

1/497

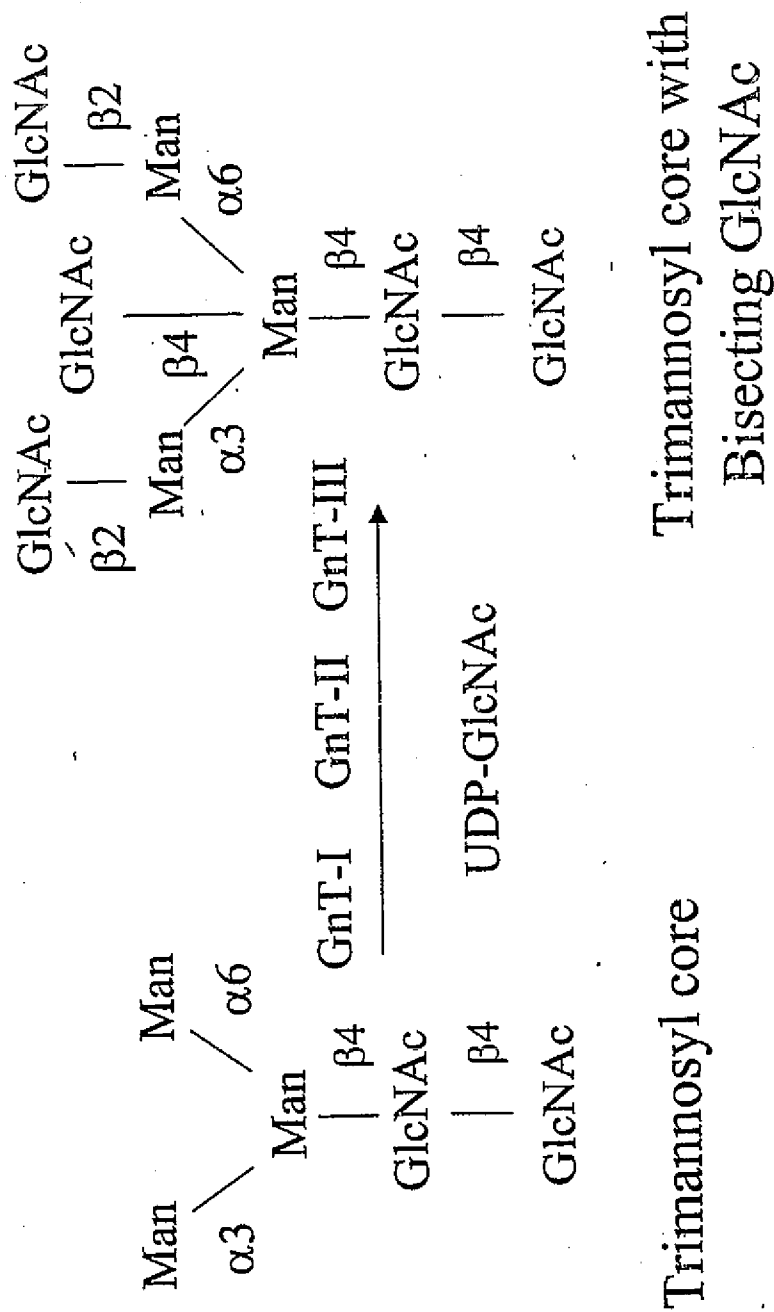


FIG. 1

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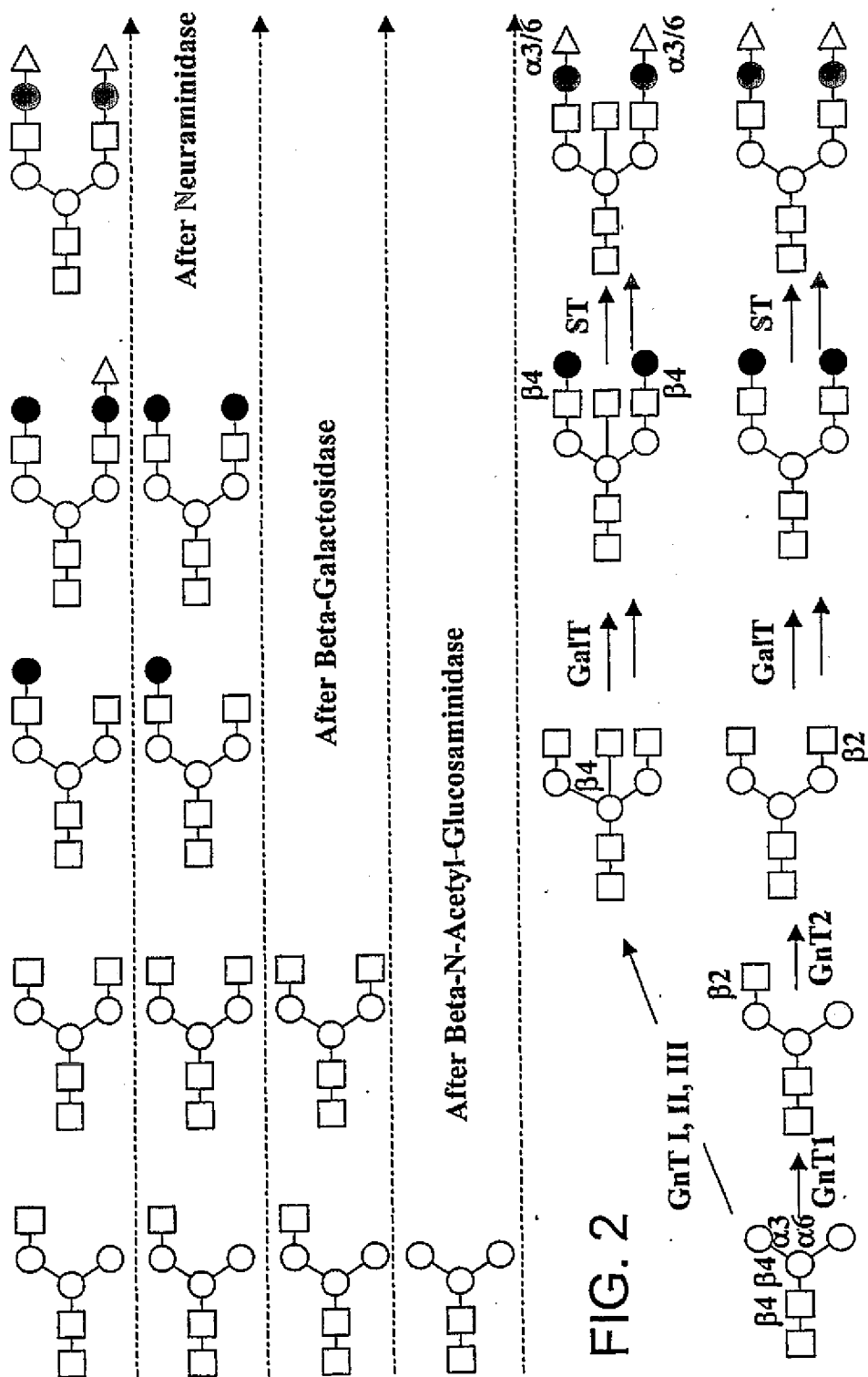


FIG. 2

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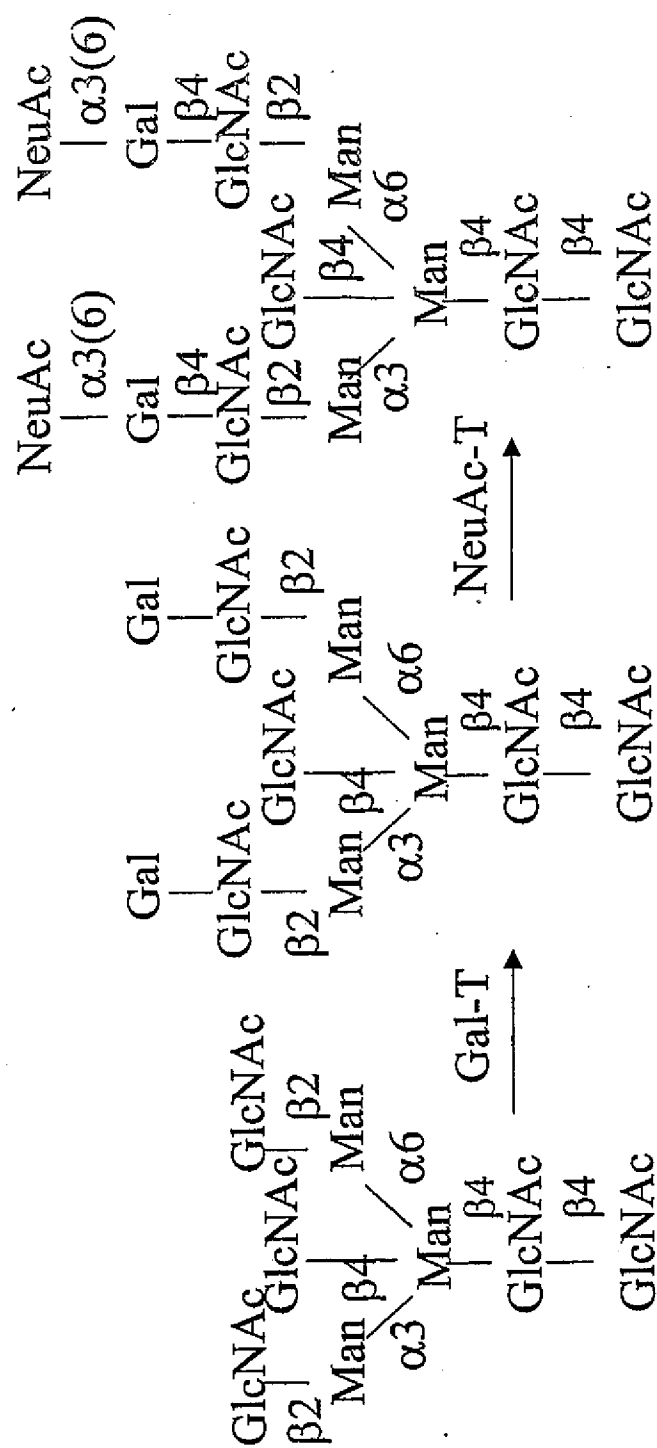


FIG. 3

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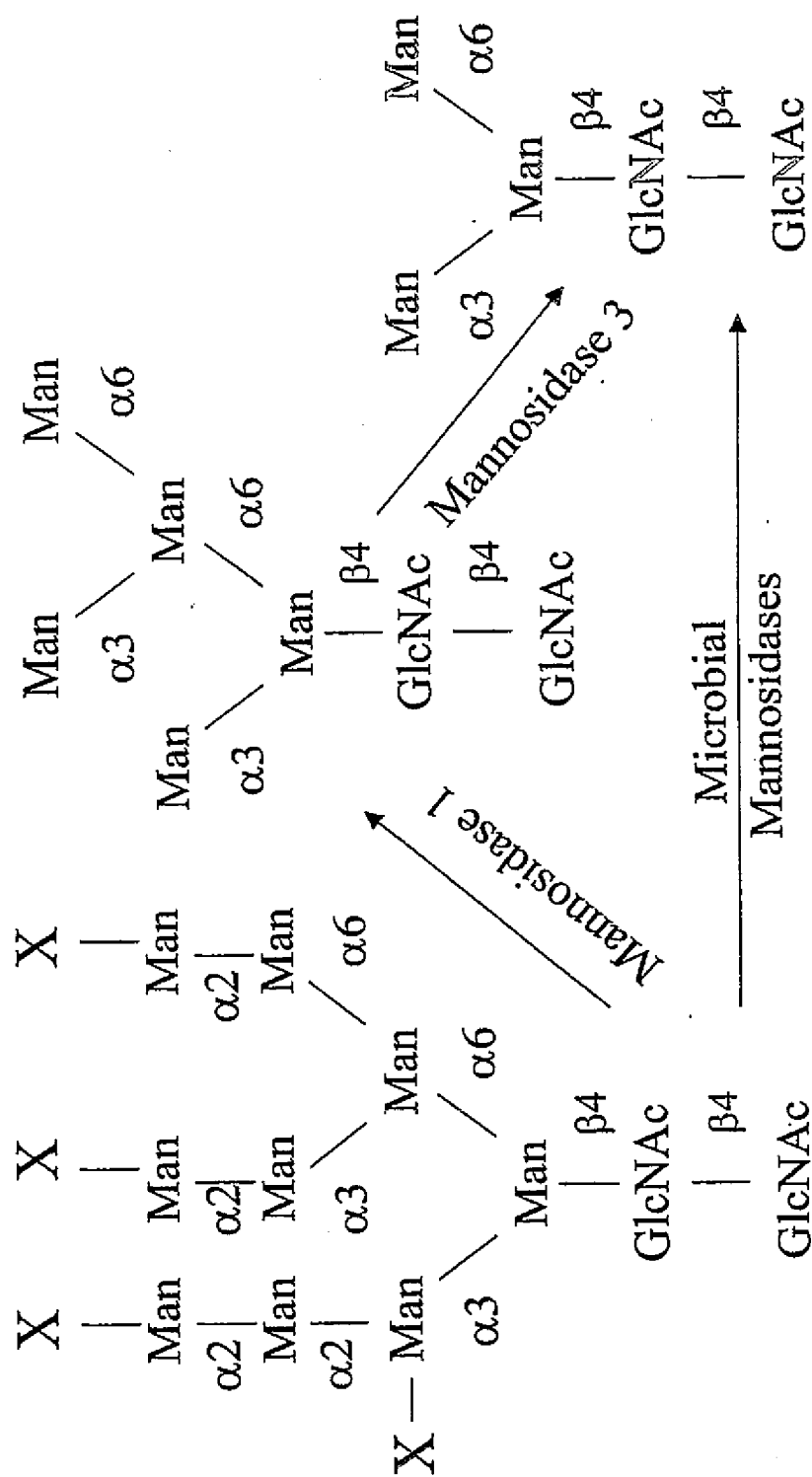


FIG. 4

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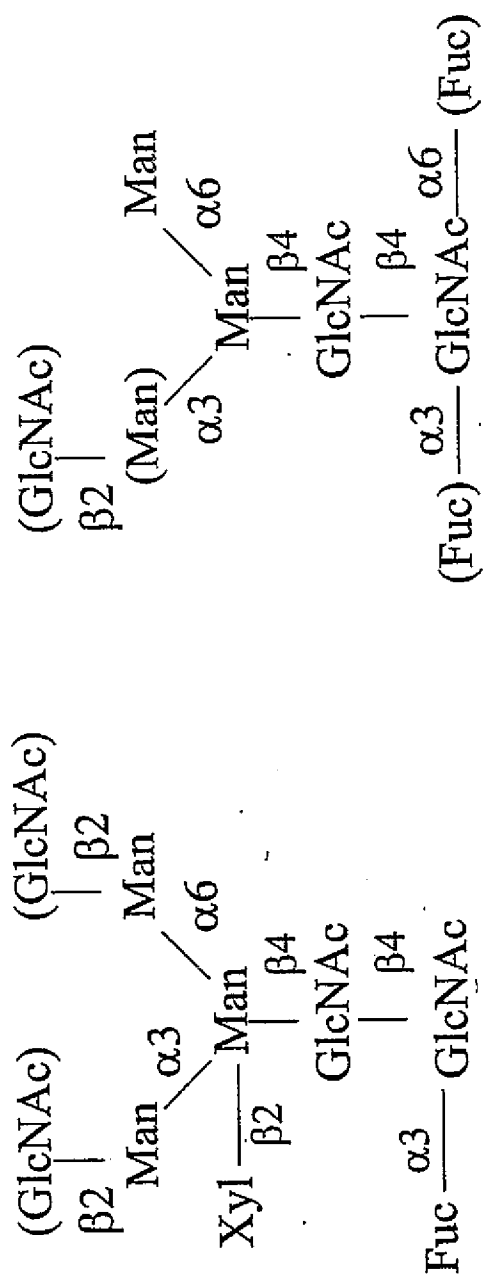


FIG. 6

FIG. 5

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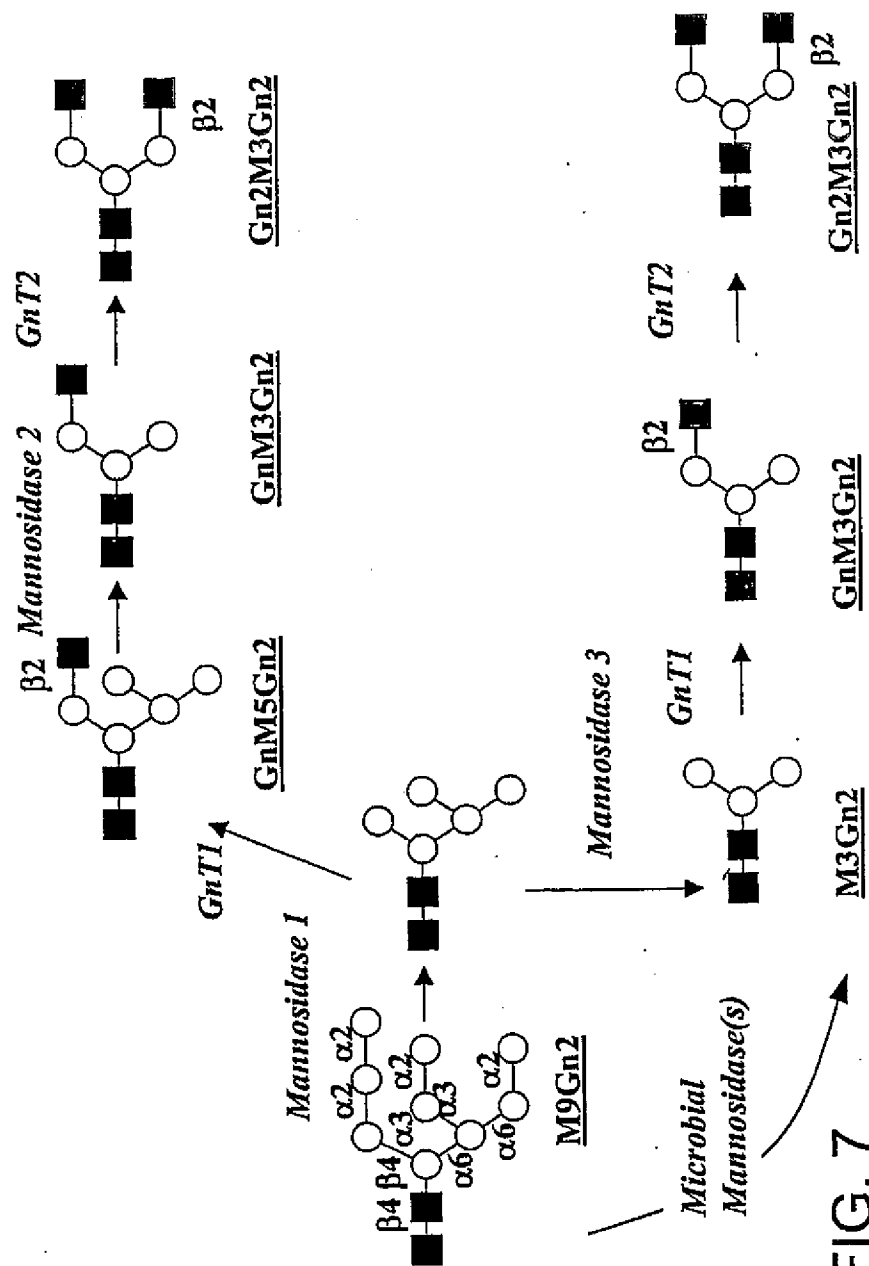


FIG. 7

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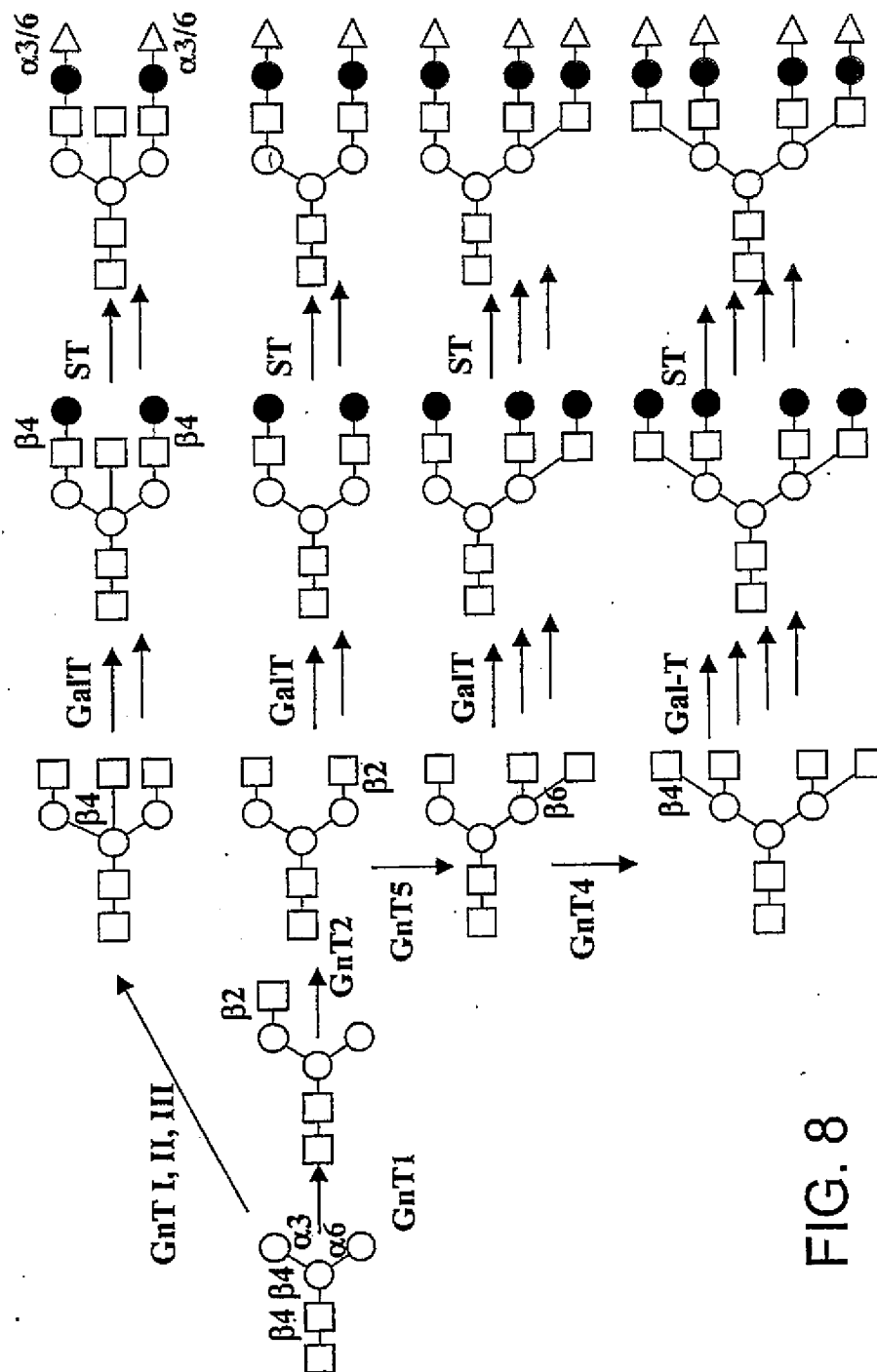


FIG. 8

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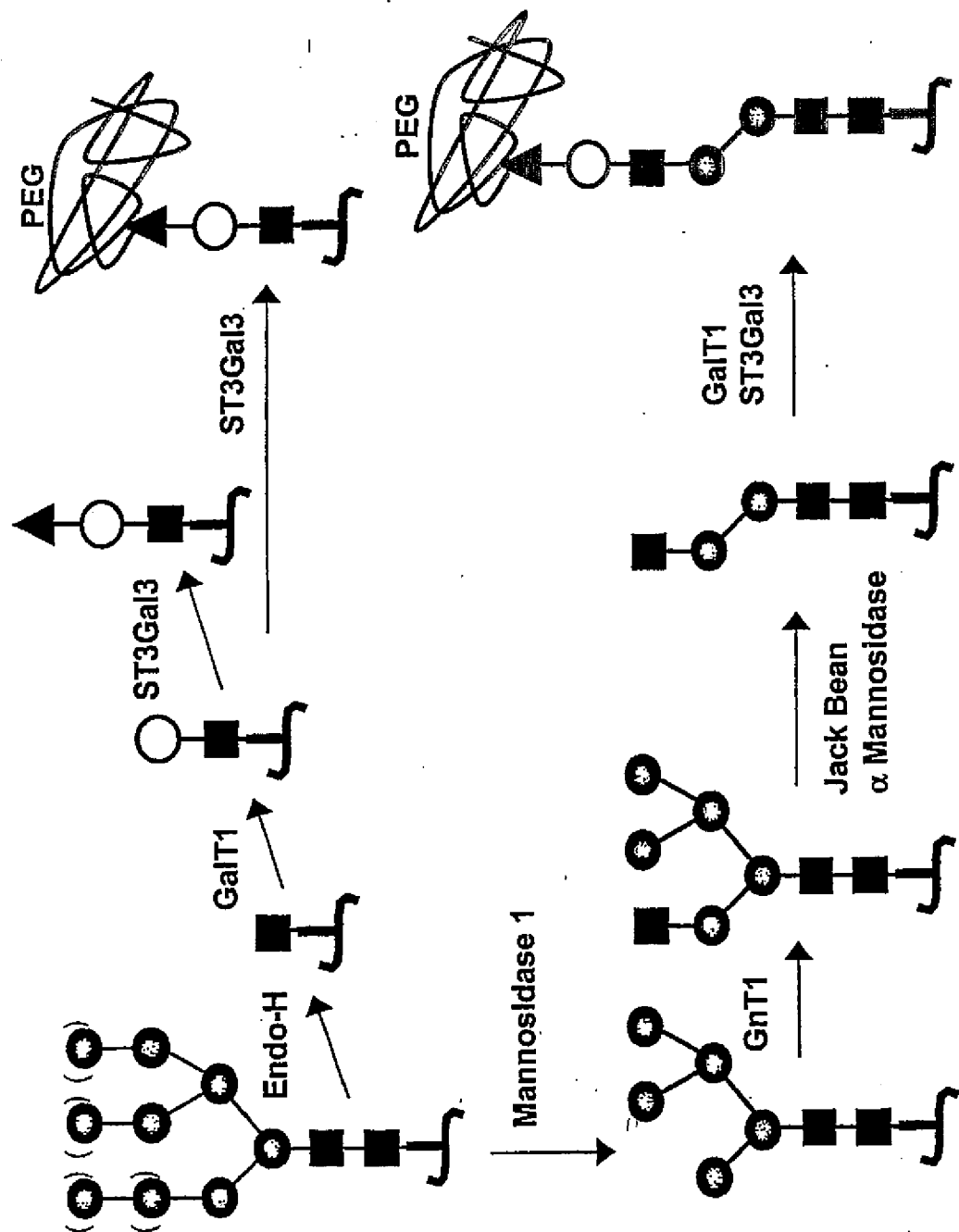
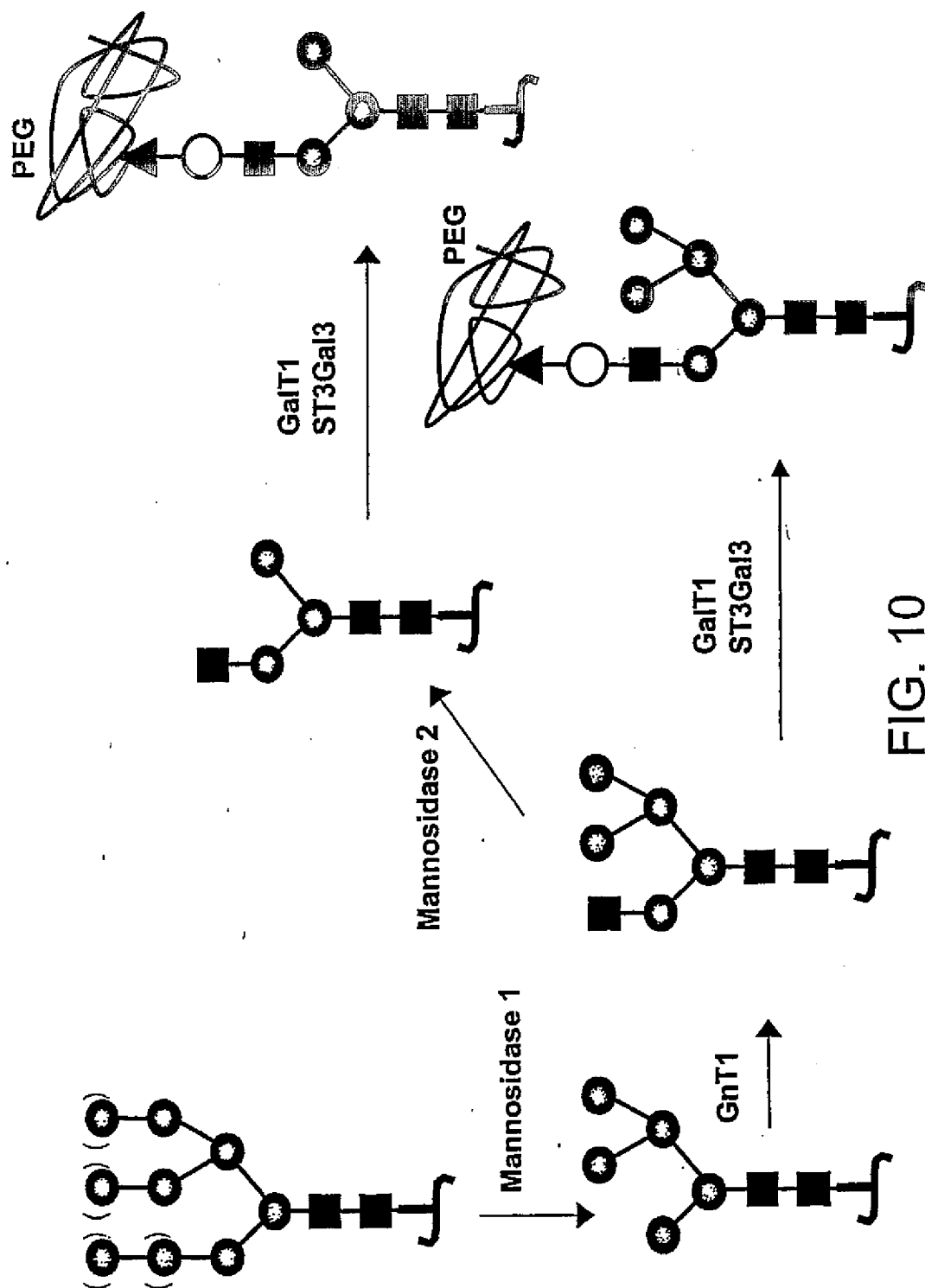


FIG. 9

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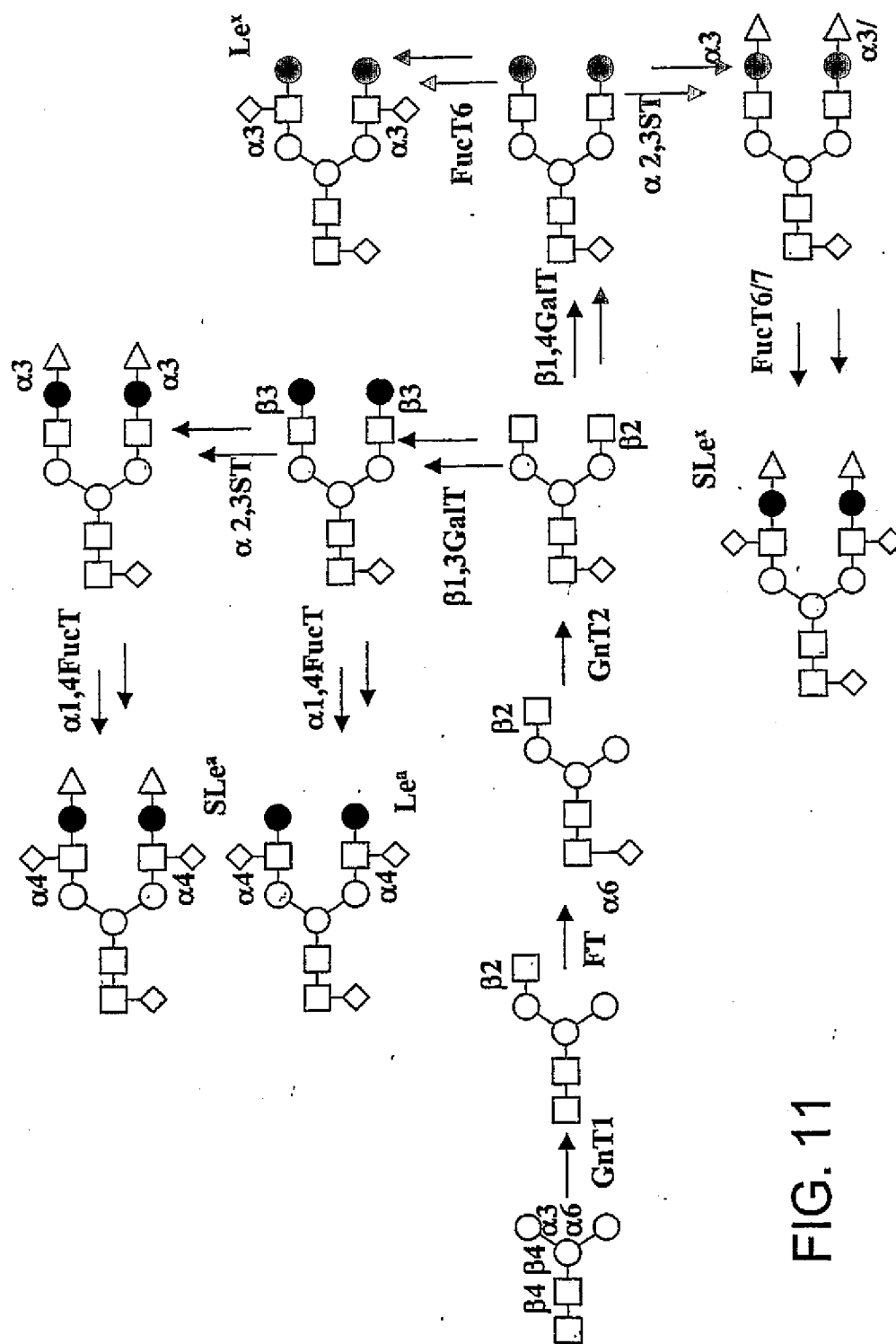


FIG. 11

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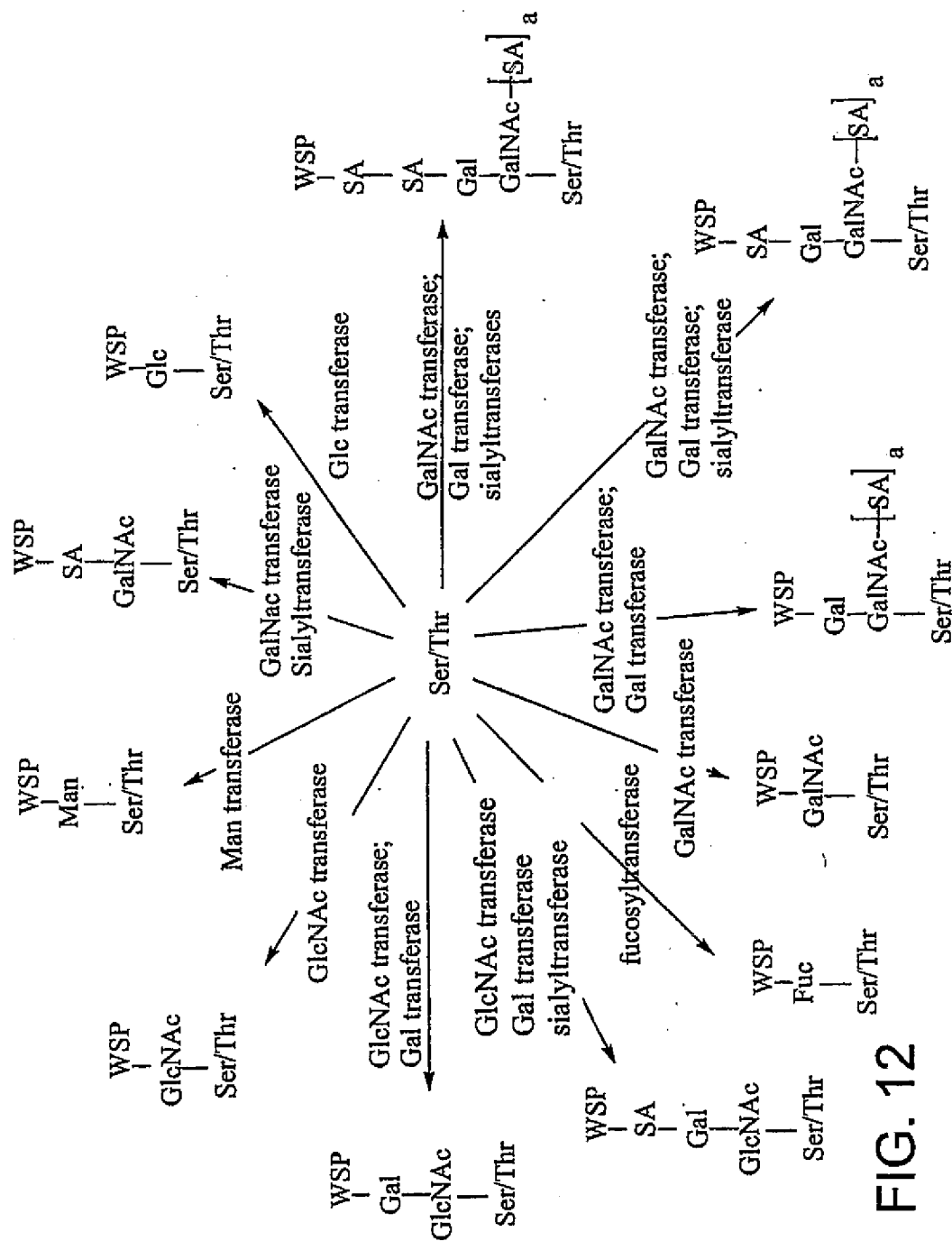


FIG. 12

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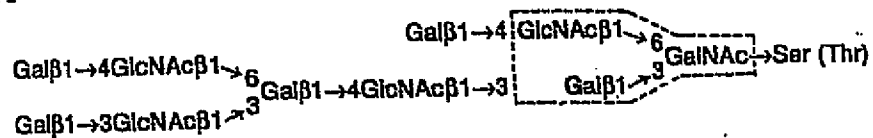
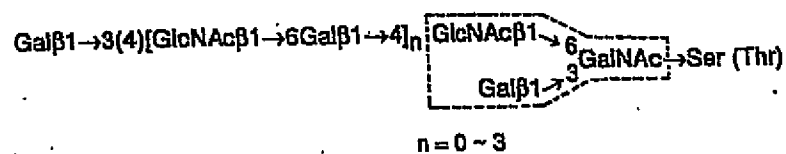
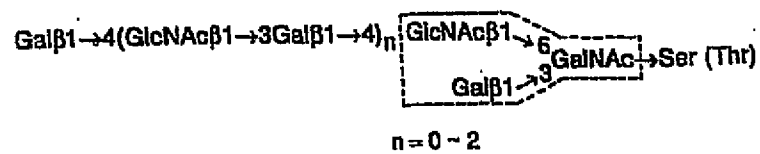
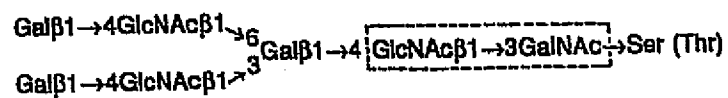
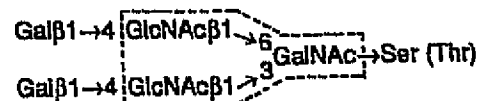
Core 1*Core 2**Core 3**Core 4*

FIG. 13

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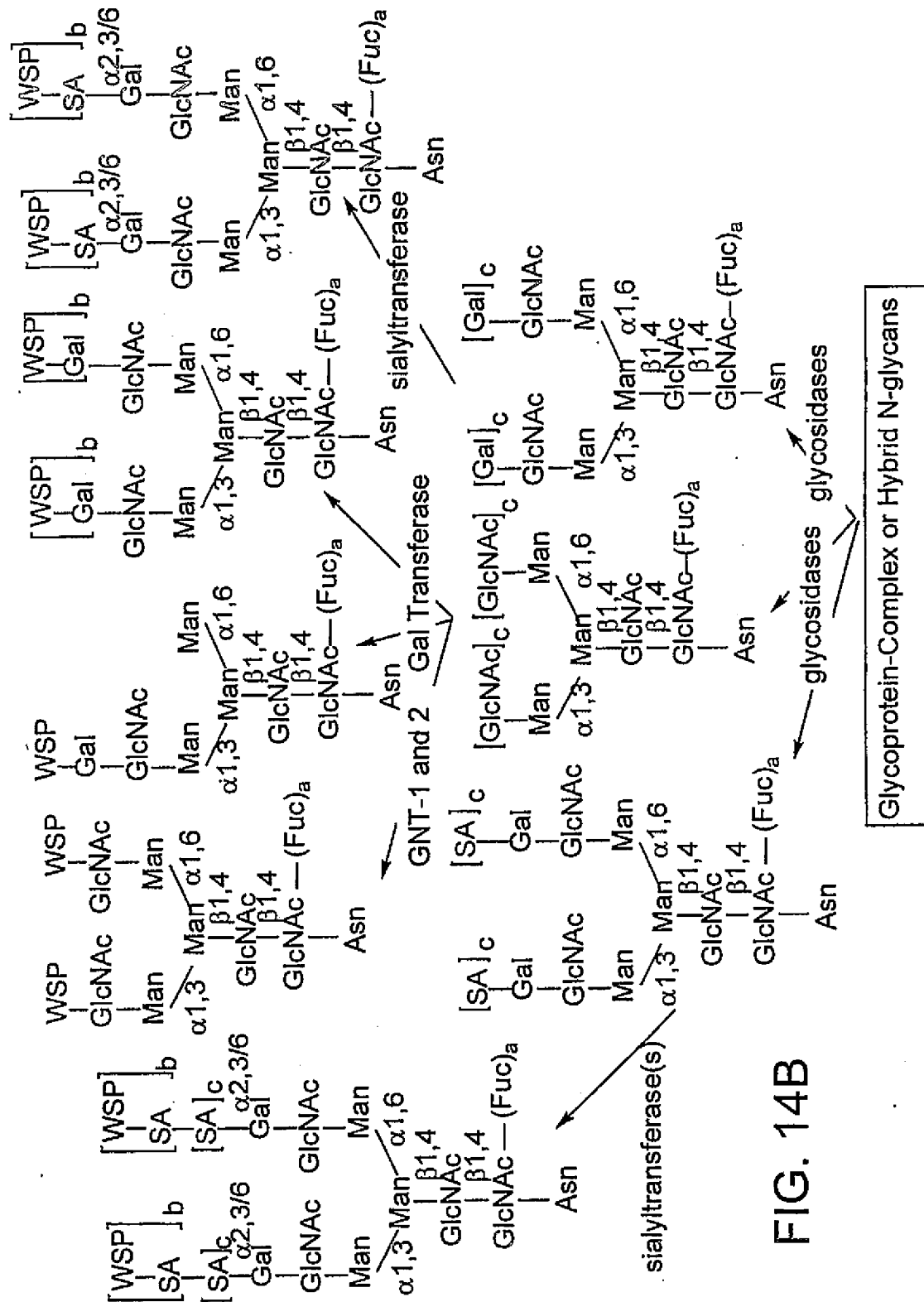


FIG. 14B

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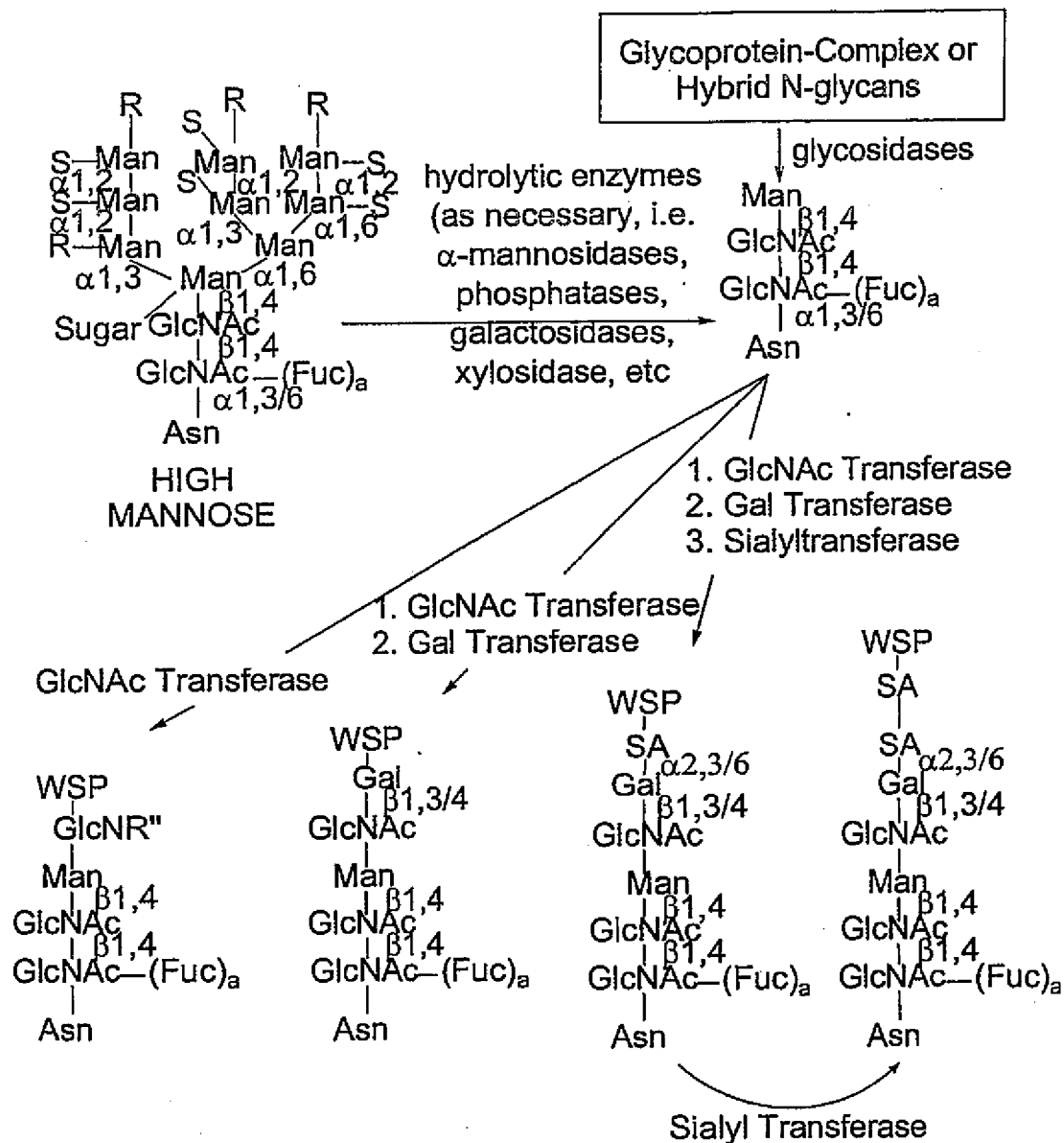


FIG. 15

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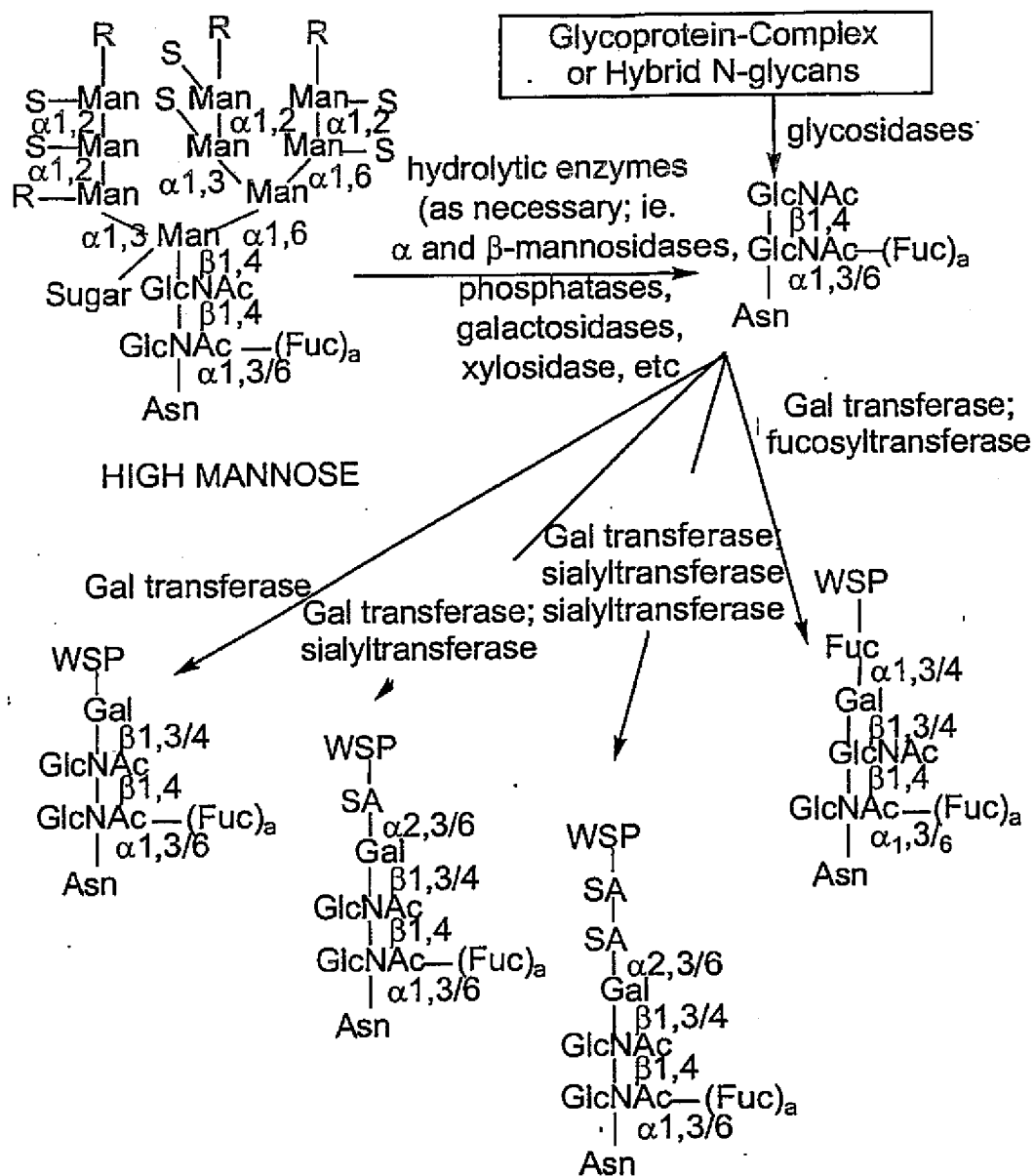


FIG. 16

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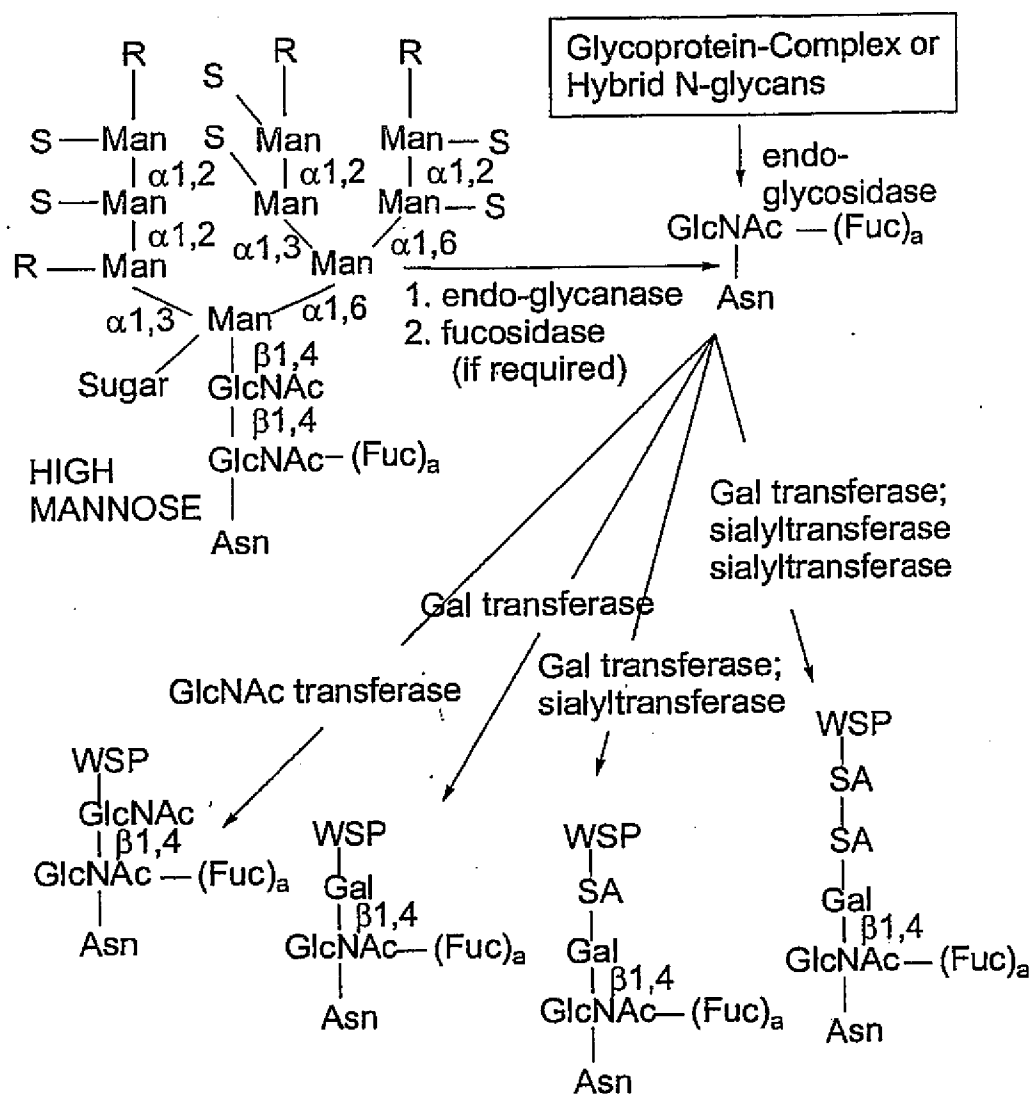
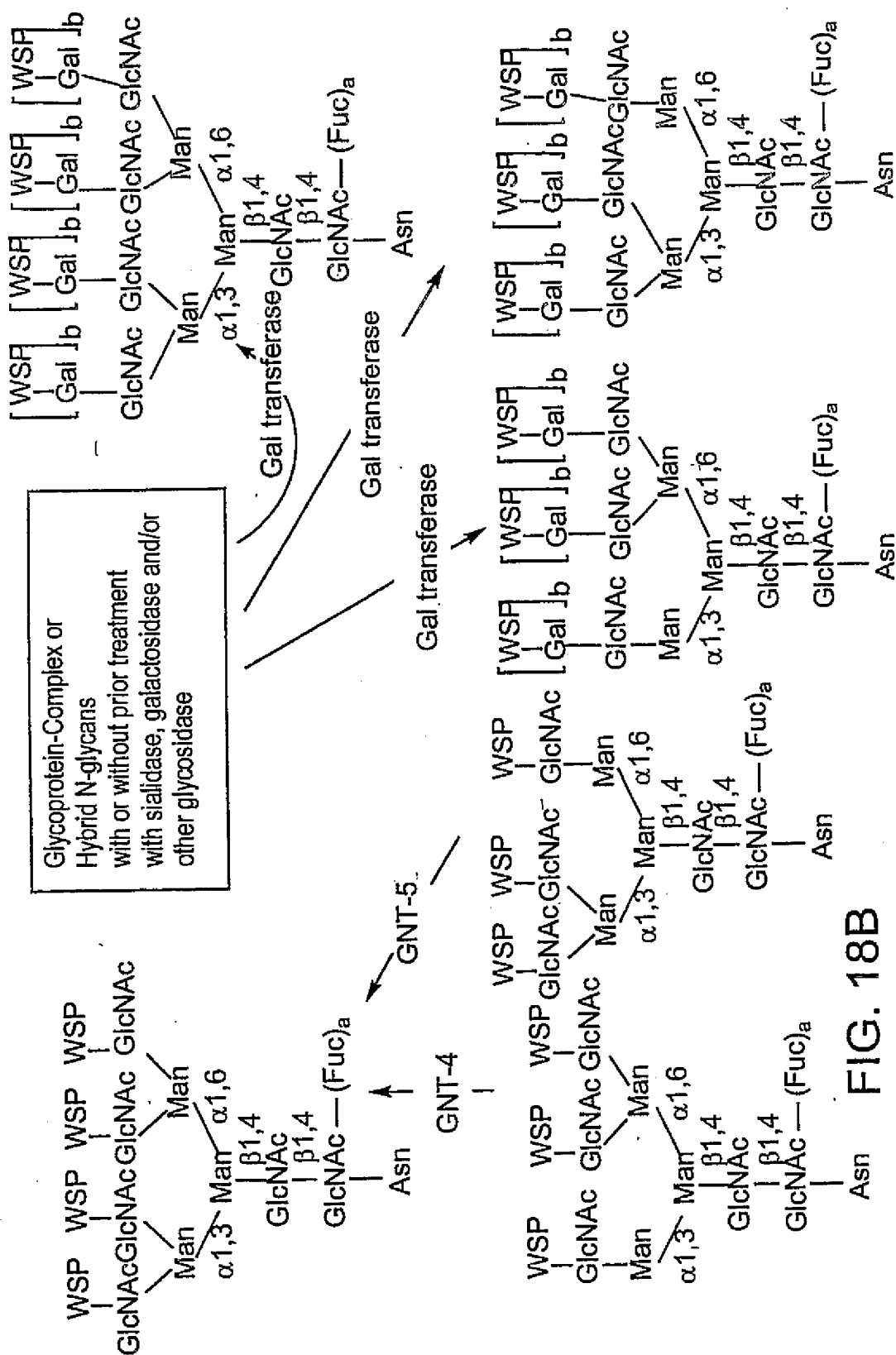


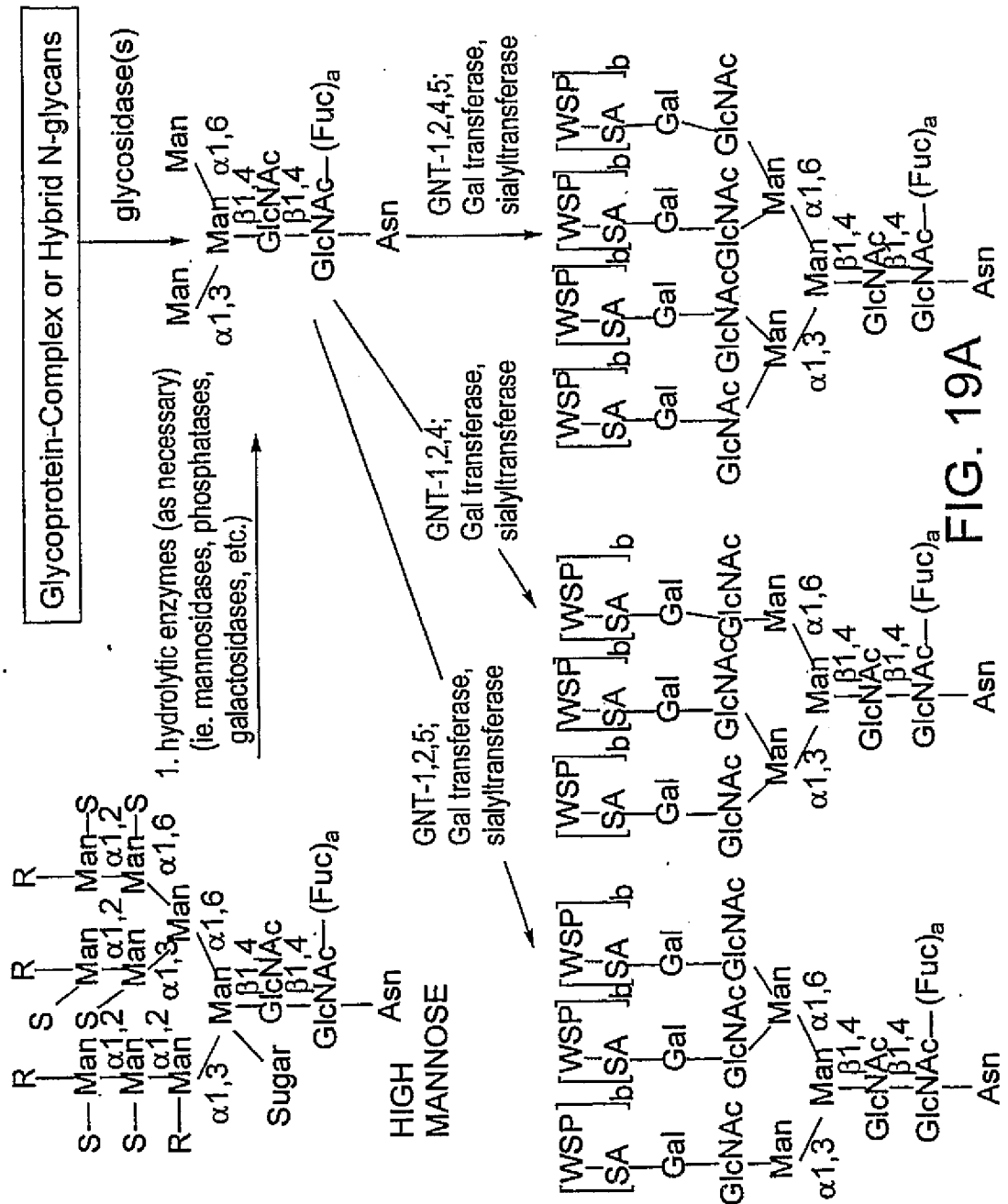
FIG. 17

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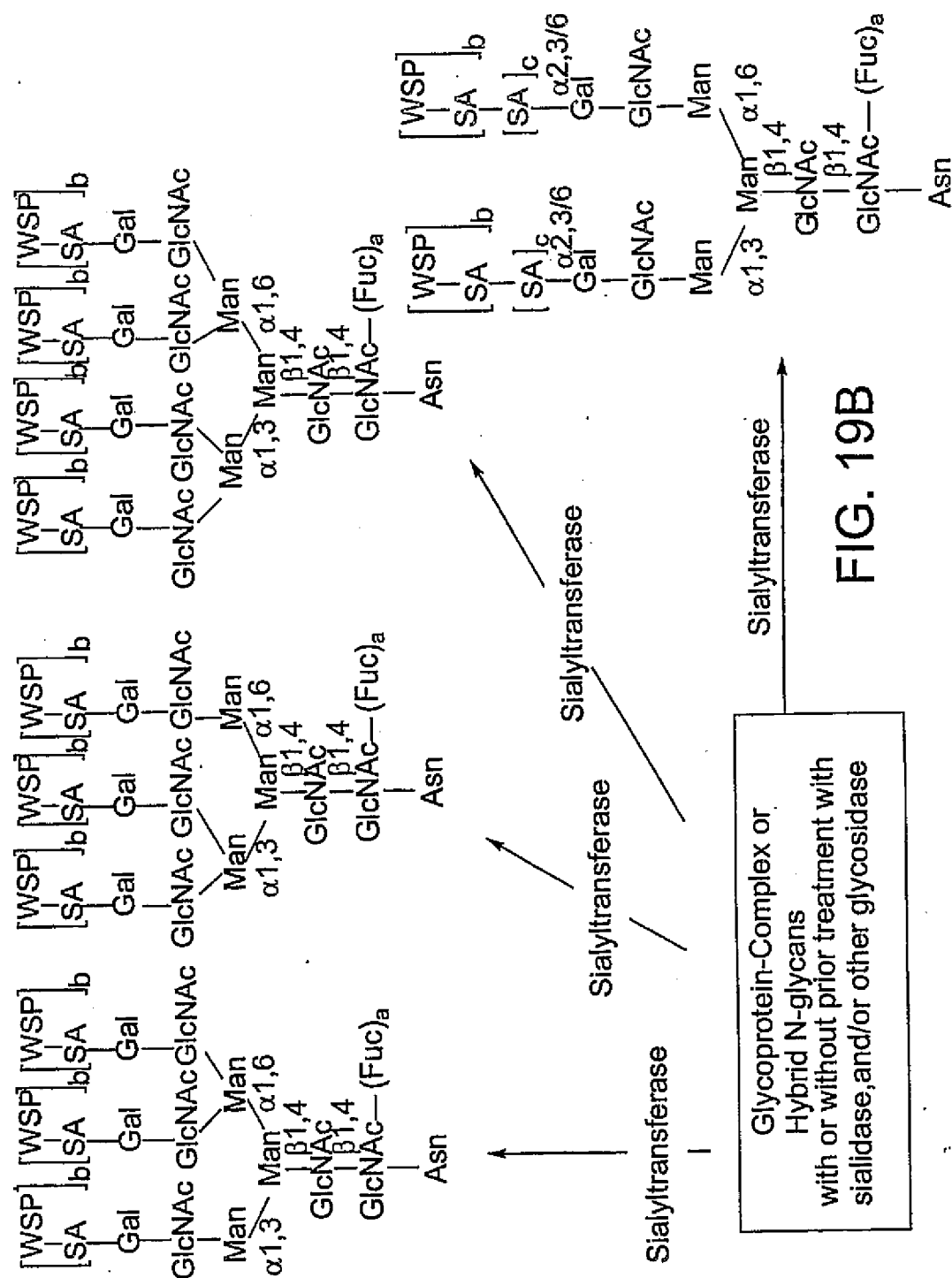


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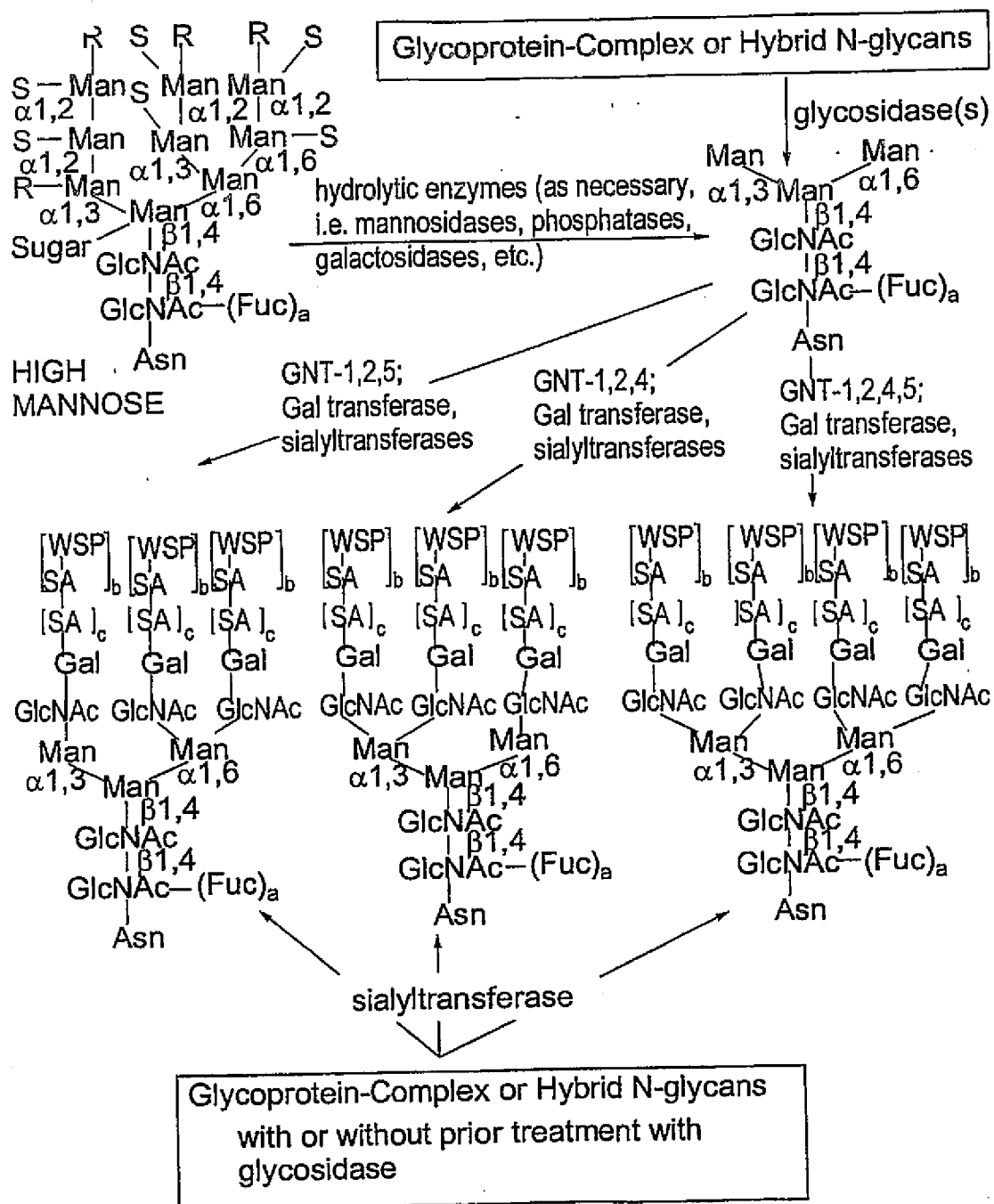


FIG. 20

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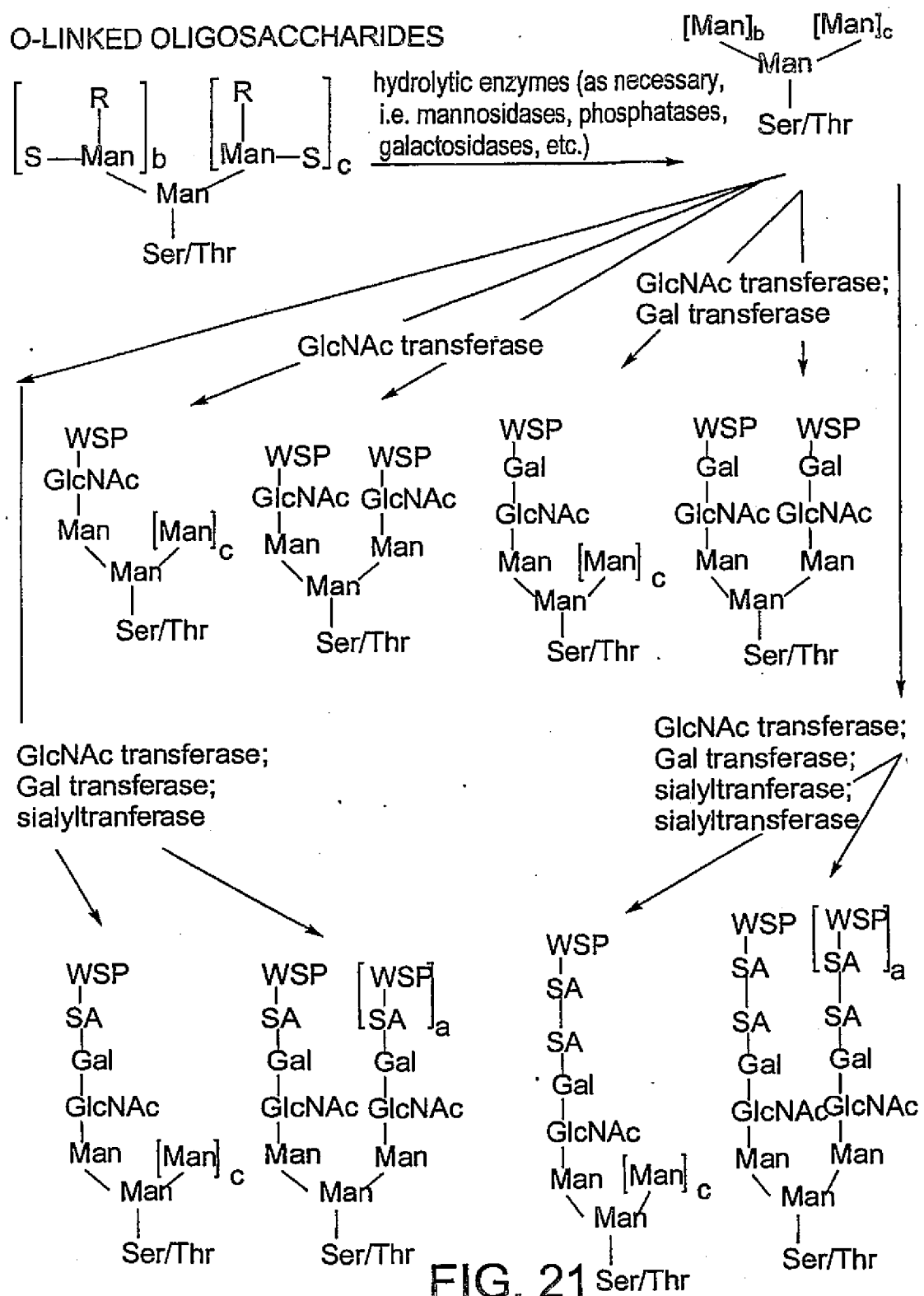
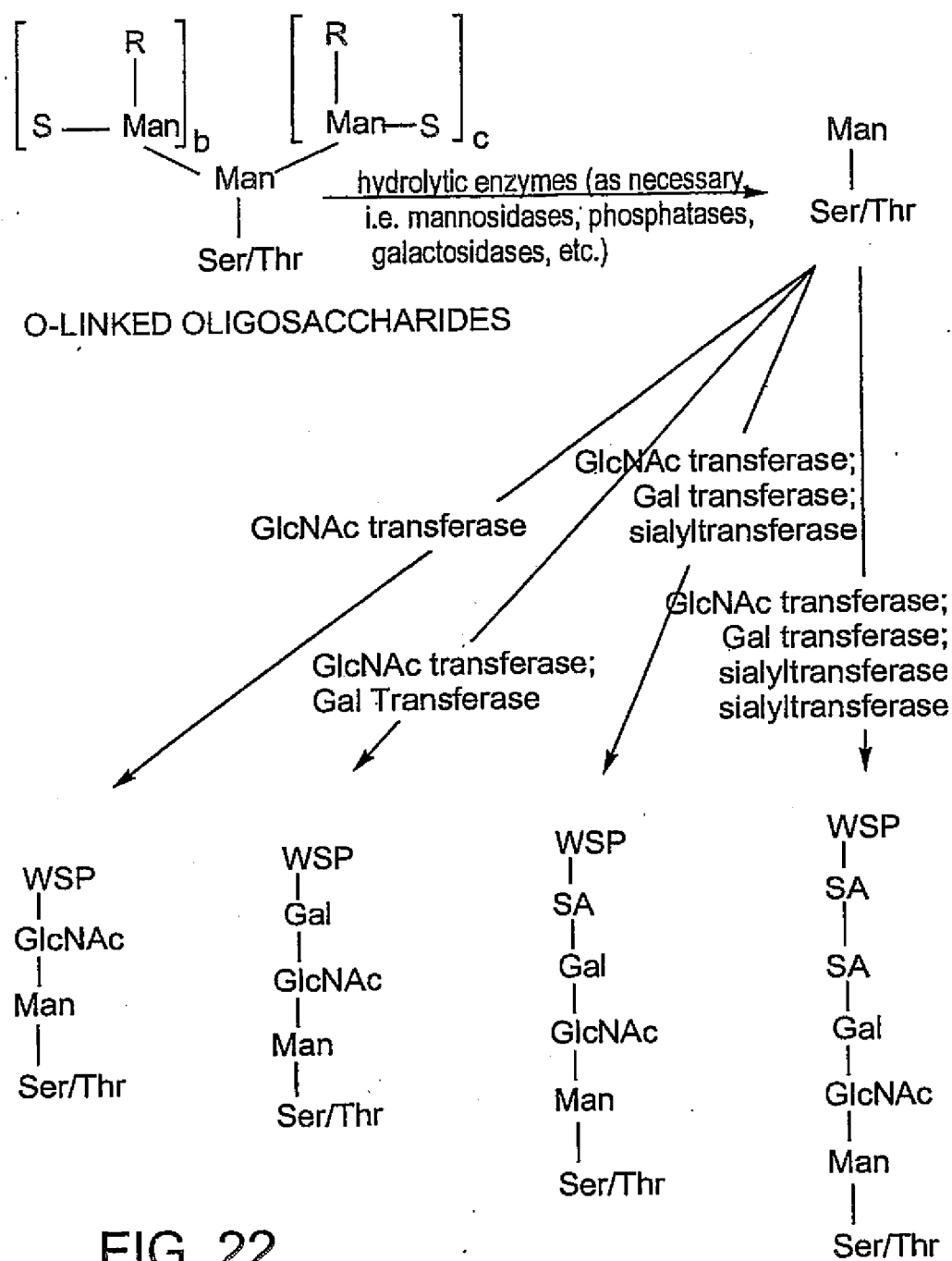


FIG. 21 Ser/Thr

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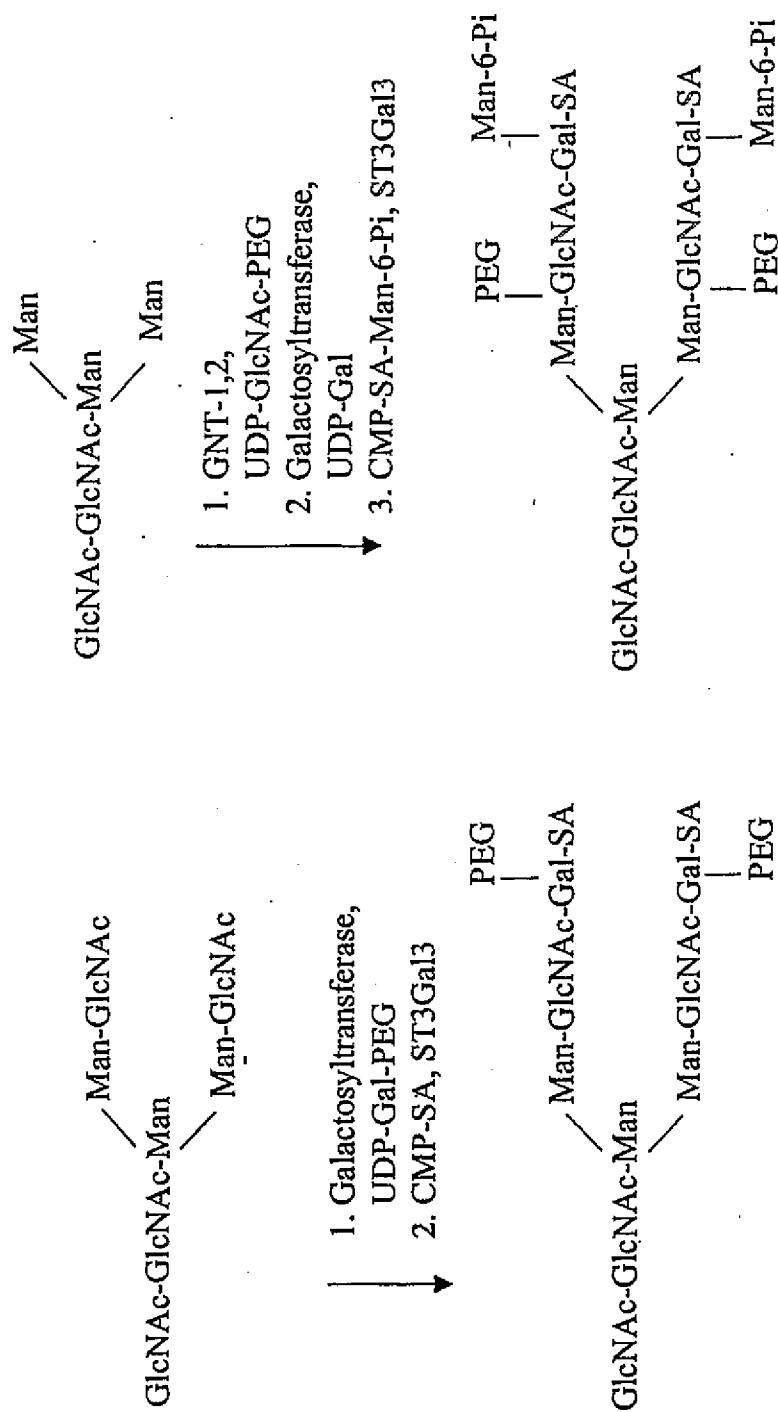


FIG. 23B

FIG. 23A

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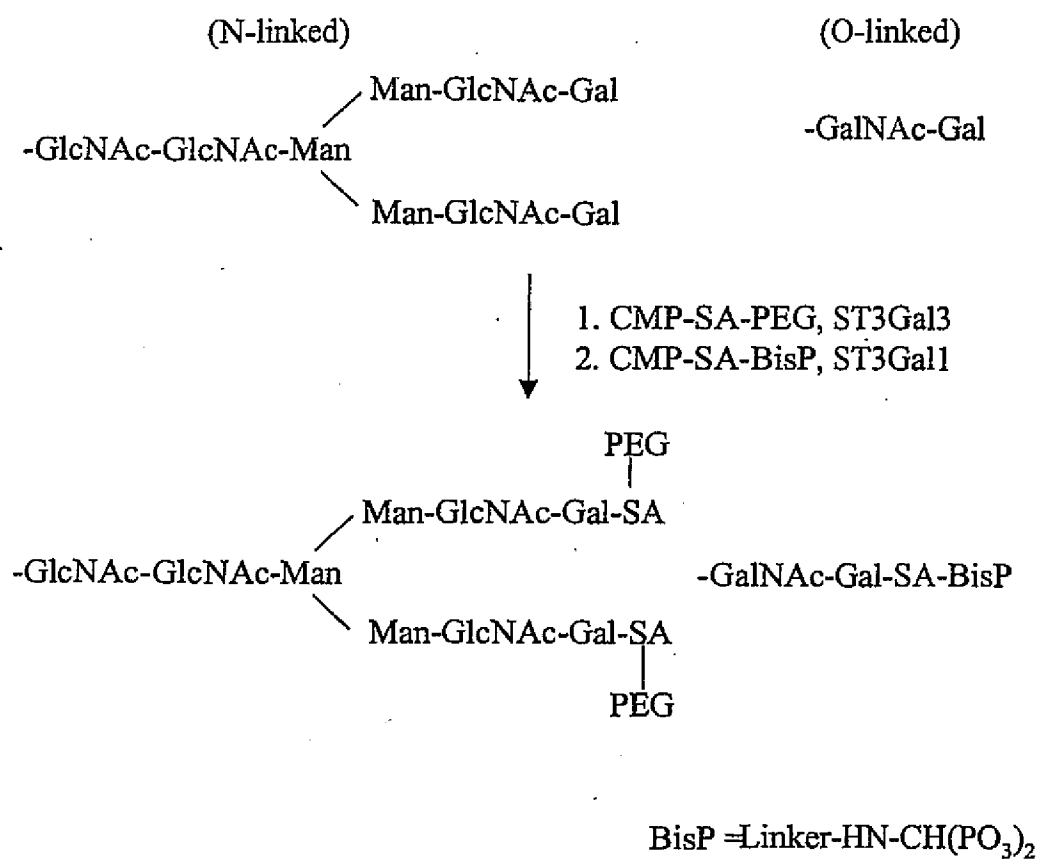


FIG. 23C

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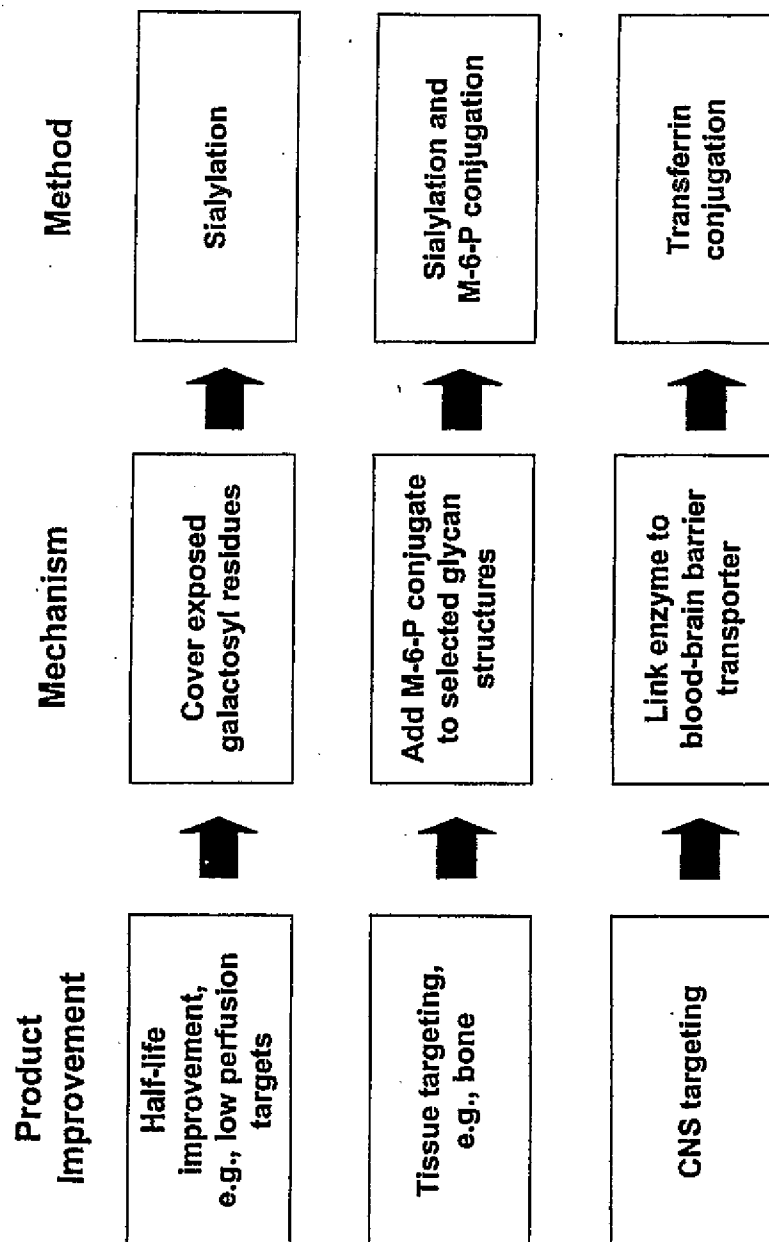


FIG. 24

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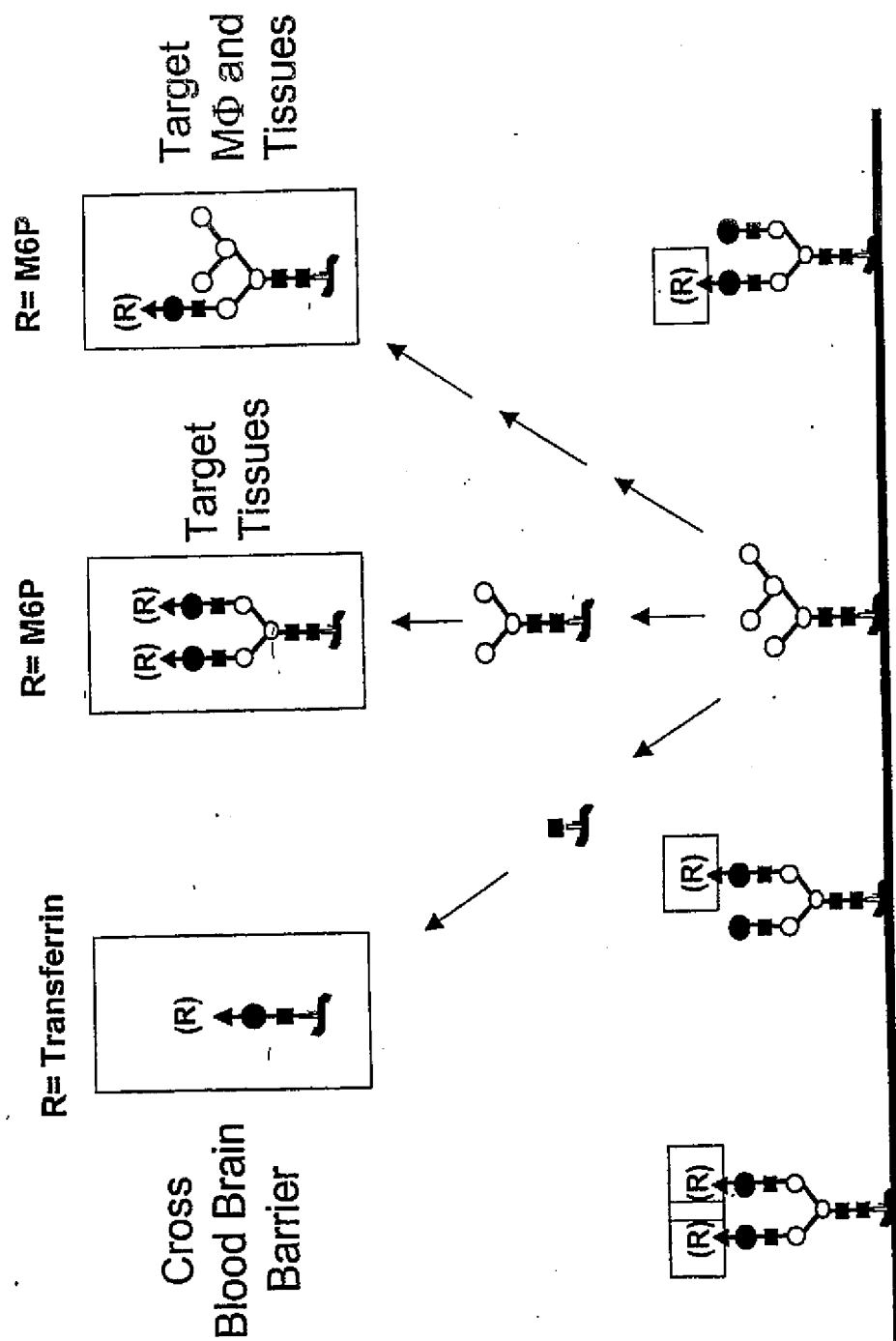


FIG. 25

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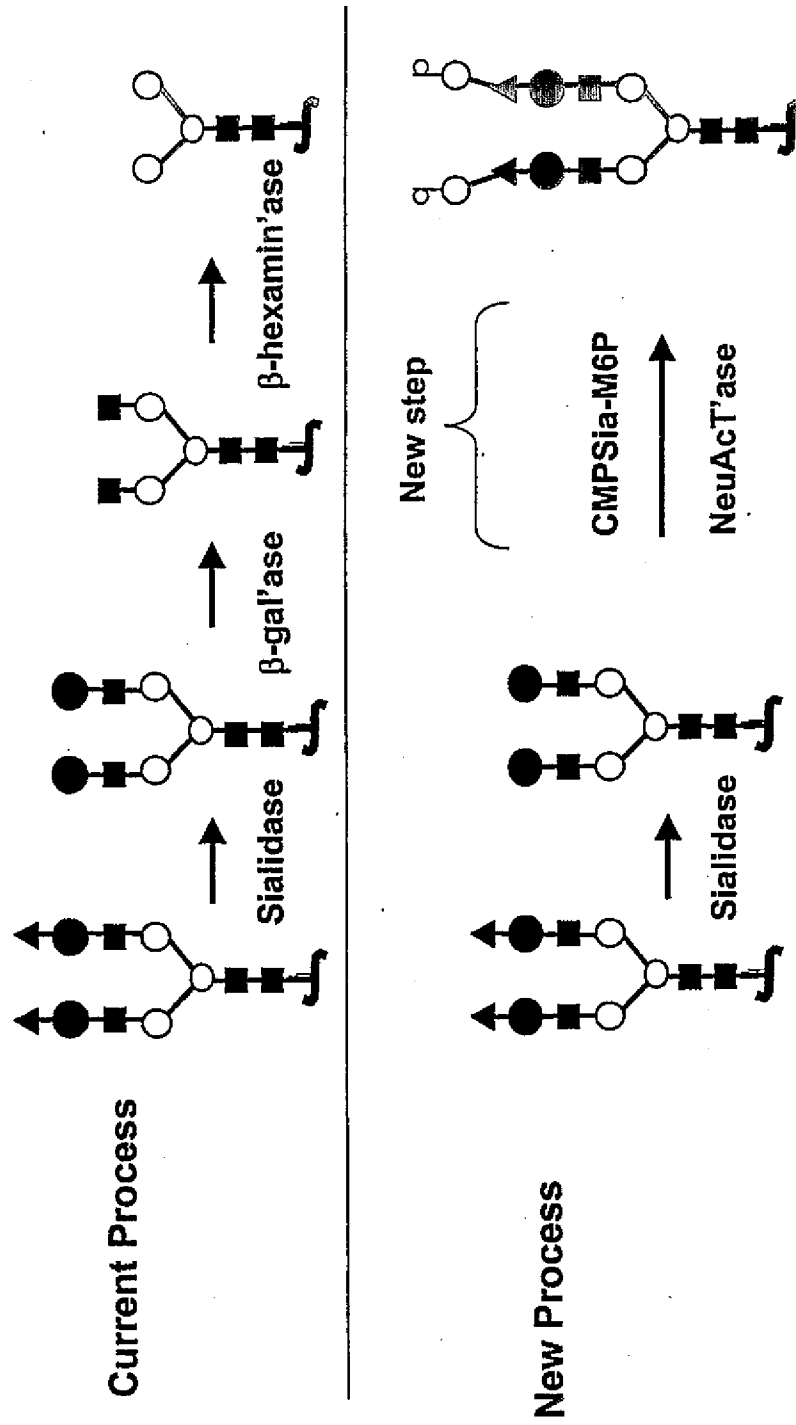


FIG. 26

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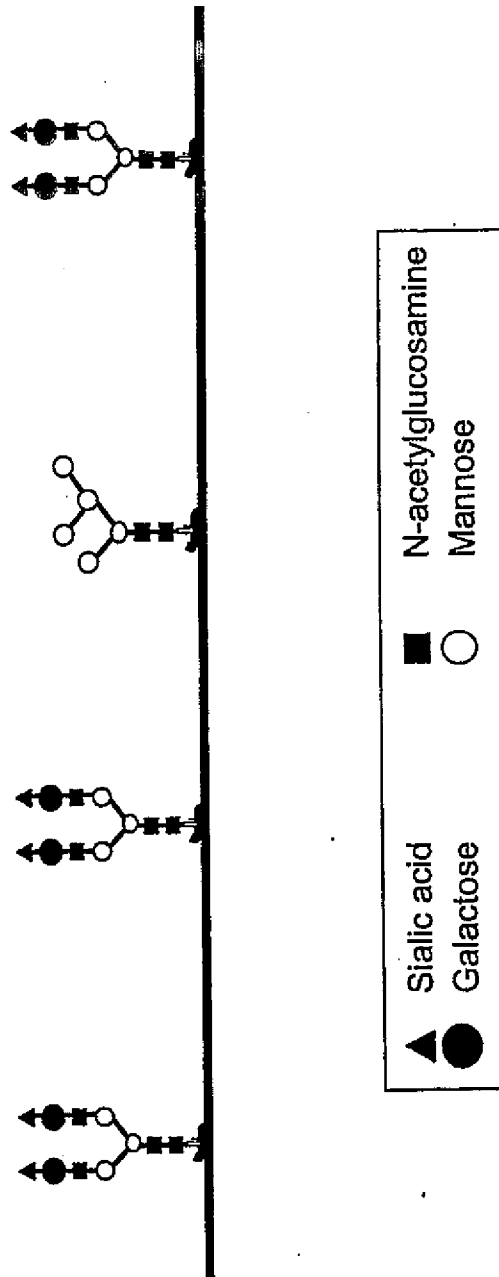


FIG. 27

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12AP1/E5 -- Viventia Biotech	AI-201 -- AutoImmune
1964 -- Aventis	AI-301 -- AutoImmune
20K growth hormone -- AMUR	AIDS vaccine -- ANRS, CIBG, Hesed
28P6/E6 -- Viventia Biotech	Biomed, Hollis-Eden, Rome, United
3-Hydroxyphthaloyl-beta-lactoglobulin --	Biomedical, American Home Products,
4-IBB ligand gene therapy --	Maxygen
64-Cu MAb conjugate TETA-1A3 --	airway receptor ligand -- IC Innovations
Mallinckrodt Institute of Radiology	AJvW 2 -- Ajinomoto
64-Cu MAb conjugate TETA-cT84.66	AK 30 NGF -- Alkermes
64-Cu Trastuzumab TETA conjugate --	Albuferon -- Human Genome Sciences
Genentech	albumin -- Biogen, DSM Anti-Infectives,
A 200 -- Amgen	Genzyme Transgenics, PPL Therapeutics,
A10255 -- Eli Lilly	TranXenoGen, Welfide Corp.
A1PDX -- Hedral Therapeutics	aldesleukin -- Chiron
A6 -- Angstrom	alefacept -- Biogen
aaAT-III -- Genzyme	Alemtuzumab
Abciximab -- Centocor	Allergy therapy -- ALK-Abello/Maxygen,
ABI.001 -- Atlantic BioPharmaceuticals	ALK-Abello/RP Scherer
ABT-828 -- Abbott	allergy vaccines -- Allergy Therapeutics
Accutin	Alnidofibatide -- Aventis Pasteur
Actinohivin	Alnorine -- SRC VB VECTOR
activin -- Biotech Australia, Human	ALP 242 -- Gruenenthal
Therapeutics, Curis	Alpha antitrypsin -- Arriva/Hyland
AD 439 -- Tanox	Immuno/ProMetic/Protease Sciences
AD 519 -- Tanox	Alpha-1 antitrypsin -- Cutter, Bayer, PPL
Adalimumab -- Cambridge Antibody Tech.	Therapeutics, Profile, ZymoGenetics,
Adenocarcinoma vaccine -- Biomira -- NIS	Arriva
Adenosine deaminase -- Enzond	Alpha-1 protease inhibitor -- Genzyme
Adenosine A2B receptor antagonists --	Transgenics, Welfide Corp.
Adenosine Therapeutics	Alpha-galactose fusion protein --
ADP-001 -- Axis Genetics	Immunomedics
AF 13948 -- Affymax	Alpha-galactosidase A -- Research
Afelimomab -- Knoll	Corporation Technologies, Genzyme
AFP-SCAN -- Immunomedics	Alpha-glucosidase -- Genzyme, Novazyme
AG 2195 -- Corixa	Alpha-lactalbumin
agalsidase alfa -- Transkaryotic Therapies	Alpha-L-iduronidase -- Transkaryotic
agalsidase beta -- Genzyme	Therapies, BioMarin
AGENT-- Antisoma	alteplase -- Genentech
AI 300 -- AutoImmune	alvircept sudotox -- NIH
AI-101 -- Teva	ALX1-11 --sNPS Pharmaceuticals
AI-102 -- Teva	Alzheimer's disease gene therapy

FIG. 28A

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AM-133 -- AMRAD	Anti-angiogenesis monoclonal antibodies --
Amb a 1 immunostim conj. -- Dynavax	KS Biomedix/Schering AG
AMD 3100 -- AnorMED -- NIS	Anti-B4 MAb-DC1 conjugate -- ImmunoGen
AMD 3465 -- AnorMED -- NIS	Anti-B7 antibody PRIMATIZED -- IDEC
AMD 3465 -- AnorMED -- NIS	Anti-B7-1 MAb 16-10A1
AMD Fab -- Genentech	Anti-B7-1 MAb 1G10
Amediplase -- Menarini, Novartis	Anti-B7-2 MAb GL-1
AM-F9	Anti-B7-2-gelonin immunotoxin --
Amoebiasis vaccine	Antibacterials/antifungals --
Amphiregulin -- Octagene	Diversa/IntraBiotics
anakinra -- Amgen	Anti-beta-amyloid monoclonal antibodies --
analgesic -- Nobex	Cambridge Antibody Tech., Wyeth-Ayerst
ancestim -- Amgen	Anti-BLyS antibodies -- Cambridge
AnergiX.RA -- Corixa, Organon	Antibody Tech. /Human Genome Sciences
Angiocidin -- InKine	Antibody-drug conjugates -- Seattle
angiogenesis inhibitors -- ILEX	Genetics/Eos
AngioMab -- Antisoma	Anti-C5 MAb BB5-1 -- Alexion
Angiopoietins -- Regeneron/Procter &	Anti-C5 MAb N19-8 -- Alexion
Gamble	Anti-C8 MAb
angiostatin -- EntreMed	anticancer cytokines -- BioPulse
Angiostatin/endostatin gene therapy --	anticancer matrix -- Telios Integra
Genetix Pharmaceuticals	Anticancer monoclonal antibodies -- ARIUS,
angiotensin-II, topical -- Maret	Immunex
Anthrax -- EluSys Therapeutics/US Army	anticancer peptides -- Maxygen, Micrologix
Medical Research Institute	Anticancer prodrug Tech. -- Alexion
Anthrax vaccine	Antibody Technologies
Anti platelet-derived growth factor D human	anticancer Troy-Bodies -- Affite -- Affitech
monoclonal antibodies -- CuraGen	anticancer vaccine -- NIH
Anti-17-1A MAb 3622W94 --	anticancers -- Epimmune
GlaxoSmithKline	Anti-CCR5/CXCR4 sheep MAb -- KS
Anti-2C4 MAb -- Genentech	Biomedix Holdings
anti-4-1BB monoclonal antibodies -- Bristol-	Anti-CD11a MAb KBA --
Myers Squibb	Anti-CD11a MAb M17
Anti-Adhesion Platform Tech. -- Cytovax	Anti-CD11a MAb TA-3 --
Anti-adipocyte MAb -- Cambridge Antibody	Anti-CD11a MAb WT.1 --
Tech./ObeSys	Anti-CD11b MAb -- Pharmacia
antiallergics -- Maxygen	Anti-CD11b MAb LM2
antiallergy vaccine -- Acambis	Anti-CD154 MAb -- Biogen
Anti-alpha-4-integrin MAb	Anti-CD16-anti-CD30 MAb -- Biotest
Anti-alpha-vb3 integrin MAb -- Applied	Anti-CD18 MAb -- Pharmacia
Molecular Evolution	Anti-CD19 MAb B43 --

FIG. 28B

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Anti-CD19 MAb -liposomal sodium butyrate conjugate –	Anti-CD4 MAb 4162W94 – GlaxoSmithKline
Anti-CD147	Anti-CD4 MAb B-F5 – Diaclone
Anti-CD19 MAb-saporin conjugate –	Anti-CD4 MAb GK1-5
Anti-CD19-dsFv-PE38-immunotoxin –	Anti-CD4 MAb KT6
Anti-CD2 MAb 12-15 –	Anti-CD4 MAb OX38
Anti-CD2 MAb B-E2 – Diaclone	Anti-CD4 MAb PAP conjugate -- Bristol-Myers Squibb
Anti-CD2 MAb OX34 –	Anti-CD4 MAb RIB 5-2
Anti-CD2 MAb OX54 –	Anti-CD4 MAb W3/25
Anti-CD2 MAb OX55 –	Anti-CD4 MAb YTA 3.1.2
Anti-CD2 MAb RM2-1	Anti-CD4 MAb YTS 177-9
Anti-CD2 MAb RM2-2	Anti-CD40 ligand MAb 5c8 -- Biogen
Anti-CD2 MAb RM2-4	Anti-CD40 MAb
Anti-CD20 MAb BCA B20	Anti-CD40 MAb 5D12 – Tanox
Anti-CD20-anti-Fc alpha RI bispecific MAb – Medarex, Tenovus	Anti-CD44 MAb A3D8
Anti-CD22 MAb-saporin-6 complex –	Anti-CD44 MAb GKWA3
Anti-CD3 immunotoxin –	Anti-CD44 MAb IM7
Anti-CD3 MAb 145-2C11 – Pharming	Anti-CD44 MAb KM81
Anti-CD3 MAb CD4IgG conjugate -- Genentech	Anti-CD44 variant monoclonal antibodies -- Corixa/Hebrew University
Anti-CD3 MAb humanised – Protein Design, RW Johnson	Anti-CD45 MAb BC8-I-131
Anti-CD3 MAb WT32	Anti-CD45RB MAb
Anti-CD3 MAb-ricin-chain-A conjugate –	Anti-CD48 MAb HuLy-m3
Anti-CD3 MAb-xanthine-oxidase conjugate –	Anti-CD48 MAb WM-63
Anti-CD30 MAb BerH2 -- Medac	Anti-CD5 MAb – Becton Dickinson
Anti-CD30 MAb-saporin conjugate	Anti-CD5 MAb OX19
Anti-CD30-scFv-ETA'-immunotoxin	Anti-CD6 MAb
Anti-CD38 MAb AT13/5	Anti-CD7 MAb-PAP conjugate
Anti-CD38 MAb-saporin conjugate	Anti-CD7 MAb-ricin-chain-A conjugate
Anti-CD3-anti-CD19 bispecific MAb	Anti-CD8 MAb – Amerimmune, Cytodyn, Becton Dickinson
Anti-CD3-anti-EGFR MAb	Anti-CD8 MAb 2-43
Anti-CD3-anti-interleukin-2-receptor MAb	Anti-CD8 MAb OX8
Anti-CD3-anti-MOV18 MAb – Centocor	Anti-CD80 MAb P16C10 – IDEC
Anti-CD3-anti-SCLC bispecific MAb	Anti-CD80 MAb P7C10 – ID Vaccine
Anti-CD4 idiotype vaccine	Anti-CD8-idarubicin conjugate
Anti-CD4 MAb – Centocor, IDEC Pharmaceuticals, Xenova Group	Anti-CEA MAb CE-25
Anti-CD4 MAb 16H5	Anti-CEA MAb MN 14 – Immunomedics
	Anti-CEA MAb MN14-PE40 conjugate – Immunomedics

FIG. 28C

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Anti-CEA MAb T84.66-interleukin-2 conjugate	Anti-heparanase human monoclonal antibodies -- Oxford
Anti-CEA sheep MAb -- KS Biomedix Holdings	Glycosciences/Medarex
Anti-cell surface monoclonal antibodies -- Cambridge Antibody Tech. /Pharmacia	Anti-hepatitis C virus human monoclonal antibodies -- XTL Biopharmaceuticals
Anti-c-erbB2-anti-CD3 bifunctional MAb -- Otsuka	Anti-HER-2 antibody gene therapy
Anti-CMV MAb -- Scotgen	Anti-herpes antibody -- Epicyte
Anti-complement	Anti-HIV antibody -- Epicyte
Anti-CTLA-4 MAb	anti-HIV catalytic antibody -- Hersed Biomed
Anti-EGFR catalytic antibody -- Hersed Biomed	anti-HIV fusion protein -- Idun
anti-EGFR immunotoxin -- IVAX	anti-HIV proteins -- Cangene
Anti-EGFR MAb -- Abgenix	Anti-HM1-24 MAb -- Chugai
Anti-EGFR MAb 528	Anti-hR3 MAb
Anti-EGFR MAb KSB 107 -- KS Biomedix	Anti-Human-Carcinoma-Antigen MAb -- Epicyte
Anti-EGFR MAb-DM1 conjugate -- ImmunoGen	Anti-ICAM-1 MAb -- Boehringer Ingelheim
Anti-EGFR MAb-LA1 --	Anti-ICAM-1 MAb 1A-29 -- Pharmacia
Anti-EGFR sheep MAb -- KS Biomedix	Anti-ICAM-1 MAb HA58
Anti-FAP MAb F19-I-131	Anti-ICAM-1 MAb YN1/1.7.4
Anti-Fas IgM MAb CH11	Anti-ICAM-3 MAb ICM3 -- ICOS
Anti-Fas MAb Jo2	Anti-idiotypic breast cancer vaccine 11D10
Anti-Fas MAb RK-8	Anti-idiotypic breast cancer vaccine ACA14C5 --
Anti-Fit-1 monoclonal antibodies -- ImClone	Anti-idiotypic cancer vaccine -- ImClone Systems/Merck KGaA ImClone, Viventia Biotech
Anti-fungal peptides -- State University of New York	Anti-idiotypic cancer vaccine 1A7 -- Titan
antifungal tripeptides -- BTG	Anti-idiotypic cancer vaccine 3H1 -- Titan
Anti-ganglioside GD2 antibody-interleukin-2 fusion protein -- Lexigen	Anti-idiotypic cancer vaccine TriAb -- Titan
Anti-GM2 MAb -- Kyowa	Anti-idiotypic Chlamydia trachomatis vaccine
Anti-GM-CSF receptor monoclonal antibodies -- AMRAD	Anti-idiotypic colorectal cancer vaccine -- Novartis
Anti-gp130 MAb -- Tosoh	Anti-idiotypic colorectal cancer vaccine -- Onyvax
Anti-HCA monoclonal antibodies -- AltaRex/Epigen	Anti-idiotypic melanoma vaccine -- IDEC Pharmaceuticals
Anti-hCG antibodies -- Abgenix/AVI BioPharma	Anti-idiotypic ovarian cancer vaccine ACA 125
	Anti-idiotypic ovarian cancer vaccine AR54 - AltaRex

FIG. 28D

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Anti-idiotypic ovarian cancer vaccine CA-125 -- AltaRex, Biomira	Anti-L-selectin monoclonal antibodies -- Protein Design Labs, Abgenix, Stanford University
Anti-IgE catalytic antibody -- Hersed Biomed	Anti-MBL monoclonal antibodies -- Alexion/Brigham and Women's Hospital
Anti-IgE MAb E26 -- Genentech	Anti-MHC monoclonal antibodies
Anti-IGF-1 MAb	Anti-MIF antibody humanised -- IDEC, Cytokine PharmaSciences
anti-inflammatory -- GeneMax	Anti-MRSA/VRSA sheep MAb -- KS Biomedix Holdings
anti-inflammatory peptide -- BTG	Anti-mu MAb -- Novartis
anti-integrin peptides -- Burnha	Anti-MUC-1 MAb
Anti-interferon-alpha-receptor MAb 64G12 -- Pharma Pacific Management	Anti-MUC 18
Anti-interferon-gamma MAb -- Protein Design Labs	Anti-Nogo-A MAb IN1
Anti-interferon-gamma polyclonal antibody - Advanced Biotherapy	Anti-nuclear autoantibodies -- Procyon
Anti-interleukin-10 MAb --	Anti-ovarian cancer monoclonal antibodies - Dompe
Anti-interleukin-12 MAb --	Anti-p185 monoclonal antibodies
Anti-interleukin-1-beta polyclonal antibody -- R&D Systems	Anti-p43 MAb
Anti-interleukin-2 receptor MAb 2A3	Antiparasitic vaccines
Anti-interleukin-2 receptor MAb 33B3-1 -- Immunotech	Anti-PDGF/bFGF sheep MAb -- KS Biomedix
Anti-interleukin-2 receptor MAb ART-18	Anti-properdin monoclonal antibodies -- Abgenix/Gliatech
Anti-interleukin-2 receptor MAb LO-Tact-1	Anti-PSMA (prostate specific membrane antigen)
Anti-interleukin-2 receptor MAb Mikbeta1	Anti-PSMA MAb J591 -- BZL Biologics
Anti-interleukin-2 receptor MAb NDS61	Anti-Rev MAb gene therapy --
Anti-interleukin-4 MAb 11B11	Anti-RSV antibodies -- Epicyte, Intracell
Anti-interleukin-5 MAb -- Wallace Laboratories	Anti-RSV monoclonal antibodies -- Medarex/MedImmune, Applied Molecular Evolution/MedImmune
Anti-interleukin-6 MAb -- Centocor, Diaclone, Pharmadigm	Anti-RSV MAb, inhalation -- Alkermes/MedImmune
Anti-interleukin-8 MAb -- Abgenix	Anti-RT gene therapy
Anti-interleukin-8 MAb -- Xenotech	Antisense K-ras RNA gene therapy
Anti-JL1 MAb	Anti-SF-25 MAb
Anti-Klebsiella sheep MAb -- KS Biomedix Holdings	Anti-sperm antibody -- Epicyte
Anti-Laminin receptor MAb-liposomal doxorubicin conjugate	Anti-Tac(Fv)-PE38 conjugate
Anti-LCG MAb -- Cytoclonal	Anti-TAPA/CD81 MAb AMP1
Anti-lipopolysaccharide MAb -- VitaResc	Anti-tat gene therapy

FIG. 28E

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Anti-TCR-alphabeta MAb H57-597	AOP-RANTES -- Senetek
Anti-TCR-alphabeta MAb R73	Apan-CH -- Praecis Pharmaceuticals
Anti-tenascin MAb BC-4-I-131	APC-8024 -- Demegen
Anti-TGF-beta human monoclonal antibodies -- Cambridge Antibody Tech., Genzyme	ApoA-1 -- Milano, Pharmacia
Anti-TGF-beta MAb 2G7 -- Genentech	Apogen -- Alexion
Antithrombin III -- Genzyme Transgenics, Aventis, Bayer, Behringwerke, CSL, Myriad	apolipoprotein A1 -- Avanir
Anti-Thy1 MAb	Apolipoprotein E -- Bio-Tech. General
Anti-Thy1.1 MAb	Applaggin -- Biogen
Anti-tissue factor/factor VIIa sheep MAb -- KS Biomedix	aprotinin -- ProdiGene
Anti-TNF monoclonal antibodies -- Centocor, Chiron, Peptech, Pharacia, Serono	APT-070C -- AdProTech
Anti-TNF sheep MAb -- KS Biomedix Holdings	AR 177 -- Aronex Pharmaceuticals
Anti-TNFalpha MAb -- Genzyme	AR 209 -- Aronex Pharmaceuticals, Antigenics
Anti-TNFalpha MAb B-C7 -- Diacione	AR545C
Anti-tooth decay MAb -- Planet BioTech.	ARGENT gene delivery systems -- ARIAD
Anti-TRAIL receptor-1 MAb -- Takeda	Arresten
Antitumour RNases -- NIH	ART-123 -- Asahi Kasei
Anti-VCAM MAb 2A2 -- Alexion	arylsulfatase B -- BioMarin
Anti-VCAM MAb 3F4 -- Alexion	Arylsulfatase B, Recombinant human -- BioMarin
Anti-VCAM-1 MAb	AS 1051 -- Ajinomoto
Anti-VEC MAb -- ImClone	ASI-BCL -- Intracell
Anti-VEGF MAb -- Genentech	Asparaginase - Merck
Anti-VEGF MAb 2C3	ATL-101 -- Alizyme
Anti-VEGF sheep MAb -- KS Biomedix Holdings	Atrial natriuretic peptide -- Pharis
Anti-VLA-4 MAb HP1/2 -- Biogen	Aurintricarboxylic acid-high molecular weight
Anti-VLA-4 MAb PS/2	Autoimmune disorders -- GPC
Anti-VLA-4 MAb R1-2	Biotech/MorphoSys
Anti-VLA-4 MAb TA-2	Autoimmune disorders and transplant rejection -- Bristol-Myers Squibb/Genzyme
Anti-VAP-1 human MAb	Tra
Anti-VRE sheep MAb -- KS Biomedix Holdings	Autoimmune disorders/cancer -- Abgenix/Chiron, CuraGen
ANUP -- TranXenoGen	Autotaxin
ANUP-1 -- Pharis	Avicidin -- NeoRx
	axogenesis factor-1 -- Boston Life Sciences
	Axokine -- Regeneron
	B cell lymphoma vaccine -- Biomira
	B7-1 gene therapy --
	BABS proteins -- Chiron

FIG. 28F

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BAM-002 -- Novelos Therapeutics	BMP 2 -- Genetics Institute/Medtronic-
Basiliximab (anti CD25 MAb) -- Novartis	Sofamor Danek, Genetics Institute/
Bay-16-9996 -- Bayer	Collagenesis, Genetics
Bay-39-9437 -- Bayer	Institute/Yamanouch
Bay-50-4798 -- Bayer	BMP 2 gene therapy
BB-10153 -- British Biotech	BMP 52 -- Aventis Pasteur, Biopharm
BBT-001 -- Bolder BioTech.	BMP-2 -- Genetics Institute
BBT-002 -- Bolder BioTech.	BMS 182248 -- Bristol-Myers Squibb
BBT-003 -- Bolder BioTech.	BMS 202448 -- Bristol-Myers Squibb
BBT-004 -- Bolder BioTech.	bone growth factors -- IsoTis
BBT-005 -- Bolder BioTech.	BPC-15 -- Pfizer
BBT-006 -- Bolder BioTech.	brain natriuretic peptide --
BBT-007 -- Bolder BioTech.	Breast cancer -- Oxford
BCH-2763 -- Shire	GlycoSciences/Medarex
BCSF -- Millenium Biologix	Breast cancer vaccine -- Therion Biologics,
BDNF -- Regeneron -- Amgen	Oregon
Becaplermin -- Johnson & Johnson, Chiron	BSSL -- PPL Therapeutics
Bectumomab -- Immunomedics	BST-2001 -- BioStratum
Beriplast -- Aventis	BST-3002 -- BioStratum
Beta-adrenergic receptor gene therapy --	BTI 322 --
University of Arkansas	butyrylcholinesterase -- Shire
bFGF -- Scios	C 6822 -- COR Therapeutics
BI 51013 -- Behringwerke AG	C1 esterase inhibitor -- Pharming
BIBH 1 -- Boehringer Ingelheim	C3d adjuvant -- AdProTech
BIM-23190 -- Beaufour-Ipsen	CAB-2.1 -- Millennium
birch pollen immunotherapy -- Pharmacia	calcitonin -- Inhale Therapeutics Systems,
bispecific fusion proteins -- NIH	Aventis, Genetronics, TranXenoGen,
Bispecific MAb 2B1 -- Chiron	Unigene, Rhone Poulenc Rohrer
Bitistatin	calcitonin -- oral -- Nobex, Emisphere,
BIWA 4 -- Boehringer Ingelheim	Pharmaceutical Discovery
blood substitute -- Northfield, Baxter Intl.	Calcitonin gene-related peptide -- Asahi
BLP-25 -- Biomira	Kasei -- Unigene
BLS-0597 -- Boston Life Sciences	calcitonin, human -- Suntory
BLyS -- Human Genome Sciences	calcitonin, nasal -- Novartis, Unigene
BLyS radiolabelled -- Human Genome	calcitonin, Panoderm -- Elan
Sciences	calcitonin, Peptitrol -- Shire
BM 06021 -- Boehringer Mannheim	calcitonin, salmon -- Therapicon
BM-202 -- BioMarin	calin -- Biopharm
BM-301 -- BioMarin	Calphobindin I
BM-301 -- BioMarin	calphobindin I -- Kowa
BM-302 -- BioMarin	calreticulin -- NYU

FIG. 28G

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Campath-1G	CD4 fusion toxin -- Senetek
Campath-1M	CD4 IgG -- Genentech
cancer therapy -- Cangene	CD4 receptor antagonists --
cancer vaccine -- Aixlie, Aventis Pasteur,	PharmacoPeia/Progenics
Center of Molecular Immunology, YM	CD4 soluble -- Progenics
BioSciences, Cytos, Genzyme,	CD4, soluble -- Genzyme Transgenics
Transgenics, GlobelImmune, Igeneon,	CD40 ligand -- Immunex
ImClone, Virogenetics, InterCell, Iomai,	CD4-ricin chain A -- Genentech
Jenner Biotherapies, Memorial Sloan-	CD59 gene therapy -- Alexion
Kettering Cancer Center, Sydney Kimmel	CD8 TIL cell therapy -- Aventis Pasteur
Cancer Center, Novavax, Protein	CD8, soluble -- Avidex
Sciences, Argonex, SIGA	CD95 ligand -- Roche
Cancer vaccine ALVAC-CEA B7.1 --	CDP 571 -- Celltech
Aventis Pasteur/Therion Biologics	CDP 850 -- Celltech
Cancer vaccine CEA-TRICOM -- Aventis	CDP-860 (PEG-PDGF MAb) -- Celltech
Pasteur/Therion Biologics	CDP 870 -- Celltech
Cancer vaccine gene therapy -- Cantab	CDS-1 -- Ernest Orlando
Pharmaceuticals	Cedelizumab -- Ortho-McNeil
Cancer vaccine HER-2/neu -- Corixa	Cetermin -- Insmed
Cancer vaccine THERATOPE -- Biomira	CETP vaccine -- Avant
cancer vaccine, PolyMASC -- Valentis	Cetrorelix
Candida vaccine -- Corixa, Inhibitex	Cetuximab
Canstatin -- ILEX	CGH 400 -- Novartis
CAP-18 -- Panorama	CGP 42934 -- Novartis
Cardiovascular gene therapy -- Collateral	CGP 51901 -- Tanox
Therapeutics	CGRP -- Unigene
carperitide -- Suntory	CGS 27913 -- Novartis
Casocidin-1 -- Pharis	CGS 32359 -- Novartis
CAT 152 -- Cambridge Antibody Tech.	Chagas disease vaccine -- Corixa
CAT 192 -- Cambridge Antibody Tech.	chemokines -- Immune Response
CAT 213 -- Cambridge Antibody Tech.	CHH 380 -- Novartis
Catalase -- Enzon	chitinase -- Genzyme, ICOS
Cat-PAD -- Circassia	Chlamydia pneumoniae vaccine -- Antex
CB 0006 -- Celltech	Biologics
CCK(27-32) -- Akzo Nobel	Chlamydia trachomatis vaccine -- Antex
CCR2-64I -- NIH	Biologics
CD, Procept -- Paligent	Chlamydia vaccine -- GlaxoSmithKline
CD154 gene therapy	Cholera vaccine CVD 103-HgR -- Swiss
CD39 -- Immunex	Serum and Vaccine Institute Berne
CD39-L2 -- Hyseq	Cholera vaccine CVD 112 -- Swiss Serum
CD39-L4 -- Hyseq	and Vaccine Institute Berne

FIG. 28H

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Cholera vaccine inactivated oral – SBL	CRL 1605 – CytRx
Vaccin	CS-560 – Sankyo
Chrysalin – Chrysalis BioTech.	CSF – ZymoGenetics
CI-782 – Hitachi Kase	CSF-G – Hangzhou, Dong-A, Hanmi
Ciliary neurotrophic factor – Fidia, Roche	CSF-GM – Cangene, Hunan, LG Chem
CIM project – Active Biotech	CSF-M – Zarix
CL 329753 – Wyeth-Ayerst	CT 1579 – Merck Frosst
CL22, Cobra – ML Laboratories	CT 1786 – Merck Frosst
Clenoliximab – IDEC	CT-112 ^Δ – BTG
Clostridium difficile antibodies – Epicyte	CTB-134L – Xenova
clotting factors – Octagene	CTC-111 – Kaketsuken
CMB 401 – Celltech	CTGF – FibroGen
CNTF – Sigma-Tau	CTLA4-Ig – Bristol-Myers Squibb
Cocaine abuse vaccine – Cantab,	CTLA4-Ig gene therapy –
ImmuLogic, Scripps	CTP-37 – AVI BioPharma
coccidiomycosis vaccine – Arizo	C-type natriuretic peptide – Suntory
collagen – Type I – Pharming	CVS 995 – Corvas Intl.
Collagen formation inhibitors – FibroGen	CX 397 – Nikko Kyodo
Collagen/hydroxyapatite/bone growth factor	CY 1747 – Epimmune
– Aventis Pasteur, Biopharm, Orquest	CY 1748 – Epimmune
collagenase – BioSpecifics	Cyanovirin-N
Colorectal cancer vaccine – Wistar Institute	Cystic fibrosis therapy – CBR/IVAX
Component B, Recombinant – Serono	CYT 351
Connective tissue growth factor inhibitors –	cytokine Traps – Regeneron
FibroGen/Taisho	cytokines – Enzon, Cytoclonal
Contortrostatin	Cytomegalovirus glycoprotein vaccine –
contraceptive vaccine – Zonagen	Chiron, Aquila Biopharmaceuticals,
Contraceptive vaccine hCG	Aventis Pasteur, Virogenetics
Contraceptive vaccine male reversible –	Cytomegalovirus vaccine live – Aventis
IMMUCON	Pasteur
Contraceptive vaccine zona pellucida –	Cytosine deaminase gene therapy –
Zonagen	GlaxoSmithKline
Copper-64 labelled MAb TETA-1A3 – NCI	DA-3003 – Dong-A
Coralyne	DAB389interleukin-6 – Senetek
Corsevin M	DAB389interleukin-7
C-peptide analogues – Schwarz	Daclizumab (anti-IL2R MAb) – Protein
CPI-1500 – Consensus	Design Labs
CRF – Neurobiological Tech.	DAMP ^Δ – Incyte Genomics
cRGDFV pentapeptide –	Daniplestim – Pharmacia
CRL 1095 – CytRx	darbepoetin alfa – Amgen
CRL 1336 – CytRx	DBI-3019 – Diabetogen

FIG. 28I

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DCC -- Genzyme	Dutepase -- Baxter Intl.
DDF -- Hyseq	DWP-401 -- Daewoong
decorin -- Integra, Telios	DWP-404 -- Daewoong
defensins -- Large Scale Biology	DWP-408 -- Daewoong
DEGR-VIIa	Dx 88 (Epi-KAL2) -- Dyax
DeImmunised antibody 3B6/22 AGEN	Dx 890 (elastin inhibitors) -- Dyax
Deimmunised anti-cancer antibodies -- Biovation/Viragen	E coli O157 vaccine -- NIH
Dendroamide A	E21-R -- BresaGen
Dengue vaccine -- Bavarian Nordic, Merck	Eastern equine encephalitis virus vaccine --
denileukin diftitox -- Ligand	Echicetin --
DES-1101 -- Desmos	Echinhibin 1 --
desirudin -- Novartis	Echistatin -- Merck
desmopressin -- Unigene	Echitamine --
Desmoteplase -- Merck, Schering AG	Ecromeximab -- Kyowa Hakko
Destabilase	EC-SOD -- PPL Therapeutics
Diabetes gene therapy -- DeveloGen, Pfizer	Eculizumab (5G1.1) -- Alexion
Diabetes therapy -- Crucell	EDF -- Ajinomoto
Diabetes type 1 vaccine -- Diamyd Therapeutics	EDN derivative -- NIH
DiaCIM -- YM BioSciences	EDNA -- NIH
dialytic oligopeptides -- Research Corp	Edobacomab -- XOMA
Diamyd -- Diamyd Therapeutics	Edrecolomab -- Centocor
DiaPep227 -- Pepgen	EF 5077
DiavaX -- Corixa	Efalizumab -- Genentech
Digoxin MAb -- Glaxo	EGF fusion toxin -- Seragen, Ligand
Diphtheria tetanus pertussis-hepatitis B vaccine -- GlaxoSmithKline	EGF-P64k vaccine -- Center of Molecular Immunology
DIR therapy -- Solis Therapeutics --	EL 246 -- LigoCyte
DNase -- Genentech	elastase inhibitor -- Synergen
Dornase alfa -- Genentech	elcatonin -- Therapicon
Dornase alfa, inhalation -- Genentech	EMD 72000 -- Merck KGaA
Doxorubicin-anti-CEA MAb conjugate -- Immunomedics	Emdogain -- BIORA
DP-107 -- Trimeris	emfilermin -- AMRAD
drotrecogin alfa -- Eli Lilly	Emoctakin -- Novartis
DTctGMCSF	enamel matrix protein -- BIORA
DTP-polio vaccine -- Aventis Pasteur	Endo III -- NYU
DU 257-KM231 antibody conjugate -- Kyowa	endostatin -- EntreMed, Pharis
dural graft matrix -- Integra	Enhancins -- Micrologix
	Enlimomab -- Isis Pharm.
	Enoxaparin sodium -- Pharmuka
	enzyme linked antibody nutrient depletion therapy -- KS Biomedix Holdings

FIG. 28J

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Eosinophil-derived neutralizing agent –	Factor VII – Novo Nordisk, Bayer, Baxter
EP-51216 – Asta Medica	Intl.
EP-51389 – Asta Medica	Factor VIIa – PPL Therapeutics,
EPH family ligands – Regeneron	ZymoGenetics
Epidermal growth factor – Hitachi Kasei,	Factor VIII – Bayer Genentech, Beaufour-
Johnson & Johnson	Ipsen, CLB, Inex, Octagen, Pharmacia,
Epidermal growth factor fusion toxin –	Pharming
Senetek	Factor VIII – PEGylated – Bayer
Epidermal growth factor-genistein –	Factor VIII fragments – Pharmacia
EPI-HNE-4 – Dyax	Factor VIII gene therapy – Targeted
EPI-KAL2 – Dyax	Genetics
Epoetin-alfa – Amgen, Dragon	Factor VIII sucrose formulation – Bayer,
Pharmaceuticals, Nanjing Huaxin	Genentech
Epratuzumab – Immunomedics	Factor VIII-2 – Bayer
Epstein-Barr virus vaccine –	Factor VIII-3 – Bayer
Aviron/SmithKline Beecham, Bioresearch	Factor Xa inhibitors – Merck, Novo Nordisk,
Eptacog alfa – Novo Nordisk	Mochida
Eptifibatide – COR Therapeutics	Factor XIII – ZymoGenetics
erb-38 –	Factors VIII and IX gene therapy – Genetics
Erlizumab – Genentech	Institute/Targeted Genetics
erythropoietin – Alkermes, ProLease, Dong-	Famoxin – Genset
A, Elanex, Genetics Institute, LG Chem,	Fas (delta) TM protein – LXR BioTech.
Protein Sciences, Serono, Snow Brand,	Fas TR – Human Genome Sciences
SRC VB VECTOR, Transkaryotic	Felvizumab – Scotgen
Therapies	FFR-VIIa – Novo Nordisk
Erythropoietin Beta – Hoffman La Roche	FG-001 – F-Gene
Erythropoietin/Epoetin alfa – Chugai	FG-002 – F-Gene
Escherichia coli vaccine – North American	FG-004 – F-Gene
Vaccine, SBL Vaccin, Swiss Serum and	FG-005 – F-Gene
Vaccine Institute Berne	FGF + fibrin – Repair
etanercept – Immunex	Fibrimage – Bio-Tech. General
examorelin – Mediolanum	fibrin-binding peptides – ISIS Innovation
Exendin 4 – Amylin	fibrinogen – PPL Therapeutics, Pharming
exonuclease VII	fibroblast growth factor – Chiron, NYU,
F 105 – Centocor	Ramot, ZymoGenetics
F-992 – Fornix	fibrolase conjugate – Schering AG
Factor IX – Alpha Therapeutics, Welfide	Filgrastim – Amgen
Corp., CSL, enetics Institute/AHP,	filgrastim – PDA modified – Xencor
Pharmacia, PPL Therapeutics	FLT-3 ligand – Immunex
Factor IX gene therapy – Cell Genesys	FN18 CRM9 –

FIG. 28K

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follistatin -- Biotech Australia, Human Therapeutics	glutamate decarboxylase -- Genzyme Transgenics
follitropin alfa -- Alkermes, ProLease, PowderJect, Serono, Akzo Nobel	Glycoprotein S3 -- Kureha
Follitropin Beta -- Bayer, Organon	GM-CSF -- Immunex
FP 59	GM-CSF tumour vaccine -- PowderJect
FSH -- Ferring	GnRH immunotherapeutic -- Protherics
FSH + LH -- Ferring	Goserelin (LhRH antagonist) -- AstraZeneca
F-spondin -- CeNeS	gp75 antigen -- ImClone
fusion protein delivery system -- UAB Research Foundation	gp96 -- Antigenics
fusion toxins -- Boston Life Sciences	GPI 0100 -- Galenica
G 5598 -- Genentech	GR 4991W93 -- GlaxoSmithKline
GA-II -- Transkaryotic Therapies	Granulocyte colony-stimulating factor -- Dong-A
Gamma-interferon analogues -- SRC VB VECTOR	Granulocyte colony-stimulating factor conjugate
Ganirelix -- Roche	grass allergy therapy -- Dynavax
gastric lipase -- Meristem	GRF1-44 -- ICN
Gavilimomab --	Growth Factor -- Chiron, Atrigel, Atrix, Innogenetics, ZymoGenetics, Novo
G-CSF -- Amgen, SRC VB VECTOR	growth factor peptides -- Biotherapeutics
GDF-1 -- CeNeS	growth hormone -- LG Chem
GDF-5 -- Biopharm	growth hormone, Recombinant human -- Serono
GDNF (glial derived neurotrophic factor) -- Amgen	GT 4086 -- Gliatech
gelsolin -- Biogen	GW 353430 -- GlaxoSmithKline
Gemtuzumab ozogamicin -- Celltech	GW-278884 -- GlaxoSmithKline
Gene-activated epoetin-alfa -- Aventis Pharma -- Transkaryotic Therapies	H 11 -- Viventia Biotech
Glanzmann thrombasthenia gene therapy --	H5N1 influenza A virus vaccine -- Protein Sciences
Glatiramer acetate -- Yeda	haemoglobin -- Biopure
glial growth factor 2 -- CeNeS	haemoglobin 3011, Recombinant -- Baxter Healthcare
GLP-1 -- Amylin, Suntory, TheraTech, Watson	haemoglobin crosfumaril -- Baxter Intl.
GLP-1 peptide analogues -- Zealand Pharmaceuticals	haemoglobin stabilized -- Ajinomoto
glucagon -- Eli Lilly, ZymoGenetics	haemoglobin, recombinant -- Apex
Glucagon-like peptide-1 7-36 amide -- Suntory	HAF -- Immune Response
Glucogen-like peptide -- Amylin	Hantavirus vaccine
Glucocerebrosidase -- Genzyme	HB 19
	HBNF -- Regeneron
	HCC-1 -- Pharis
	hCG -- Milkhaus

FIG. 28L

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hCG vaccine -- Zonagen	Herpes simplex glycoprotein DNA vaccine --
HE-317 -- Hollis-Eden Pharmaceuticals	Merck, Wyeth-Lederle Vaccines-Malvern,
Heat shock protein cancer and influenza	Genentech, GlaxoSmithKline, Chiron,
vaccines -- StressGen	Takeda
Helicobacter pylori vaccine -- Acambis,	Herpes simplex vaccine -- Cantab
AstraZeneca/CSL, Chiron, Provalis	Pharmaceuticals, CEL-SCI, Henderson
Helistat-G -- GalaGen	Morley
Hemolink -- Hemosol	Herpes simplex vaccine live -- ImClone
hepapoietin -- Snow Brand	Systems/Wyeth-Lederle, Aventis Pasteur
heparanase -- InSight	HGF derivatives -- Dompe
heparinase I -- Ibex	hIAPP vaccine -- Crucell
heparinase III -- Ibex	Hib-hepatitis B vaccine -- Aventis Pasteur
Hepatitis A vaccine -- American Biogenetic	HIC 1
Sciences	HIP -- Altachem
Hepatitis A vaccine inactivated	Hirudins -- Biopharma, Cangene, Dongkook,
Hepatitis A vaccine Nothav -- Chiron	Japan Energy Corporation, Pharmacia
Hepatitis A-hepatitis B vaccine --	Corporation, SIR International, Sanofi-
GlaxoSmithKline	Synthelabo, Sotragene, Rhein Biotech
hepatitis B therapy -- Tripep	HIV edible vaccine -- ProdiGene
Hepatitis B vaccine -- Amgen, Chiron SpA,	HIV gp120 vaccine -- Chiron, Ajinomoto,
Meiji Milk, NIS, Prodeva, PowderJect,	GlaxoSmithKline, ID Vaccine, Progenics,
Rhein Biotech	VaxGen
Hepatitis B vaccine recombinant -- Evans	HIV gp120 vaccine gene therapy --
Vaccines, Epitex Combiotech, Genentech,	HIV gp160 DNA vaccine -- PowderJect,
MedImmune, Merck Sharp & Dohme,	Aventis Pasteur, Oncogen, Hyland
Rhein Biotech, Shantha Biotechnics,	Immuno, Protein Sciences
Vector, Yeda	HIV gp41 vaccine -- Panacos
Hepatitis B vaccine recombinant TGP 943 --	HIV HGP-30W vaccine -- CEL-SCI
Takeda	HIV immune globulin -- Abbott, Chiron
Hepatitis C vaccine -- Bavarian Nordic,	HIV peptides -- American Home Products
Chiron, Innogenetics Acambis,	HIV vaccine -- Applied bioTech., Axis
Hepatitis D vaccine -- Chiron Vaccines	Genetics, Biogen, Bristol-Myers Squibb,
Hepatitis E vaccine recombinant --	Genentech, Korea Green Cross, NIS,
Genelabs/GlaxoSmithKline, Novavax	Oncogen, Protein Sciences Corporation,
hepatocyte growth factor -- Panorama,	Terumo, Tonen Corporation, Wyeth-
Sosei	Ayerst, Wyeth-Lederle Vaccines-Malvern,
hepatocyte growth factor kringle fragments --	Advanced BioScience Laboratories,
- EntreMed	Bavarian Nordic, Bavarian Nordic/Statens
Her-2/Neu peptides -- Corixa	Serum Institute, GeneCure, Immune
	Response, Progenics, Therion Biologics,
	United Biomedical, Chiron

FIG. 28M

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HIV vaccine vCP1433 -- Aventis Pasteur	Human monoclonal antibodies --
HIV vaccine vCP1452 -- Aventis Pasteur	Medarex/Northwest Biotherapeutics,
HIV vaccine vCP205 -- Aventis Pasteur	Medarex/Seattle Genetics
HL-9 -- American BioScience	human netrin-1 -- Exelixis
HM-9239 -- Cytran	human papillomavirus antibodies -- Epicyte
HML-103 -- Hemosol	Human papillomavirus vaccine -- Biotech
HML-104 -- Hemosol	Australia, IDEC, StressGen
HML-105 -- Hemosol	Human papillomavirus vaccine MEDI 501 --
HML-109 -- Hemosol	Medimmune/GlaxoSmithKline
HML-110 -- Hemosol	Human papillomavirus vaccine MEDI
HML-121 -- Hemosol	503/MEDI 504 --
hNLP -- Pharis	Medimmune/GlaxoSmithKline
Hookworm vaccine	Human papillomavirus vaccine TA-CIN --
host-vector vaccines -- Henogen	Cantab Pharmaceuticals
HPM 1 -- Chugai	Human papillomavirus vaccine TA-HPV --
HPV vaccine -- MediGene	Cantab Pharmaceuticals
HSA -- Meristem	Human papillomavirus vaccine TH-GW --
HSF -- StressGen	Cantab/GlaxoSmithKline
HSP carriers -- Weizmann, Yeda, Peptor	human polyclonal antibodies -- Biosite/Eos
HSPPC-70 -- Antigenics	BioTech./ Medarex
HSPPC-96, pathogen-derived -- Antigenics	human type II anti factor VIII monoclonal
HSV 863 -- Novartis	antibodies -- ThromboGenics
HTLV-I DNA vaccine	humanised anti glycoprotein Ib murine
HTLV-I vaccine	monoclonal antibodies -- ThromboGenics
HTLV-II vaccine -- Access	HumaRAD -- Intracell
HU 901 -- Tanox	HuMax EGFR -- Genmab
Hu23F2G -- ICOS	HuMax-CD4 -- Medarex
HuHMFG1	HuMax-IL15 -- Genmab
HumaLYM -- Intracell	HYB 190 -- Hybridon
Human krebs statika -- Yamanouchi	HYB 676 -- Hybridon
human monoclonal antibodies --	I-125 MAb A33 -- Celltech
Abgenix/Biogen, Abgenix/ Corixa,	Ibritumomab tiuxetan -- IDEC
Abgenix/Immunex, Abgenix/Lexicon,	IBT-9401 -- Ibex
Abgenix/ Pfizer, Athersys/Medarex,	IBT-9402 -- Ibex
Biogen/MorphoSys, CAT/Searle,	IC 14 -- ICOS
Centocor/Medarex, Corixa/Kirin Brewery,	Idarubicin anti-Ly-2.1 --
Corixa/Medarex, Eos BioTech./Medarex,	IDEC 114 -- IDEC
Eos/Xenerex, Exelixis/Protein Design	IDEC 131 -- IDEC
Labs, ImmunoGen/ Raven, Medarex/	IDEC 152 -- IDEC
B.Twelve, MorphoSys/ImmunoGen, XTL	IDM 1 -- IDM
Biopharmaceuticals/Dyax,	IDPS -- Hollis-Eden Pharmaceuticals

FIG. 28N

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iduronate-2-sulfatase -- Transkaryotic Therapies	insulin -- AutoImmune, Altea, Biobras, BioSante, Bio-Tech. General, Chong Kun Dang, Emisphere, Flamel, Provalis, Rhein Biotech, TranXenoGen
IGF/IBP-2-13 -- Pharis	insulin (bovine) -- Novartis
IGN-101 -- Igeneon	insulin analogue -- Eli Lilly
IK HIR02 -- Iketon	Insulin Aspart -- Novo Nordisk
IL-11 -- Genetics Institute/AHP	insulin detemir -- Novo Nordisk
IL-13-PE38 -- NeoPharm	insulin glargine -- Aventis
IL-17 receptor -- Immunex	insulin inhaled -- Inhale Therapeutics Systems, Alkermes
IL-18BP -- Yeda	insulin oral -- Inovax
IL-1Hy1 -- Hyseq	insulin, AeroDose -- AeroGen
IL-1 β -- Celltech	insulin, AERx -- Aradigm
IL-1 β adjuvant -- Celltech	insulin, BEODAS -- Elan
IL-2 -- Chiron	insulin, Biphasix -- Helix
IL-2 + IL-12 -- Hoffman La-Roche	insulin, buccal -- Generex
IL-6/sIL-6R fusion -- Hadasit	insulin, I2R -- Flemington
IL-6R derivative -- Tosoh	insulin, intranasal -- Bentley
IL-7-Dap 389 fusion toxin -- Ligand	insulin, oral -- Nobex, Unigene
IM-862 -- Cytran	insulin, Orasome -- Endorex
IMC-1C11 -- ImClone	insulin, ProMaxx -- Epic
imiglucerase -- Genzyme	insulin, Quadrant -- Elan
Immune globulin intravenous (human) -- Hoffman La Roche	insulin, recombinant -- Aventis
immune privilege factor -- Proneuron	insulin, Spiros -- Elan
Immunocal -- Immunotec	insulin, Transfersome -- IDEA
Immunogene therapy -- Briana Bio-Tech	insulin, Zymo, recombinant -- Novo Nordisk
Immunoliposomal 5-fluorodeoxyuridine-dipalmitate --	insulinotropin -- Scios
immunosuppressant vaccine -- Aixdie	Insulysin gene therapy --
immunotoxin -- Antisoma, NIH	integrin antagonists -- Merck
ImmuRAIT-Re-188 -- Immunomedics	interferon (Alpha2) -- SRC VB VECTOR, Viragen, Dong-A, Hoffman La-Roche, Genentech
imreg-1 -- Imreg	interferon -- BioMedicines, Human Genome Sciences
infertility -- Johnson & Johnson, E-TRANS	interferon (Alfa-n3) -- Interferon Sciences Intl.
Infliximab -- Centocor	interferon (Alpha), Biphasix -- Helix
Influenza virus vaccine -- Aventis Pasteur, Protein Sciences	
inhibin -- Biotech Australia, Human Therapeutics	
Inhibitory G protein gene therapy	
INKP-2001 -- InKine	
Inolimomab -- Diaclone	

FIG. 280

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interferon (Alpha)—Amgen, BioNative,	IL-2/ diphtheria toxin — Ligand
Novartis, Genzyme Transgenics,	Interleukin-3 — Cangene
Hayashibara, Inhale Therapeutics	Interleukin-4 — Immunology Ventures,
Systems, Medusa, Flamel, Dong-A,	Sanofi Winthrop, Schering-Plough,
GeneTrol, Nastech, Shantha,	Immunex/ Sanofi Winthrop, Bayer, Ono
Wassermann, LG Chem, Sumitomo,	interleukin-4 + TNF-Alpha — NIH
Aventis, Behring EGIS, Pepgen, Servier,	interleukin-4 agonist — Bayer
Rhein Biotech,	interleukin-4 fusion toxin — Ligand
interferon (Alpha2A)	Interleukin-4 receptor — Immunex, Immun
interferon (Alpha2B) — Enzon, Schering-	Interleukin-6 — Ajinomoto, Cangene, Yeda,
Plough, Biogen, IDEA	Genetics Institute, Novartis
interferon (Alpha-N1) — GlaxoSmithKline	interleukin-6 fusion protein
interferon (beta) — Rentschler, GeneTrol,	Interleukin-6 fusion toxin — Ligand, Serono
Meristem, Rhein Biotech, Toray, Yeda,	interleukin-7 — IC Innovations
Daiichi, Mochida	interleukin-7 receptor — Immunex
interferon (Beta1A) — Serono, Biogen	interleukin-8 antagonists — Kyowa
interferon (beta1A), inhale — Biogen	Hakko/Millennium/Pfizer
interferon (B1b)— Chiron	interleukin-9 antagonists — Genaera
interferon (tau)— Pepgen	Interleukin-10 — DNAX, Schering-Plough
Interferon alfacon-1 — Amgen	Interleukin-10 gene therapy —
Interferon alpha-2a vaccine	interleukin-12 — Genetics Institute, Hoffman
Interferon Beta 1b — Schering/Chiron,	La-Roche
InterMune	interleukin-13 — Sanofi
Interferon Gamma — Boehringer Ingelheim,	interleukin-13 antagonists — AMRAD
Sheffield, Rentschler, Hayashibara	Interleukin-13-PE38QQR
interferon receptor, Type I — Serono	interleukin-15 — Immunex
interferon(Gamma1B) — Genentech	interleukin-16 — Research Corp
Interferon-alpha-2b + ribavirin — Biogen,	interleukin-18 — GlaxoSmithKline
ICN	Interleukin-18 binding protein — Serono
Interferon-alpha-2b gene therapy —	lor-P3 — Center of Molecular Immunology
Schering-Plough	IP-10 — NIH
Interferon-con1 gene therapy —	IPF — Metabolex
interleukin-1 antagonists — Dompe	IR-501 — Immune Response
Interleukin-1 receptor antagonist — Abbott	ISIS 9125 — Isis Pharmaceuticals
Bioresearch, Pharmacia	ISURF No. 1554 — Millennium
Interleukin-1 receptor type I — Immunex	ISURF No. 1866 — Iowa State Univer.
interleukin-1 receptor Type II — Immunex	ITF-1697 — Italfarmaco
Interleukin-1 trap — Regeneron	IxC 162 — Ixion
Interleukin-1-alpha — Immunex/Roche	J 695 — Cambridge Antibody Tech.,
interleukin-2 — SRC VB VECTOR,	Genetics Inst., Knoll
Ajinomoto, Biomira, Chiron	Jagged + FGF — Repair

FIG. 28P

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JKC-362 -- Phoenix Pharmaceuticals	leptin, 2nd-generation -- Amgen
JTP-2942 -- Japan Tobacco	leridistim -- Pharmacia
Juman monoclonal antibodies -- Medarex/Raven	leuprolide, ProMaxx -- Epic
K02 -- Axy's Pharmaceuticals	leuprorelin, oral -- Unigene
Keliximab -- IDEC	LeuTech -- Papatin
Keyhole limpet haemocyanin	LEX 032 -- SuperGen
KGF -- Amgen	LiDEPT -- Novartis
KM 871 -- Kyowa	Lintuzumab (anti-CD33 MAb) -- Protein Design Labs
KPI 135 -- Scios	lipase -- Altus Biologics
KPI-022 -- Scios	lipid A vaccine -- EntreMed
Kringle 5	lipid-linked anchor Tech. -- ICRT, ID Biomedical
KSB 304	liposome-CD4 Tech. -- Sheffield
KSB-201 -- KS Biomedix	Listeria monocytogenes vaccine
L 696418 -- Merck	LMB 1
L 703801 -- Merck	LMB 7
L1 -- Acorda	LMB 9 -- Battelle Memorial Institute, NIH
L-761191 -- Merck	LM-CD45 -- Cantab Pharmaceuticals
lactoferrin -- Meristem, Pharming, Agennix	lovastatin -- Merck
lactoferrin cardio -- Pharming	LSA-3
LAG-3 -- Serono	LT- β receptor -- Biogen
LAIT -- GEMMA	lung cancer vaccine -- Corixa
LAK cell cytotoxin -- Arizona	lusupultide -- Scios
lamellarins -- PharmaMar/University of Malaga	L-Vax -- AVAX
laminin A peptides -- NIH	LY 355455 -- Eli Lilly
lanotepase -- Genetics Institute	LY 366405 -- Eli Lilly
laronidase -- BioMarin	LY-355101 -- Eli Lilly
Lassa fever vaccine	Lyme disease DNA vaccine -- Vical/Aventis Pasteur
LCAT -- NIH	Lyme disease vaccine -- Aquila
LDP 01 -- Millennium	Biopharmaceuticals, Aventis, Pasteur, Symbicom, GlaxoSmithKline, Hyland
LDP 02 -- Millennium	Immuno, MedImmune
Lecithinized superoxide dismutase -- Seikagaku	Lymphocytic choriomeningitis virus vaccine
LeIF adjuvant -- Corixa	lymphoma vaccine -- Biomira, Genitope
leishmaniasis vaccine -- Corixa	LYP18
lenercept -- Hoffman La-Roche	lys plasminogen, recombinant
Lenograstim -- Aventis, Chugai	Lysosomal storage disease gene therapy -- Avigen
lepirudin -- Aventis	lysostaphin -- Nutrition 21
leptin -- Amgen, IC Innovations	
Leptin gene therapy -- Chiron Corporation	

FIG. 28Q

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M 23 -- Gruenenthal	MEDI 507 -- BioTransplant
M1 monoclonal antibodies -- Acorda	melanin concentrating hormone --
Therapeutics	Neurocrine Biosciences
MA 16N7C2 -- Corvas Intl.	melanocortins -- OMRF
malaria vaccine -- GlaxoSmithKline,	Melanoma monoclonal antibodies -- Viragen
AdProTech, Antigenics, Apovia, Aventis	melanoma vaccine -- GlaxoSmithKline,
Pasteur, Axis Genetics, Behringwerke,	Akzo Nobel, Avant, Aventis Pasteur,
CDCP, Chiron Vaccines, Genzyme	Bavarian Nordic, Biovector, CancerVax,
Transgenics, Hawaii, MedImmune, NIH,	Genzyme Molecular Oncology, Humbolt,
NYU, Oxon, Roche/Saramane, Biotech	ImClone Systems, Memorial, NYU, Oxon
Australia, Rx Tech	Melanoma vaccine Magevac -- Therion
Malaria vaccine CDC/NIIMALVAC-1	memory enhancers -- Scios
malaria vaccine, multicomponent	meningococcal B vaccine -- Chiron
mammaglobin -- Corixa	meningococcal vaccine -- CAMR
mammastatin -- Biotherapeutics	Meningococcal vaccine group B conjugate -
mannan-binding lectin -- NatImmu	- North American Vaccine
mannan-MUC1 -- Psiron	Meningococcal vaccine group B
MAP 30	recombinant -- BioChem Vaccines,
Marinovir -- Phytera	Microscience
MARstem -- Maret	Meningococcal vaccine group Y conjugate -
MB-015 -- Mochida	- North American Vaccine
MBP -- ImmuLogic	Meningococcal vaccine groups A B and C
MCI-028 -- Mitsubishi-Tokyo	conjugate -- North American Vaccine
MCIF -- Human Genome Sciences	Mepolizumab -- GlaxoSmithKline
MDC -- Advanced BioScience -- Akzo	Metastatin -- EntreMed, Takeda
Nobel, ICOS	Met-CkB7 -- Human Genome Sciences
MDX 11 -- Medarex	met-enkephalin -- TNI
MDX 210 -- Medarex	METH-1 -- Human Genome Sciences
MDX 22 -- Medarex	methioninase -- AntiCancer
MDX 22	Methionine lyase gene therapy --
MDX 240 -- Medarex	AntiCancer
MDX 33	Met-RANTES -- Genexa Biomedical,
MDX 44 -- Medarex	Serono
MDX 447 -- Medarex	Metreleptin
MDX H210 -- Medarex	Microtubule inhibitor MAb
MDX RA -- Houston BioTech., Medarex	Immunogen/Abgenix
ME-104 -- Pharmexa	MGDF -- Kirin
Measles vaccine	MGV -- Progenics
Mecasemin -- Cephalon/Chiron, Chiron	micrin -- Endocrine
MEDI 488 -- MedImmune	microplasmin -- ThromboGenics
MEDI 500	MIF -- Genetics Institute

FIG. 28R

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migration inhibitory factor -- NIH	MAB 45-2D9- -- haematoporphyrin conjugate
Mim CD4.1 -- Xycte Therapies	MAB 4B4
mirostipen -- Human Genome Sciences	MAB 4E3-CPA conjugate -- BCM Oncologia
Mitumomab (BEC-2) -- ImClone Systems, Merck KGaA	MAB 4E3-daunorubicin conjugate
MK 852 -- Merck	MAB 50-6
MLN 1202 (Anti-CCR2 monoclonal antibody) -- Millenium Pharmaceuticals	MAB 50-61A -- Institut Pasteur
Mobenakin -- NIS	MAB 5A8 -- Biogen
molgramostim -- Genetics Institute, Novartis	MAB 791T/36-methotrexate conjugate
monoclonal antibodies -- Abgenix/Celltech, Immusol/ Medarex, Viragen/ Roslin Institute, Cambridge Antibody Tech./Elan	MAB 7c11.e8
MAB 108 --	MAB 7E11 C5-selenocystamine conjugate
MAB 10D5 --	MAB 93KA9 -- Novartis
MAB 14.18-interleukin-2 immunocytokine -- Lexigen	MAB A5B7-cisplatin conjugate -- Biodynamics Research, Pharmacia
MAB 14G2a --	MAB A5B7-I-131
MAB 15A10 --	MAB A7
MAB 170 -- Biomira	MAB A717 -- Exocell
MAB 177Lu CC49 --	MAB A7-zinostatin conjugate
MAB 17F9	MAB ABX-RB2 -- Abgenix
MAB 1D7	MAB ACA 11
MAB 1F7 -- Immune Network	MAB AFP-I-131 -- Immunomedics
MAB 1H10-doxorubicin conjugate	MAB AP1
MAB 26-2F	MAB AZ1
MAB 2A11	MAB B3-LysPE40 conjugate
MAB 2E1 -- RW Johnson	MAB B4 -- United Biomedical
MAB 2F5	MAB B43 Genistein-conjugate
MAB 31.1 -- International BioImmune Systems	MAB B43.13-Tc-99m -- Biomira
MAB 32 -- Cambridge Antibody Tech., Peptech	MAB B43-PAP conjugate
MAB 323A3 -- Centocor	MAB B4G7-gelonin conjugate
MAB 3C5	MAB BCM 43-daunorubicin conjugate -- BCM Oncologia
MAB 3F12	MAB BIS-1
MAB 3F8	MAB BMS 181170 -- Bristol-Myers Squibb
MAB 42/6	MAB BR55-2
MAB 425 -- Merck KGaA	MAB BW494
MAB 447-52D -- Merck Sharp & Dohme	MAB C 242-DM1 conjugate -- ImmunoGen
	MAB C242-PE conjugate
	MAB c30-6
	MAB CA208-cytorhodin-S conjugate -- Hoechst Japan
	MAB CC49 -- Enzon

FIG. 28S

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MAb ch14.18 --	MAb LL2-I-131 -- Immunomedics
MAb CH14.18-GM-CSF fusion protein --	MAb LL2-Y-90
Lexigen	MAb LS2D617 -- Hybritech
MAb chCE7	MAb LYM-1-gelonin conjugate
MAb CI-137 -- AMRAD	MAb LYM-1-I-131
MAb cisplatin conjugate	MAb LYM-1-Y-90
MAb CLB-CD19	MAb LYM-2 -- Peregrine
MAb CLB-CD19v	MAb M195
MAb CLL-1 -- Peregrine	MAb M195-bismuth 213 conjugate --
MAb CLL-1-GM-CSF conjugate	Protein Design Labs
MAb CLL-1-IL-2 conjugate -- Peregrine	MAb M195-gelonin conjugate
MAb CLN IgG -- doxorubicin conjugates	MAb M195-I-131
MAb conjugates -- Tanox	MAb M195-Y-90
MAb D612	MAb MA 33H1 -- Sanofi
MAb Dal B02	MAb MAD11
MAb DC101 -- ImClone	MAb MGB2
MAb EA 1 --	MAb MINT5
MAb EC708 -- Biovation	MAb MK2-23
MAb EP-5C7 -- Protein Design Labs	MAb MOC31 ETA(252-613) conjugate
MAb ERIC-1 -- ICRT	MAb MOC-31-In-111
MAb F105 gene therapy	MAb MOC-31-PE conjugate
MAb FC 2.15	MAb MR6 --
MAb G250 -- Centocor	MAb MRK-16 -- Aventis Pasteur
MAb GA6	MAb MS11G6
MAb GA733	MAb MX-DTPA BrE-3
MAb Gliomab-H -- Viventia Biotech	MAb MY9
MAb HB2-saporin conjugate	MAb Nd2 -- Tosoh
MAb HD 37 --	MAb NG-1 -- Hygeia
MAb HD37-ricin chain-A conjugate	MAb NM01 -- Nissin Food
MAb HNK20 -- Acambis	MAb OC 125
MAb huN901-DM1 conjugate --	MAb OC 125-CMA conjugate
ImmunoGen	MAb OKI-1 -- Ortho-McNeil
MAb I-131 CC49 -- Corixa	MAb OX52 -- Bioproducts for Science
MAb ICO25	MAb PMA5
MAb ICR12-CPG2 conjugate	MAb PR1
MAb ICR-62	MAb prost 30
MAb IRac-ricin A conjugate	MAb R-24
MAb K1	MAb R-24 α Human GD3 -- Celltech
MAb KS1-4-methotrexate conjugate	MAb RFB4-ricin chain A conjugate
MAb L6 -- Bristol-Myers Squibb, Oncogen	MAb RFT5-ricin chain A conjugate
MAb LiCO 16-88	MAb SC 1

FIG. 28T

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MAB SM-3 -- ICRT	Muc-1 vaccine -- Corixa
MAB SMART 1D10 -- Protein Design Labs	mucosal tolerance -- Aberdeen
MAB SMART ABL 364 -- Novartis	mullerian inhibiting subst
MAB SN6f	muplestim -- Genetics Institute, Novartis,
MAB SN6f-deglycosylated ricin A chain	DSM Anti-Infectives
conjugate --	murine MAB -- KS Biomedix
MAB SN6j	Mutant somatropin -- JCR Pharmaceutical
MAB SN7-ricin chain A conjugate	MV 833 -- Toagosei
MAB T101-Y-90 conjugate -- Hybritech	Mycoplasma pulmonis vaccine
MAB T-88 -- Chiron	Mycoprex -- XOMA
MAB TB94 -- Cancer ImmunoBiology	myeloperoxidase -- Henogen
MAB TEC 11	myostatin -- Genetics Institute
MAB TES-23 -- Chugai	Nacolomab tafenatox -- Pharmacia
MAB TM31 -- Avant	Nagrecor -- Scios
MAB TNT-1 -- Cambridge Antibody Tech.,	nagrestipen -- British Biotech
Peregrine	NAP-5 -- Corvas Intl.
MAB TNT-3	NAPc2 -- Corvas Intl.
MAB TNT-3 -- IL2 fusion protein --	nartograstim -- Kyowa
MAB TP3-At-211	Natalizumab -- Protein Design Labs
MAB TP3-PAP conjugate --	Nateplase -- NIH, Nihon Schering
MAB UJ13A -- ICRT	nateplase -- Schering AG
MAB UN3	NBI-3001 -- Neurocrine Biosci.
MAB ZME-018-gelonin conjugate	NBI-5788 -- Neurocrine Biosci.
MAB-BC2 -- GlaxoSmithKline	NBI-6024 -- Neurocrine Biosci.
MAB-DM1 conjugate -- ImmunoGen	Nef inhibitors -- BRI
MAB-ricin-chain-A conjugate -- XOMA	Neisseria gonorrhoea vaccine -- Antex
MAB-temoporfin conjugates	Biologics
Monopharm C -- Viventia Biotech	Neomycin B-arginine conjugate
monteplase -- Eisai	Nerelimomab -- Chiron
montirelin hydrate -- Gruenenthal	Nerve growth factor -- Amgen -- Chiron,
moroctocog alfa -- Genetics Institute	Genentech
Moroctocog-alfa -- Pharmacia	Nerve growth factor gene therapy
MP 4	nesiritide citrate -- Scios
MP-121 -- Biopharm	neuregulin-2 -- CeNeS
MP-52 -- Biopharm	neurocan -- NYU
MRA -- Chugai	neuronal delivery system -- CAMR
MS 28168 -- Mitsui Chemicals, Nihon	Neurophil inhibitory Factor -- Corvas
Schering	Neuroprotective vaccine -- University of
MSH fusion toxin -- Ligand	Auckland
MSI-99 -- Genaera	neurotrophic chimaeras -- Regeneron
MT 201 -- Micromet	neurotrophic factor -- NsGene, CereMedix

FIG. 28U

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NeuroVax -- Immune Response	Oncophage -- Antigenics
neurturin -- Genentech	Oncostatin M -- Bristol-Myers Squibb
neutral endopeptidase -- Genentech	OncoVax-CL -- Jenner Biotherapies
NGF enhancers -- NeuroSearch	OncoVax-P -- Jenner Biotherapies
NHL vaccine -- Large Scale Biology	oncept -- Yeda
NIP45 -- Boston Life Sciences	onychomycosis vaccine -- Boehringer
NKI-B20	Ingelheim
NM 01 -- Nissin Food	opebecan -- XOMA
NMI-139 -- NitroMed	opioids -- Arizona
NMMP -- Genetics Institute	Oprelvekin -- Genetics Institute
NN-2211 -- Novo Nordisk	Oregovomab -- AltaRex
Noggin -- Regeneron	Org-33408 b -- Akzo Nobel
Nonacog alfa	Orolip DP -- EpiCept
Norelin -- Biostar	oryzacystatin
Norwalk virus vaccine	OSA peptides -- GenSci Regeneration
NRLU 10 -- NeoRx	osteoblast-cadherin GF -- Pharis
NRLU 10 PE -- NeoRx	Osteocalcin-thymidine kinase gene therapy
NT-3 -- Regeneron	osteogenic protein -- Curis
NT-4/5 -- Genentech	osteopontin -- OraPharma
NU 3056	osteoporosis peptides -- Integra, Telios
NU 3076	osteoprotegerin -- Amgen, SnowBrand
NX 1838 -- Gilead Sciences	otitis media vaccines -- Antex Biologics
NY ESO-1/CAG-3 antigen -- NIH	ovarian cancer -- University of Alabama
NYVAC-7 -- Aventis Pasteur	OX40-IgG fusion protein -- Cantab, Xenova
NZ-1002 -- Novazyme	P 246 -- Diatide
obesity therapy -- Nobex	P 30 -- Alfacell
OC 10426 -- Ontogen	p1025 -- Active Biotech
OC 144093 -- Ontogen	P-113 ^A -- Demegen
OCIF -- Sankyo	P-16 peptide -- Transition Therapeutics
Oct-43 -- Otsuka	p43 -- Ramot
Odulimomab -- Immunotech	P-50 peptide -- Transition Therapeutics
OK PSA - liposomal	p53 + RAS vaccine -- NIH, NCI
OKT3-gamma-1-ala-ala	PACAP(1-27) analogue
OM 991	paediatric vaccines -- Chiron
OM 992	Pafase -- ICOS
Omalizumab -- Genentech	PAGE-4 plasmid DNA -- IDEC
oncoimmunin-L -- NIH	PAI-2 -- Biotech Australia, Human
Oncolysin B -- ImmunoGen	Therapeutics
Oncolysin CD6 -- ImmunoGen	Palifermin (keratinocyte growth factor) --
Oncolysin M -- ImmunoGen	Amgen
Oncolysin S -- ImmunoGen	Palivizumab -- MedImmune

FIG. 28V

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PAM 4 -- Merck	PEG-uricase -- Mountain View
pamiteplase -- Yamanouchi	Pegvisomant -- Genentech
pancreatin, Minitabs -- Eurand	PEGylated proteins, PolyMASC -- Valentis
Pangen -- Fournier	PEGylated recombinant native human leptin
Pantarin -- Selective Genetics	-- Roche
Parainfluenza virus vaccine -- Pharmacia,	Pemtumomab
Pierre Fabre	Penetratin -- Cyclacel
paraoxanase -- Esperion	Pepscan -- Antisoma
parathyroid hormone -- Abiogen, Korea	peptide G -- Peptech, ICRT
Green Cross	peptide vaccine -- NIH, NCI
Parathyroid hormone (1-34) --	Pexelizumab
Chugai/Suntory	pexiganan acetate -- Genaera
Parkinson's disease gene therapy -- Cell	Pharmaprojects No. 3179 -- NYU
Genesys/ Ceregene	Pharmaprojects No. 3390 -- Ernest Orlando
Parvovirus vaccine -- MedImmune	Pharmaprojects No. 3417 -- Sumitomo
PCP-Scan -- Immunomedics	Pharmaprojects No. 3777 -- Acambis
PDGF -- Chiron	Pharmaprojects No. 4209 -- XOMA
PDGF cocktail -- Theratechnologies	Pharmaprojects No. 4349 -- Baxter Intl.
peanut allergy therapy -- Dynavax	Pharmaprojects No. 4651
PEG anti-ICAM MAb -- Boehringer	Pharmaprojects No. 4915 -- Avanir
Ingelheim	Pharmaprojects No. 5156 -- Rhizogenics
PEG asparaginase -- Enzon	Pharmaprojects No. 5200 -- Pfizer
PEG glucocerebrosidase	Pharmaprojects No. 5215 -- Origene
PEG hirudin -- Knoll	Pharmaprojects No. 5216 -- Origene
PEG interferon-alpha-2a -- Roche	Pharmaprojects No. 5218 -- Origene
PEG interferon-alpha-2b + ribavirin --	Pharmaprojects No. 5267 -- ML
Biogen, Enzon, ICN Pharmaceuticals,	Laboratories
Schering-Plough	Pharmaprojects No. 5373 -- MorphoSys
PEG MAb A5B7 --	Pharmaprojects No. 5493 -- Metabolex
Pegacaristim -- Amgen -- Kirin Brewery --	Pharmaprojects No. 5707 -- Genentech
ZymoGenetics	Pharmaprojects No. 5728 -- Autogen
Pegaldesleukin -- Research Corp	Pharmaprojects No. 5733 -- BioMarin
pegaspargase -- Enzon	Pharmaprojects No. 5757 -- NIH
pegfilgrastim -- Amgen	Pharmaprojects No. 5765 -- Gryphon
PEG-interferon Alpha -- Viragen	Pharmaprojects No. 5830 -- AntiCancer
PEG-interferon Alpha 2A -- Hoffman La-	Pharmaprojects No. 5839 -- Dyax
Roche	Pharmaprojects No. 5849 -- Johnson &
PEG-interferon Alpha 2B -- Schering-	Johnson
Plough	Pharmaprojects No. 5860 -- Mitsubishi-
PEG-r-hirudin -- Abbott	Tokyo
PEG-rHuMGDF -- Amgen	

FIG. 28W

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Pharmaprojects No. 5869 -- Oxford GlycoSciences	Plasminogen activators -- Abbott Laboratories, American Home Products, Boehringer Mannheim, Chiron
Pharmaprojects No. 5883 -- Asahi Brewery	Corporation, DuPont Pharmaceuticals, Eli Lilly, Shionogi, Genentech, Genetics Institute, GlaxoSmithKline, Hemispherx Biopharma, Merck & Co, Novartis, Pharmacia Corporation, Wakamoto, Yeda
Pharmaprojects No. 5947 -- StressGen	plasminogen-related peptides -- Bio-Tech. General/MGH
Pharmaprojects No. 5961 -- Theratechnologies	platelet factor 4 -- RepliGen
Pharmaprojects No. 5962 -- NIH	Platelet-derived growth factor -- Amgen -- ZymoGenetics
Pharmaprojects No. 5966 -- NIH	plusonemin-- Hayashibara
Pharmaprojects No. 5994 -- Pharming	PMD-2850 -- Protherics
Pharmaprojects No. 5995 -- Pharming	Pneumococcal vaccine -- Antex Biologics, Aventis Pasteur
Pharmaprojects No. 6023 -- IMMUCON	Pneumococcal vaccine intranasal -- BioChem Vaccines/Biovector
Pharmaprojects No. 6063 -- Cytoclonal	PR1A3
Pharmaprojects No. 6073 -- SIDDCO	PR-39
Pharmaprojects No. 6115 -- Genzyme	pralmorelin -- Kaken
Pharmaprojects No. 6227 -- NIH	Pretarget-Lymphoma -- NeoRx
Pharmaprojects No. 6230 -- NIH	Priliximab -- Centocor
Pharmaprojects No. 6236 -- NIH	PRO 140 -- Progenics
Pharmaprojects No. 6243 -- NIH	PRO 2000 -- Procept
Pharmaprojects No. 6244 -- NIH	PRO 367 -- Progenics
Pharmaprojects No. 6281 -- Senetek	PRO 542 -- Progenics
Pharmaprojects No. 6365 -- NIH	pro-Apo A-I -- Esperion
Pharmaprojects No. 6368 -- NIH	prolactin -- Genzyme
Pharmaprojects No. 6373 -- NIH	Prosaptide TX14(A) -- Bio-Tech. General
Pharmaprojects No. 6408 -- Pan Pacific	prostate cancer antibodies -- Immunex, UroCor
Pharmaprojects No. 6410 -- Athersys	prostate cancer antibody therapy -- Genentech/UroGenesys, Genotherapeutics
Pharmaprojects No. 6421 -- Oxford GlycoSciences	prostate cancer immunotherapeutics -- The PSMA Development Company
Pharmaprojects No. 6522 -- Maxygen	prostate cancer vaccine -- Aventis Pasteur, Zonagen, Corixa, Dendreon, Jenner
Pharmaprojects No. 6523 -- Pharis	Biotherapies, Therion Biologics
Pharmaprojects No. 6538 -- Maxygen	
Pharmaprojects No. 6554 -- APALEXO	
Pharmaprojects No. 6560 -- Ardana	
Pharmaprojects No. 6562 -- Bayer	
Pharmaprojects No. 6569 -- Eos	
Phenoxazine	
Phenylase -- Ibex	
Pigment epithelium derived factor -- plasminogen activator inhibitor-1, recombinant -- DuPont Pharmaceuticals	

FIG. 28X

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prostate-specific antigen -- EntreMed	RD 62198
protein A -- RepliGen	rDnase -- Genentech
protein adhesives -- Enzon	RDP-58 -- SangStat
protein C -- Baxter Intl., PPL Therapeutics,	RecepTox-Fce -- Keryx
ZymoGenetics	RecepTox-GnRH -- Keryx, MTR
protein C activator -- Gilead Sciences	Technologies
protein kinase R antags -- NIH	RecepTox-MBP -- Keryx, MTR
protirelin -- Takeda	Technologies
protocadherin 2 -- Caprion	recFSH -- Akzo Nobel, Organon
Pro-urokinase -- Abbott, Bristol-Myers	REGA 3G12
Squibb, Dainippon, Tosoh -- Welfide	Regavirumab -- Teijin
P-selectin glycoprotein ligand-1 -- Genetics	relaxin -- Connetics Corp
Institute	Renal cancer vaccine -- Macropharm
pseudomonal infections -- InterMune	repifermin -- Human Genome Sciences
Pseudomonas vaccine -- Cytovax	Respiratory syncytial virus PFP-2 vaccine --
PSGL-Ig -- American Home Products	Wyeth-Lederle
PSP-94 -- Procyon	Respiratory syncytial virus vaccine --
PTH 1-34 -- Nobex	GlaxoSmithKline, Pharmacia, Pierre Fabre
Quilimmune-M -- Antigenics	Respiratory syncytial virus vaccine
R 744 -- Roche	inactivated
R 101933	Respiratory syncytial virus-parainfluenza
R 125224 -- Sankyo	virus vaccine -- Aventis Pasteur,
RA therapy -- Cardion	Pharmacia
Rabies vaccine recombinant -- Aventis	Reteplase -- Boehringer Mannheim,
Pasteur, BioChem Vaccines, Kaketsuken	Hoffman La-Roche
Pharmaceuticals	Retropep -- Retroscreen
RadioTheraCIM -- YM BioSciences	RFB4 (dsFv) PE38
Ramot project No. 1315 -- Ramot	RFI 641 -- American Home Products
Ramot project No. K-734A -- Ramot	RFTS -- UAB Research Foundation
Ramot project No. K-734B -- Ramot	RG 12986 -- Aventis Pasteur
Ranibizumab (Anti-VEGF fragment) --	RG 83852 -- Aventis Pasteur
Genentech	RG-1059 -- RepliGen
RANK -- Immunex	rGCR -- NIH
ranpirnase -- Alfacell	rGLP-1 -- Restoragen
ranpirnase-anti-CD22 MAb -- Alfacell	rGRF -- Restoragen
RANTES inhibitor -- Milan	rh Insulin -- Eli Lilly
RAPID drug delivery systems -- ARIAD	RHAMM targeting peptides -- Cangene
rasburicase -- Sanofi	rHb1.1 -- Baxter Intl.
rBPI-21, topical -- XOMA	rhCC10 -- Claragen
RC 529 -- Corixa	rhCG -- Serono
rCFTR -- Genzyme Transgenics	Rheumatoid arthritis gene therapy

FIG. 28Y

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Rheumatoid arthritis vaccine -- Veterans Affairs Medical Center	SB RA 31012 --
rhLH -- Serono	SC 56929 -- Pharmacia
Ribozyme gene therapy -- Genset	SCA binding proteins -- Curis, Enzon
Rickettsial vaccine recombinant	scFv(14E1)-ETA Berlex Laboratories, Schering AG
RIGScan CR -- Neoprobe	ScFv(FRP5)-ETA --
RIP-3 -- Rigel	ScFv6C6-PE40 --
Rituximab -- Genentech	SCH 55700 -- Celltech
RK-0202 -- RxKinetix	Schistosomiasis vaccine -- Glaxo Wellcome/Medeva, Brazil
RLT peptide -- Esperion	SCPF -- Advanced Tissue Sciences
rM/NEI -- IVAX	scuPA-suPAR complex -- Hadasit
rmCRP -- Immtech	SD-9427 -- Pharmacia
RN-1001 -- Renovo	SDF-1 -- Ono
RN-3 -- Renovo	SDZ 215918 -- Novartis
RNase conjugate -- Immunomedics	SDZ 280125 -- Novartis
RO 631908 -- Roche	SDZ 89104 -- Novartis
Rotavirus vaccine -- Merck	SDZ ABL 364 -- Novartis
RP 431 -- DuPont Pharmaceuticals	SDZ MMA 383 -- Novartis
RP-128 -- Resolution	Secretin -- Ferring, Repligen
RPE65 gene therapy --	serine protease inhbs -- Pharis
RPR 110173 -- Aventis Pasteur	sermorelin acetate -- Serono
RPR 115135 -- Aventis Pasteur	SERP-1 -- Viron
RPR 116258A -- Aventis Pasteur	sertenef -- Daiippon
rPSGL-Ig -- American Home Products	serum albumin, Recombinant human -- Aventis Behring
r-SPC surfactant -- Byk Gulden	serum-derived factor -- Hadasit
RSV antibody -- Medimmune	Sevirumab -- Novartis
Ruplizumab -- Biogen	SGN 14 -- Seattle Genetics
rV-HER-2/neu -- Therion Biologics	SGN 15 -- Seattle Genetics
SA 1042 -- Sankyo	SGN 17/19 -- Seattle Genetics
sacrosidase -- Orphan Medical	SGN 30 -- Seattle Genetics
Sant 7	SGN-10 -- Seattle Genetics
Sargramostim -- Immunex	SGN-11 -- Seattle Genetics
saruplase -- Gruenenthal	SH 306 -- DuPont Pharmaceuticals
Satumomab -- Cytogen	Shanvac-B -- Shantha
SB 1 -- COR Therapeutics	Shigella flexneri vaccine -- Avant, Acambis, Novavax
SB 207448 -- GlaxoSmithKline	Shigella sonnei vaccine --
SB 208651 -- GlaxoSmithKline	siCAM-1 -- Boehringer Ingelheim
SB 240683 -- GlaxoSmithKline	Silteplase -- Genzyme
SB 249415 -- GlaxoSmithKline	
SB 249417 -- GlaxoSmithKline	
SB 6 -- COR Therapeutics	

FIG. 28Z

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SIV vaccine -- Endocon, Institut Pasteur	Staphylococcus aureus vaccine conjugate --
SK 896 -- Sanwa Kagaku Kenkyusho	Nabi
SK-827 -- Sanwa Kagaku Kenkyusho	Staphylococcus therapy -- Tripep
Skeletex -- CellFactors	Staphylokinase -- Biovation, Prothera,
SKF 106160 -- GlaxoSmithKline	Thrombogenetics
S-nitroso-AR545C --	Streptococcal A vaccine -- M6
SNTP -- Active Biotech	Pharmaceuticals, North American Vaccine
somatomedin-1 -- GroPep, Mitsubishi-	Streptococcal B vaccine -- Microscience
Tokyo, NIH	Streptococcal B vaccine recombinant --
somatomedin-1 carrier protein -- Insmmed	Biochem Vaccines
somatostatin -- Ferring	Streptococcus pyogenes vaccine
Somatotropin/	STRL-33 -- NIH
Human Growth Hormone -- Bio-Tech.	Subalin -- SRC VB VECTOR
General, Eli Lilly	SUIS -- United Biomedical
somatropin -- Bio-Tech. General, Alkermes,	SUIS-LHRH -- United Biomedical
ProLease, Aventis Behring, Biovector,	SUN-E3001 -- Suntory
Cangene, Dong-A, Eli Lilly, Emisphere,	super high affinity monoclonal antibodies --
Enact, Genentech, Genzyme Transgenics,	YM BioSciences
Grandis/InfiMed, CSL, InfiMed, MacroMed,	Superoxide dismutase -- Chiron, Enzon,
Novartis, Novo Nordisk, Pharmacia	Ube Industries, Bio-Tech, Yeda
Serono, TranXenoGen	superoxide dismutase-2 -- OXIS
somatropin derivative -- Schering AG	suppressin -- UAB Research Foundation
somatropin, AIR -- Eli Lilly	SY-161-P5 -- ThromboGenics
Somatropin, inhaled -- Eli Lilly/Alkermes	SY-162 -- ThromboGenics
somatropin, Kabi -- Pharmacia	Systemic lupus erythematosus vaccine --
somatropin, Orasome -- Novo Nordisk	MedClone/VivoRx
Sonermin -- Dainippon Pharmaceutical	T cell receptor peptides -- Xoma
SP(V5.2)C -- Supertek	T cell receptor peptide vaccine
SPf66	T4N5 liposomes -- AGI Dermatics
sphingomyelinase -- Genzyme	TACI, soluble -- ZymoGenetics
SR 29001 -- Sanofi	targeted apoptosis -- Antisoma
SR 41476 -- Sanofi	tasonermin -- Boehringer Ingelheim
SR-29001 -- Sanofi	TASP
SS1(dsFV)-PE38 -- NeoPharm	TASP-V
β 2 microglobulin -- Avidex	Tat peptide analogues -- NIH
β 2-microglobulin fusion proteins -- NIH	TBP I -- Yeda
β -amyloid peptides -- CeNeS	TBP II
β -defensin -- Pharis	TBV25H -- NIH
Staphylococcus aureus infections --	Tc 99m ior cea1 -- Center of Molecular
Inhibitex/ZLB	Immunology
	Tc 99m P 748 -- Diatide

FIG. 28AA

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Tc 99m votumumab -- Intracell	Tissue factor -- Genentech
Tc-99m rh-Annexin V -- Theseus Imaging	Tissue factor pathway inhibitor
teceleukin -- Biogen	TJN-135 -- Tsumura
tenecteplase -- Genentech	TM 27 -- Avant
Teriparatide -- Armour Pharmaceuticals, Asahi Kasei, Eli Lilly	TM 29 -- Avant
terlipressin -- Ferring	TMC-151 -- Tanabe Seiyaku
testisin -- AMRAD	TNF tumour necrosis factor -- Asahi Kasei
Tetra fibrin -- Roche	TNF Alpha -- Cytimmune
TFPI -- EntreMed	TNF antibody -- Johnson & Johnson
tgD-IL-2 -- Takeda	TNF binding protein -- Amgen
TGF-Alpha -- ZymoGenetics	TNF degradation product -- Oncotech
TGF- β -- Kolon	TNF receptor -- Immunex
TGF- β 2 -- Insmed	TNF receptor 1, soluble -- Amgen
TGF- β 3 -- OSI	TNF Tumour necrosis factor-alpha -- Asahi Kasei, Genentech, Mochida
Thalassaemia gene therapy -- Crucell	TNF-Alpha inhibitor -- Tripep
TheraCIM-h-R3 -- Center of Molecular Immunology, YM BioSciences	TNFR:Fc gene therapy -- Targeted Genetics
Theradigm-HBV -- Epimmune	TNF-SAM2
Theradigm-HPV -- Epimmune	Tolerimab -- Innogenetics
Theradigm-malaria -- Epimmune	Toxoplasma gondii vaccine -- GlaxoSmithKline
Theradigm-melanoma -- Epimmune	TP 9201 -- Telios
TheraFab -- Antisoma	TP10 -- Avant
ThGRF 1-29 -- Theratechnologies	TP20 -- Avant
ThGRF 1-44 -- Theratechnologies	tPA -- Centocor
Thrombin receptor activating peptide -- Abbott	trafermin -- Scios
thrombomodulin -- Iowa, Novocastra	TRAIL/Apo2L -- Immunex
Thrombopoietin -- Dragon Pharmaceuticals, Genentech	TRAIL-R1 MAb -- Cambridge Antibody Technologies
thrombopoietin, Pliva -- Recepton	transferrin-binding proteins -- CAMR
Thrombospondin 2 --	Transforming growth factor-beta-1 -- Genentech
thrombostatin -- Thromgen	transport protein -- Genesis
thymalfasin -- SciClone	Trastuzumab -- Genentech
thymocartin -- Gedeon Richter	TRH -- Ferring
thymosin Alpha1 -- NIH	Triabin -- Schering AG
thyroid stimulating hormone -- Genzyme	Triconal
tICAM-1 -- Bayer	Triflavin
Tick anticoagulant peptide -- Merck	troponin I -- Boston Life Sciences
TIF -- Xoma	TRP-2 ^A -- NIH
Tifacogin -- Chiron, NIS, Pharmacia	trypsin inhibitor -- Mochida

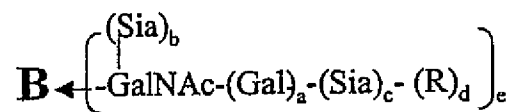
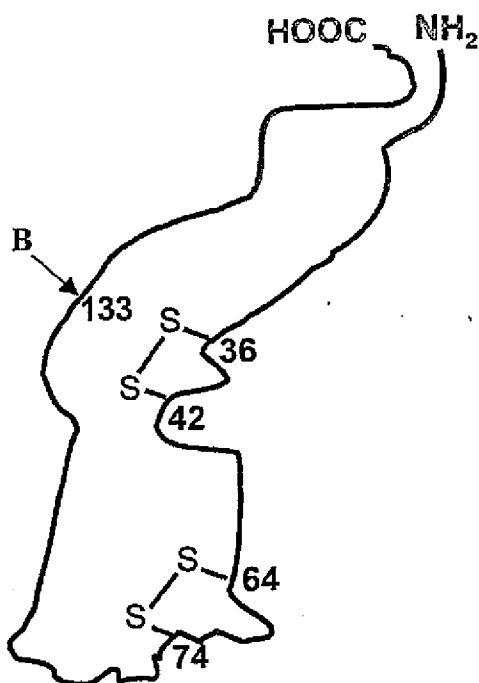
FIG. 28BB

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TSP-1 gene therapy –	Vascular endothelial growth factors – R&D
TT-232	Systems
TTS-CD2 – Active Biotech	vascular targeting agents – Peregrine
Tuberculosis vaccine – Aventis Pasteur,	vasopermeation enhancement agents --
Genesis	Peregrine
Tumor Targeted Superantigens – Active	vasostatin – NIH
Biotech – Pharmacia	VCL – Bio-Tech. General
tumour vaccines – PhotoCure	VEGF – Genentech, Scios
tumour-activated prodrug antibody	VEGF inhibitor – Chugai
conjugates – Millennium/ImmunoGen	VEGF-2 – Human Genome Sciences
tumstatin – ILEX	VEGF-Trap – Regeneron
Tuvirumab – Novartis	viscumin, recombinant – Madaus
TV-4710 – Teva	Vitaxin
TWEAK receptor -- Immunex	Vitrax -- ISTA Pharmaceuticals
TXU-PAP	West Nile virus vaccine -- Bavarian Nordic
TY-10721 – TOA Eiyo	WP 652
Type I diabetes vaccine -- Research Corp	WT1 vaccine -- Corixa
Typhoid vaccine CVD 908	WX-293 – Willex BioTech.
U 143677 -- Pharmacia	WX-360 -- Willex BioTech.
U 81749 -- Pharmacia	WX-UK1 – Willex BioTech.
UA 1248 – Arizona	XMP-500 – XOMA
UGIF – Sheffield	XomaZyme-791 – XOMA
UIC 2	XTL 001 – XTL Biopharmaceuticals
UK 101	XTL 002 – XTL Biopharmaceuticals
UK-279276 – Corvas Intl.	yeast delivery system -- GlobelImmune
urodilatin – Pharis	Yersinia pestis vaccine
urofollitrophin – Serono	YIGSR-Stealth – Johnson & Johnson
Urokinase – Abbott	Yisum Project No. D-0460 -- Yisum
uteroferrin-- Pepgen	YM 207 – Yamanouchi
V 20 – GLYCODesign	YM 337 -- Protein Design Labs
V2 vasopressin receptor gene therapy	Yttrium-90 labelled biotin
vaccines -- Active Biotech	Yttrium-90-labeled anti-CEA MAb T84.66 –
Varicella zoster glycoprotein vaccine --	ZD 0490 – AstraZeneca
Research Corporation Technologies	ziconotide – Elan
Varicella zoster virus vaccine live – Cantab	ZK 157138 -- Berlex Laboratories
Pharmaceuticals	Zolimomab aritox
Vascular endothelial growth factor –	Zorcell – Immune Response
Genentech, University of California	ZRXL peptides -- Novartis

FIG. 28CC

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a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, sialyl or
oligosialyl

FIG. 29A

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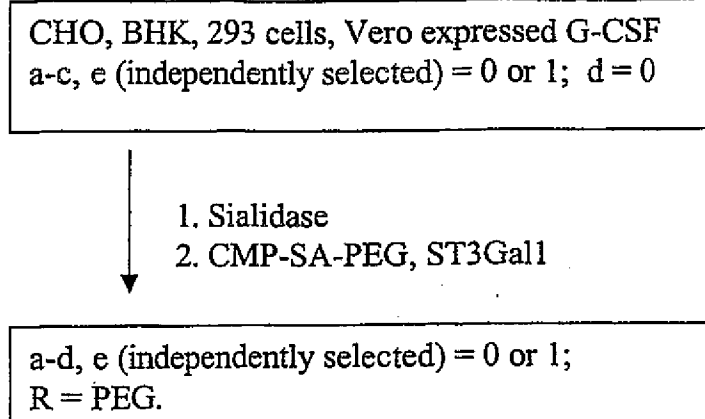


FIG. 29B

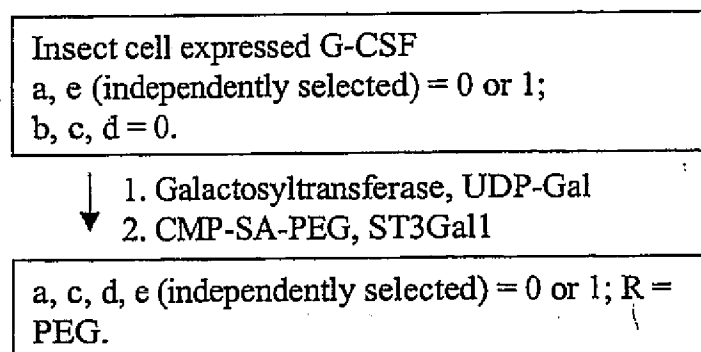


FIG. 29C

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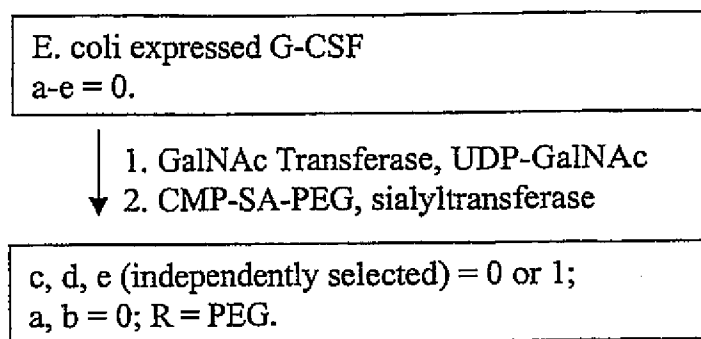


FIG. 29D

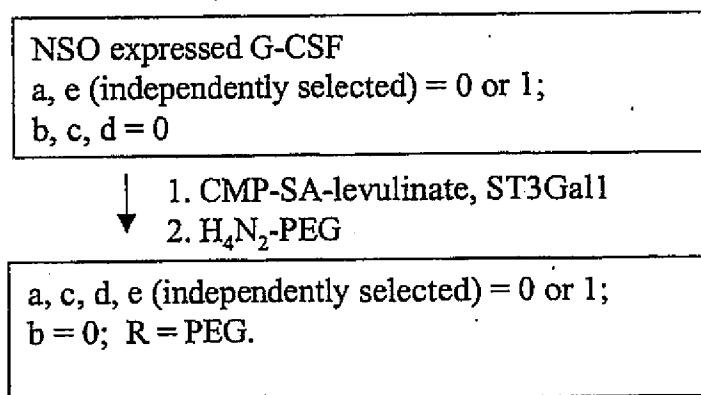


FIG. 29E

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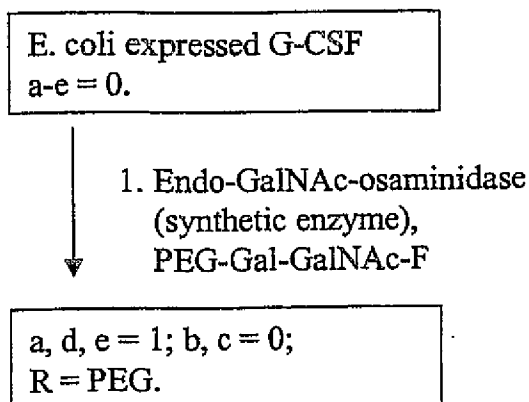


FIG. 29F

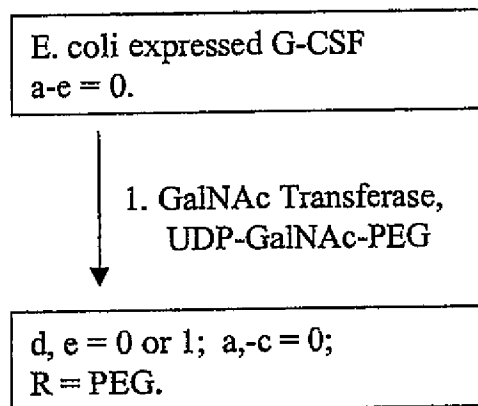
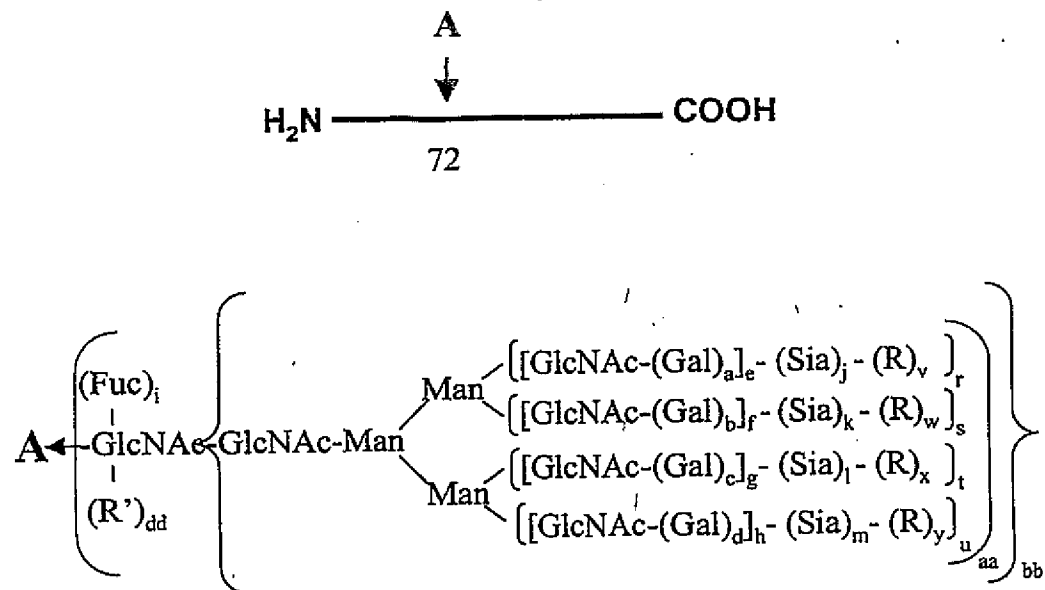


FIG. 29G

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a-d, i, n-u (independently selected) = 0 or 1.

aa, bb, cc, dd, ee (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 30A

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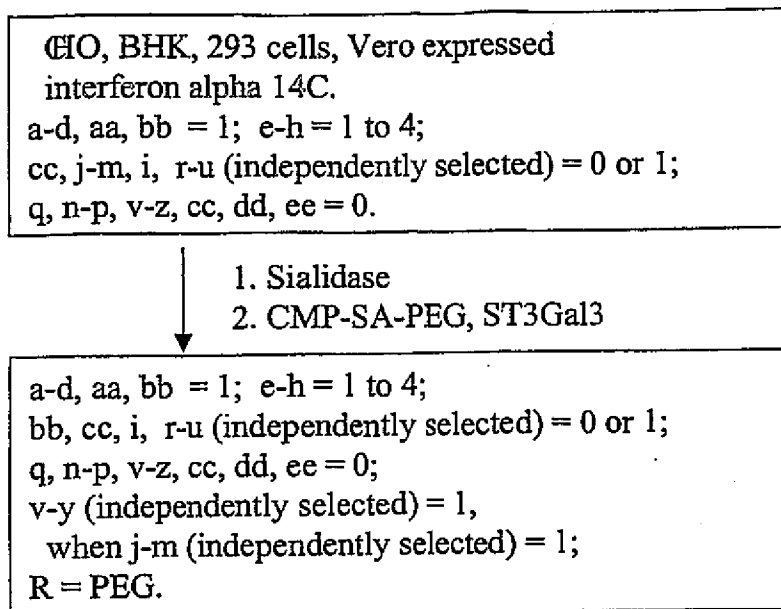


FIG. 30B

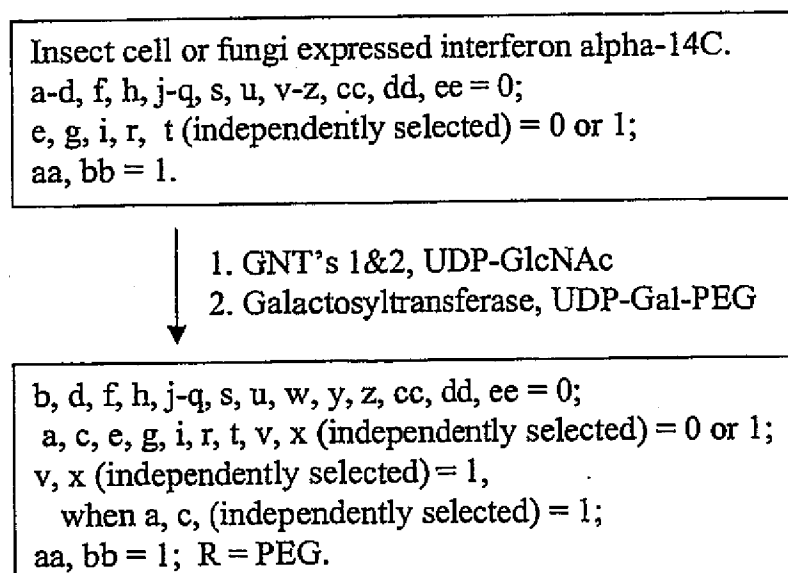


FIG. 30C

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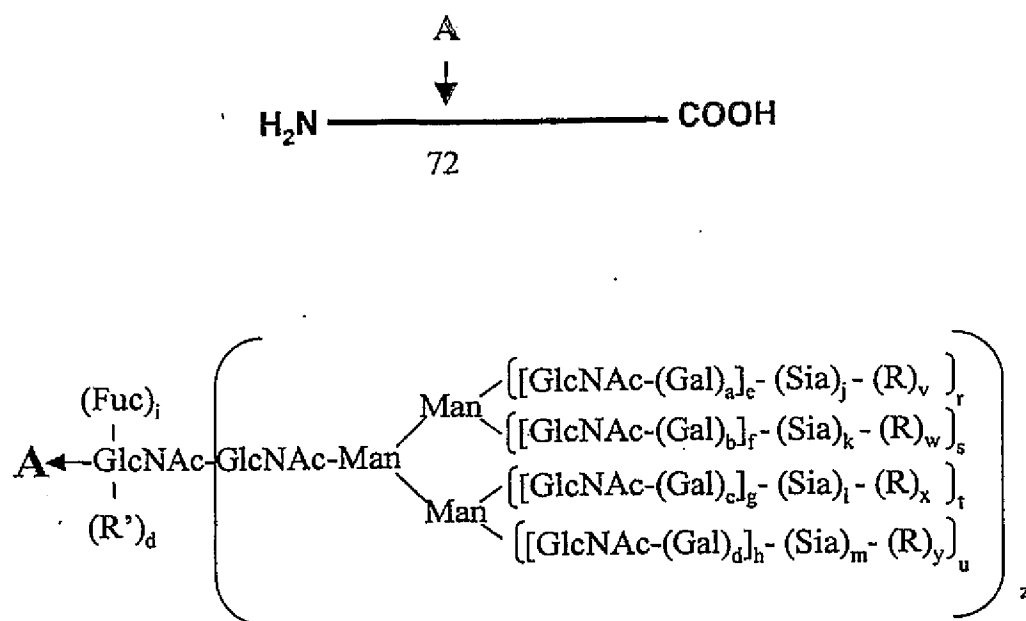
Yeast expressed interferon alpha-14C.
a-q, cc, dd, ee, v-z = 0;
r-y (independently selected) = 0 to 1;
aa, bb = 1;
R (branched or linear) = Man, oligomannose or
polysaccharide.

- ↓
1. Endo-H
2. Galactosyltransferase, UDP-Gal
3.. CMP-SA-PEG, ST3Gal3

a-z, bb = 0; aa = 1; R' = -Gal-Sia-PEG.

FIG. 30D

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1.

R = polymer; R' = sugar, glycoconjugate.

FIG. 30E

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CHO, BHK, 293 cells, Vero expressed
interferon alpha-14C.

$h = 1$ to 3 ;

$a-g, j-m, i$ (independently selected) = 0 or 1 ;

$r-u$ (independently selected) = 0 or 1 ;

$n, v-y = 0; z = 1$.



1. CMP-SA-PEG, ST3Gal3

$h = 1$ to 3 ;

$a-g, i$ (independently selected) = 0 or 1 ;

$r-u$ (independently selected) = 0 or 1 ;

$j-m, v-y$ (independently selected) = 0 or 1 ;

$z = 1; n = 0; R = \text{PEG}$.

FIG. 30F

Insect cell or fungi expressed
interferon alpha-14C.

$a-d, f, h, j-n, s, u, v-y = 0$;

e, g, i, r, t (independently selected) = 0 or 1 ;

$z = 1$.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

$a-m, r-y$ (independently selected) = 0 or 1 ;

$z = 1; n = 0; R = \text{PEG}$.

FIG. 30G

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Yeast expressed interferon alpha-14C.

a-n = 0; r-y (independently selected) = 0 to 1;
z = 1; R (branched or linear) = Man,
oligomannose.

1. mannosidases
2. GNT's 1,2,4,5, UDP-GlcNAc
3. Galactosyltransferase, UDP-Gal
4. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
z = 1; n = 0; R = PEG.

FIG. 30H

NSO expressed interferon alpha 14C.

a-i, r-u (independently selected) = 0 or 1;
j-m, n, v-y = 0; z = 1.

1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
2. H₄N₂-PEG

a-i, j-m, r-y (independently selected) = 0 or 1;
n = 0; z = 1; R = PEG.

FIG. 30I

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CHO, BHK, 293 cells, Vero expressed
interferon alpha-14C.
h = 1 to 3;
a-g, j-m, i (independently selected) = 0 or 1;
r-u (independently selected) = 0 or 1;
n, v-y = 0; z = 1.



1. CMP-SA-PEG, α 2,8-ST

h = 1 to 3;
a-g, i, r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0 to 2;
v-y (independently selected) = 1,
when j-m (independently selected) is 2;
z = 1; n = 0; R = PEG.

FIG. 30J

CHO, BHK, 293 cells, Vero expressed
Interferon alpha-14C.
a-g, j-m, r-u (independently selected) = 0 or 1;
h = 1 to 3; n, v-y = 0; z = 1.



1. Sialidase
2. Trans-sialidase, PEG-Sia-lactose

a-g, j-m, r-y (independently selected) = 0 or 1;
h = 1 to 3; n = 0; z = 1; R = PEG.

FIG. 30K

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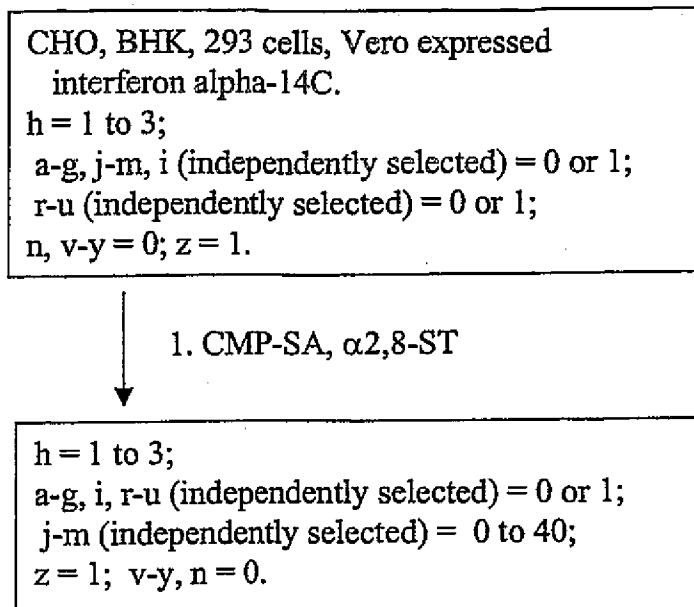


FIG. 30L

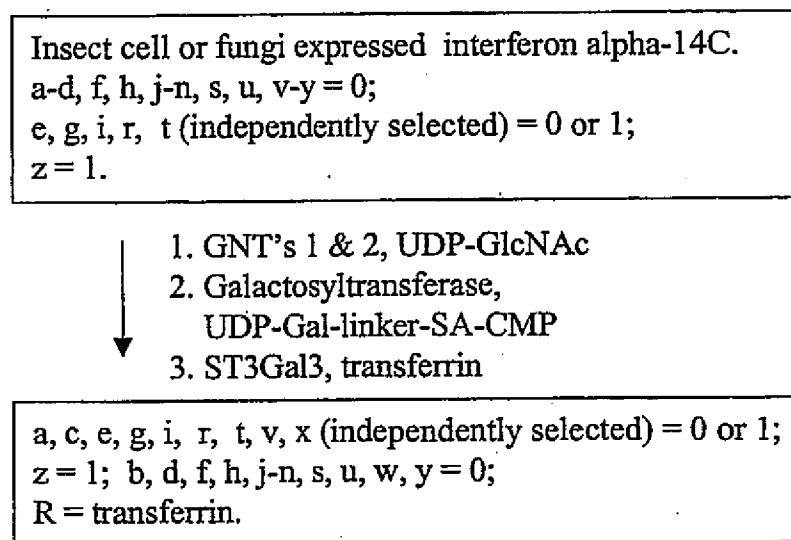


FIG. 30M

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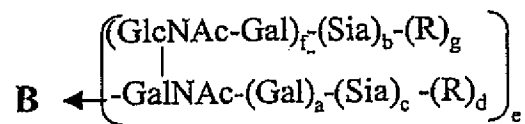
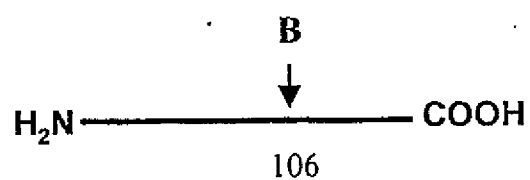
Insect cell or fungi expressed interferon alpha-14C.
a-d, f, h, j-n, s, u, v-y = 0;
e, g, i, r, t (independently selected) = 0 or 1; z = 1.

- ↓
1. endoglycanase
 2. Galactosyltransferase,
UDP-Gal-linker-SA-CMP
 3. ST3Gal3, transferrin

i (independently selected) = 0 or 1;
a-h, j-m, r-z = 0;
n = 1; R' = -Gal-linker-transferrin.

FIG. 30N

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a-c, e, f (independently selected) = 0 or 1;
 d, g = 0; R = polymer, glycoconjugate.

FIG. 300

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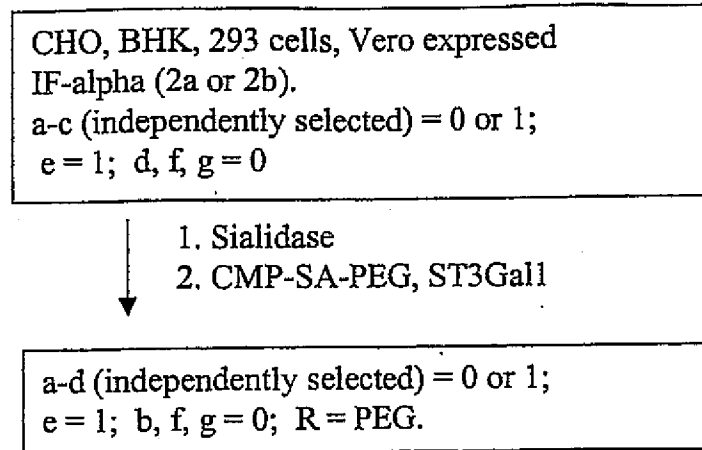


FIG. 30P

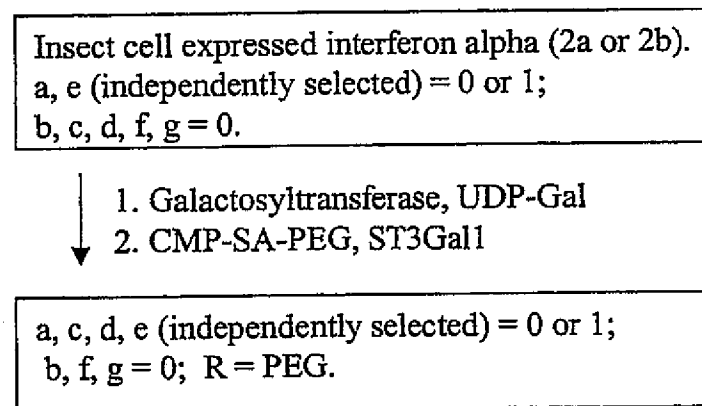


FIG. 30Q

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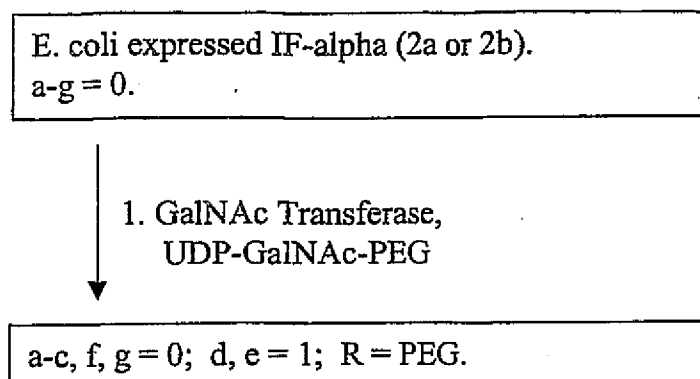


FIG. 30R

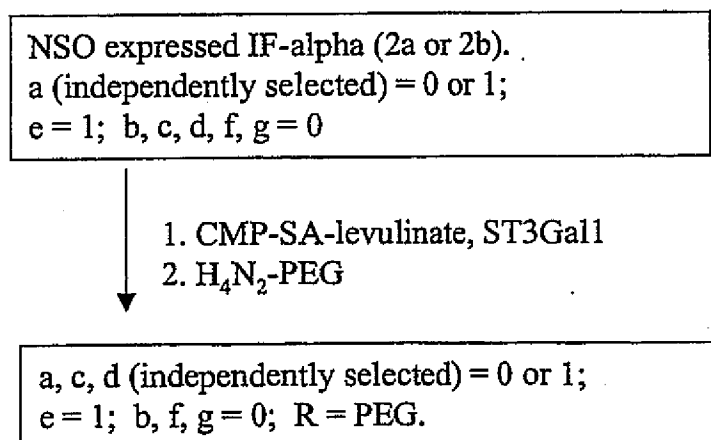


FIG. 30S

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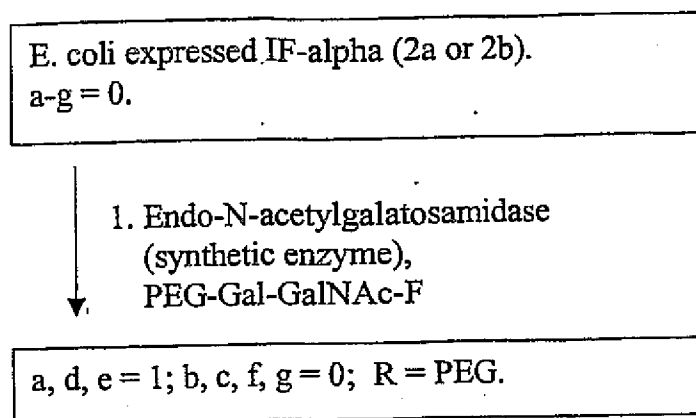


FIG. 30T

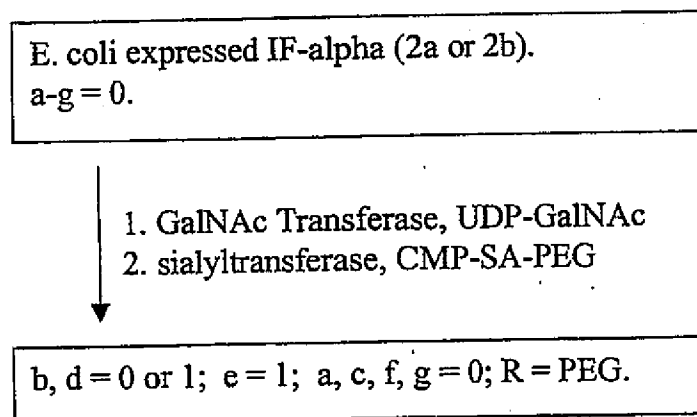


FIG. 30U

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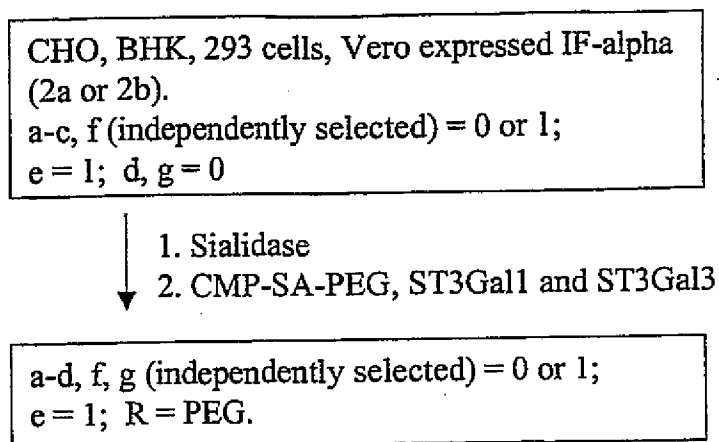


FIG. 30V

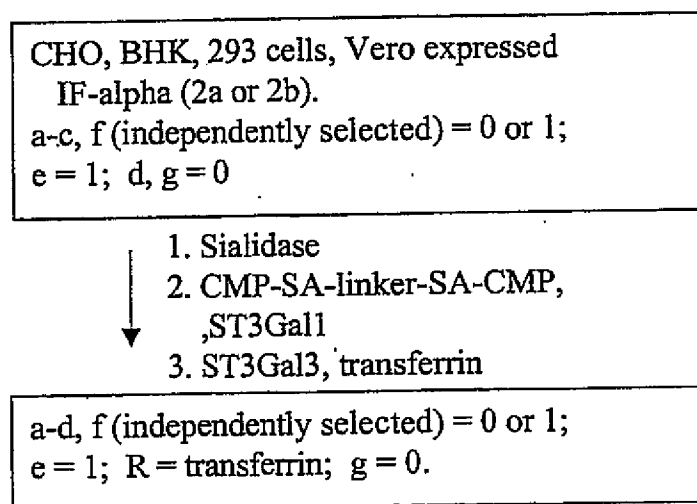


FIG. 30W

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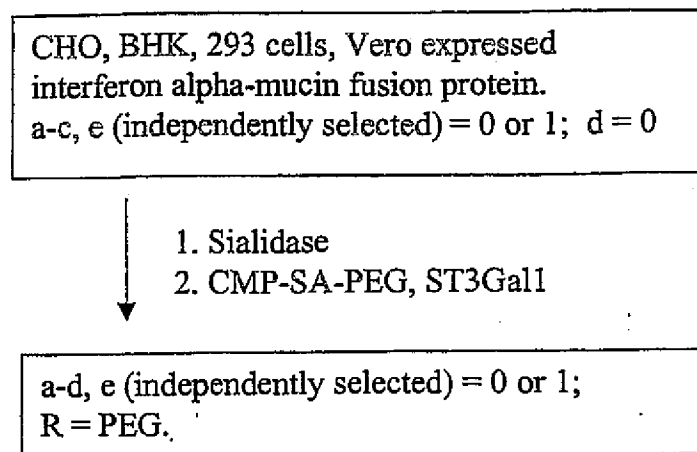


FIG. 30Y

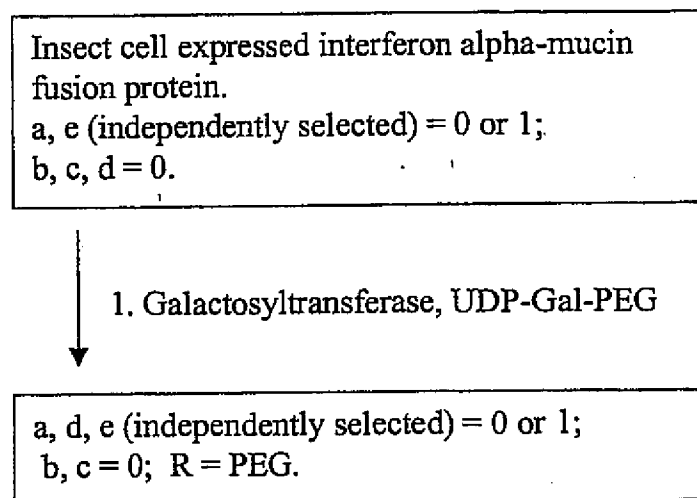


FIG. 30Z

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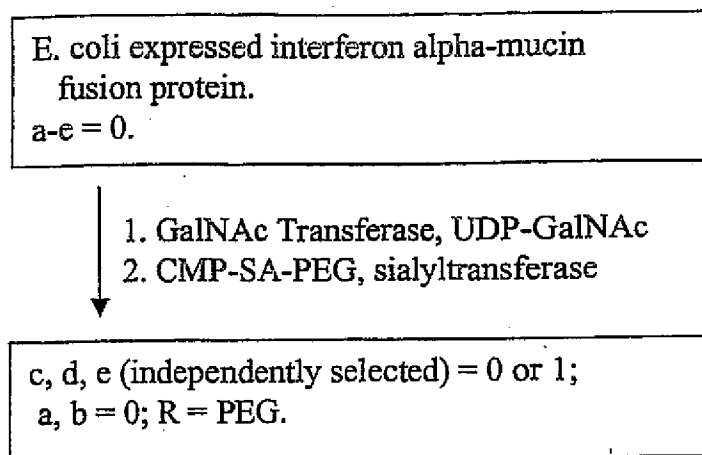
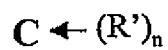
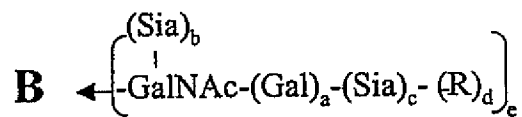
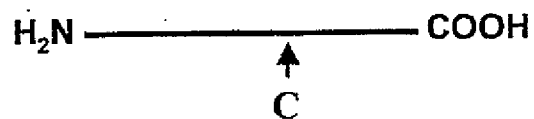
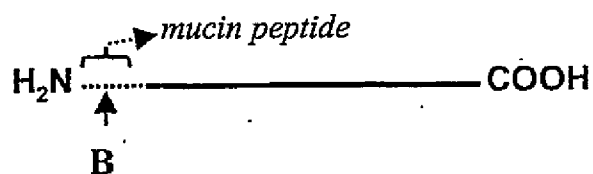
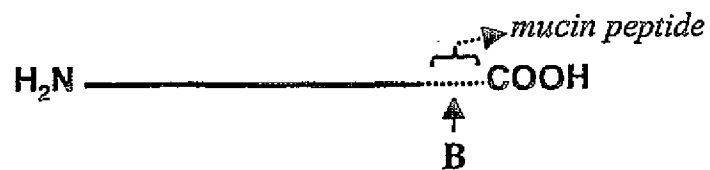


FIG. 30AA

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a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 30BB

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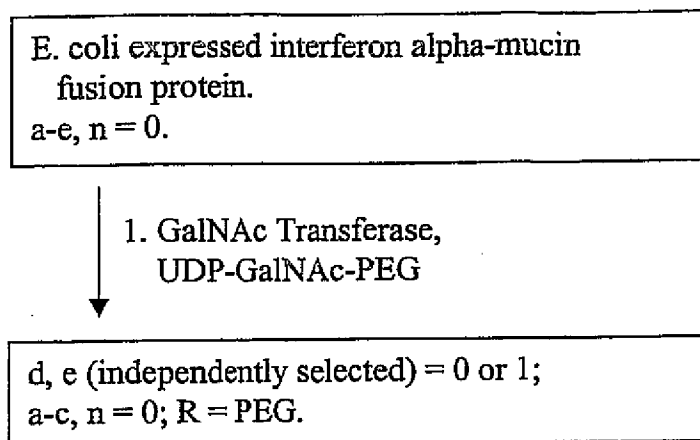


FIG. 30CC

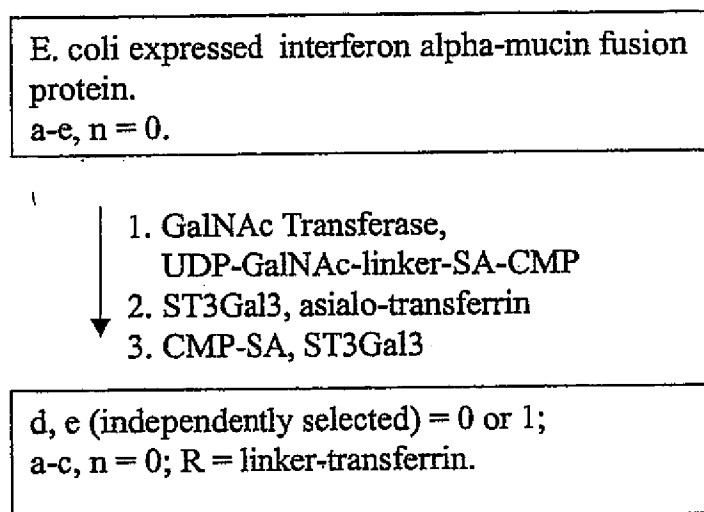


FIG. 30DD

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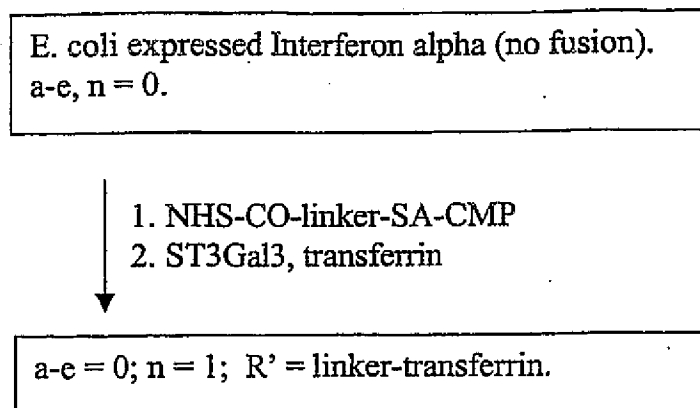
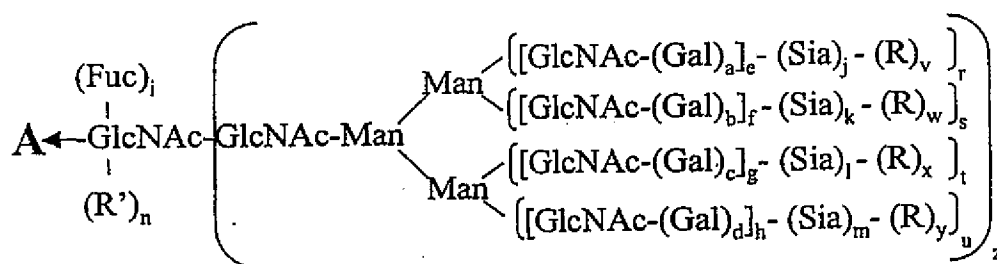
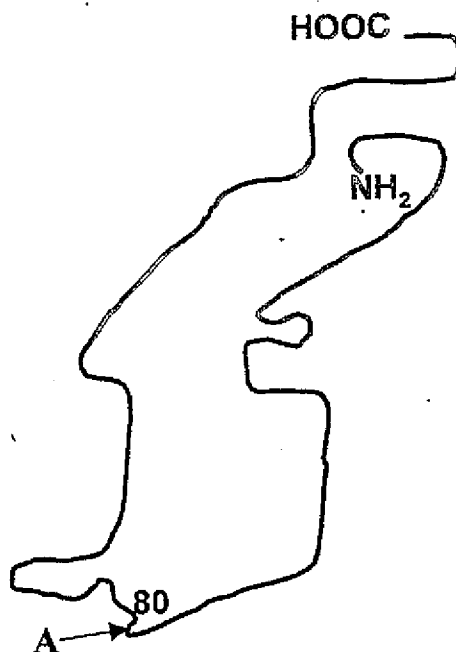


FIG. 30EE

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer

FIG. 31A

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CHO, BHK, 293 cells, Vero expressed IF-beta
 h = 1 to 3;
 a-g, j-m, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 n, v-y = 0; z = 1.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

h = 1 to 3;
 a-g, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 j-m, v-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 31B

Insect cell expressed IF-beta
 a-d, f, h, j-n, s, u, v-y = 0;
 e, g, i, r, t (independently selected) = 0 or 1;
 z = 1.



1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
2. CMP-SA-PEG, ST3Gal3,
buffer, salt

b, d, f, h, k, m, n, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 j, l, v, x (independently selected) = 0 or 1;
 z = 1; R = PEG.

FIG. 31C

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Yeast expressed IF-beta

a-n = 0; z = 1;

r-y (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; n = 1; R' = -Gal-Sia-PEG.

FIG. 31D

CHO, BHK, 293 cells, Vero expressed IF-beta

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.

- ↓
1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;

a-g, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

j-m, v-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 31E

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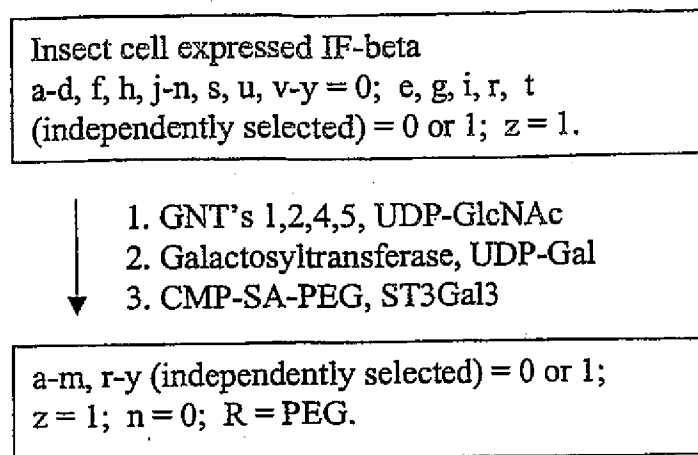


FIG. 31F

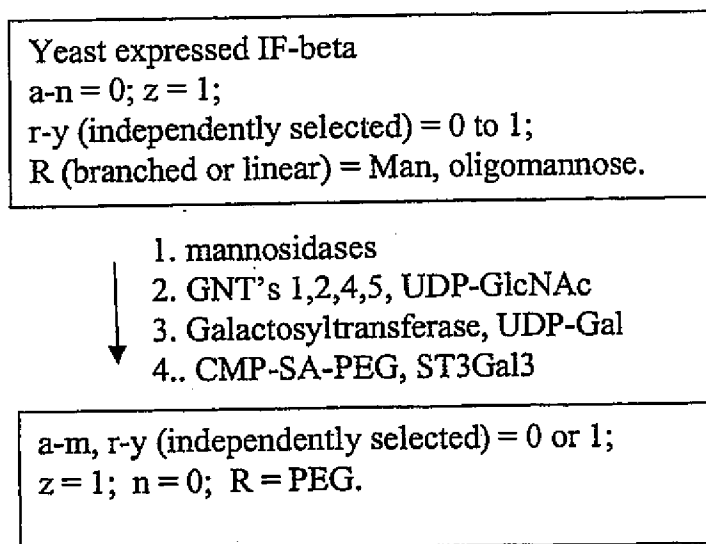


FIG. 31G

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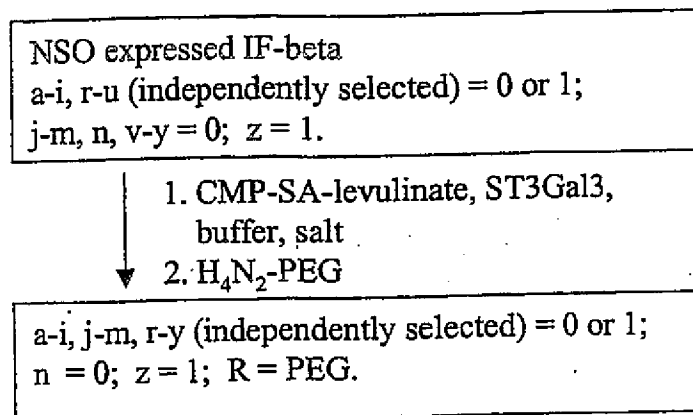


FIG. 31H

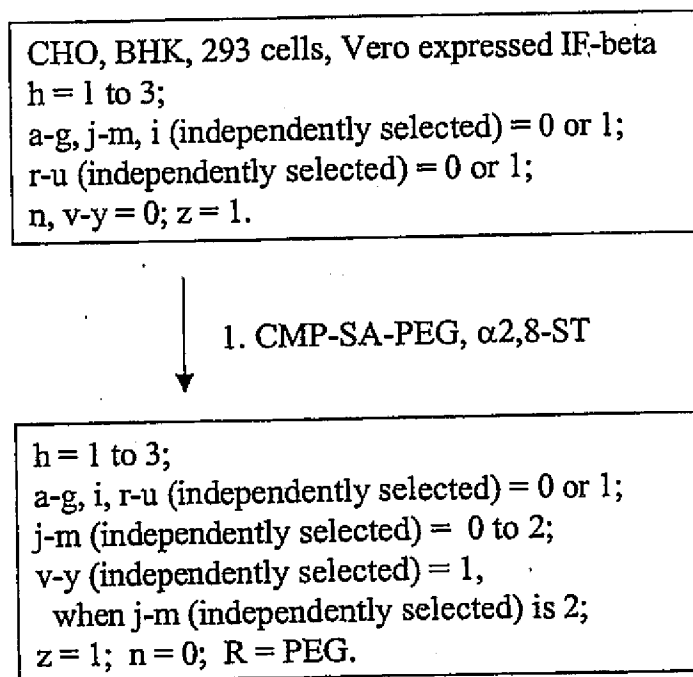


FIG. 31I

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CHO, BHK, 293 cells, Vero expressed IF-beta
 a-g, j-m, r-u (independently selected) = 0 or 1;
 h = 1 to 3; n, v-y = 0; z = 1.



1. Sialidase
2. Trans-sialidase, PEG-Sia-lactose

a-g, j-m, r-y (independently selected) = 0 or 1;
 h = 1 to 3; n = 0; z = 1; R = PEG.

FIG. 31J

CHO, BHK, 293 cells, Vero expressed Ifn-beta.
 a-d, i-m, r-u, z (independently selected) = 0 or 1;
 e-h = 1; n, v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;
 e-h = 1; n=0;
 v-y (independently selected) = 0 or 1; R = PEG.

FIG. 31K

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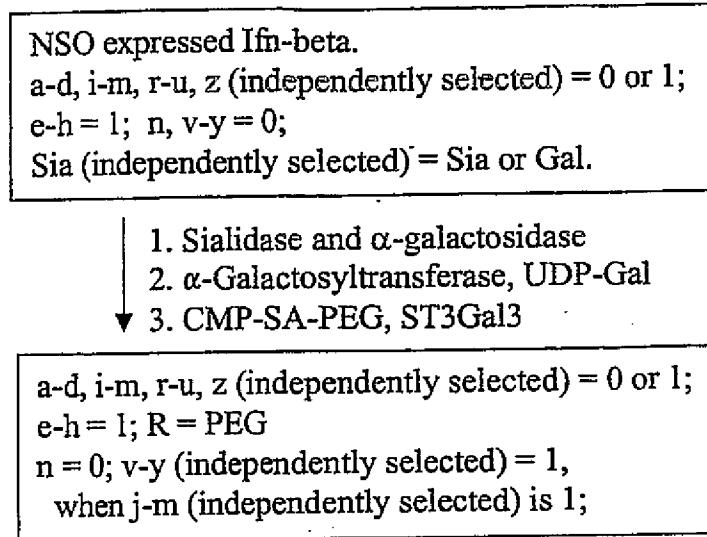


FIG. 31L

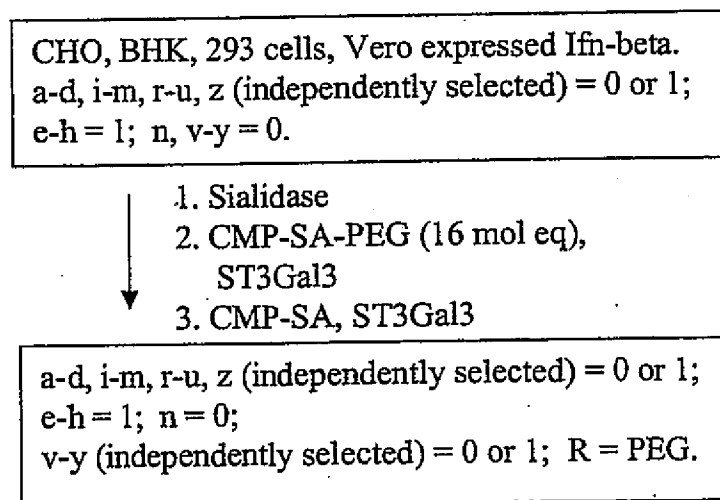


FIG. 31M

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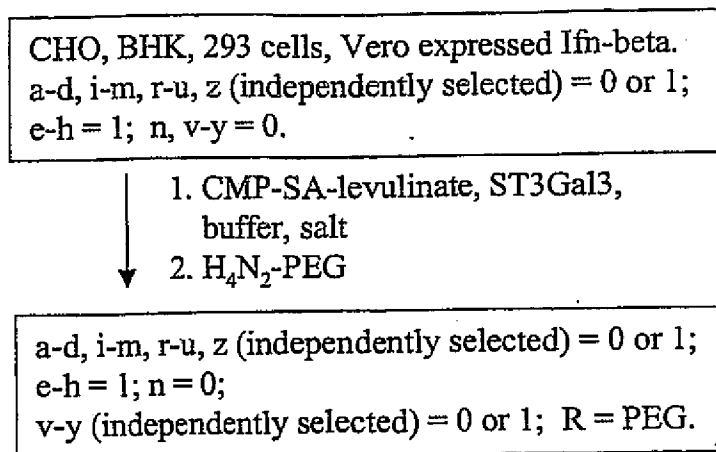


FIG. 31N

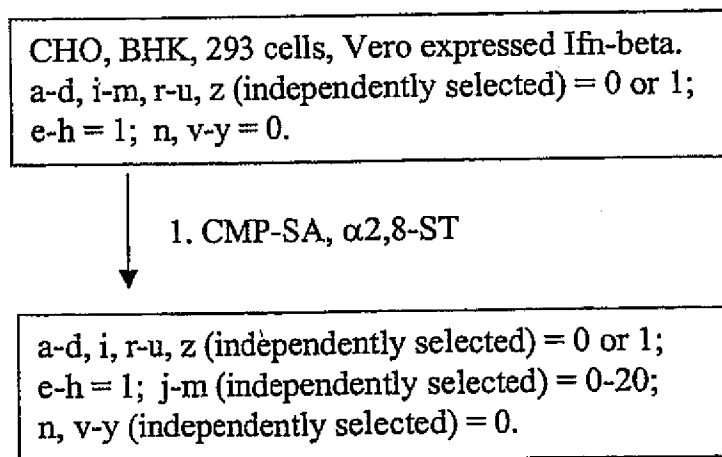
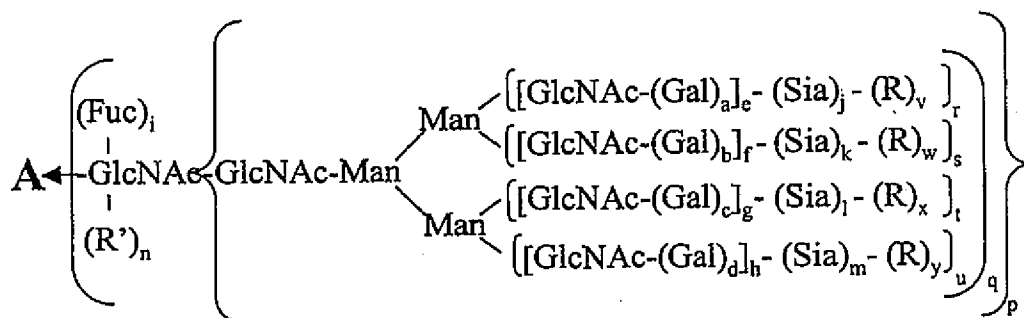
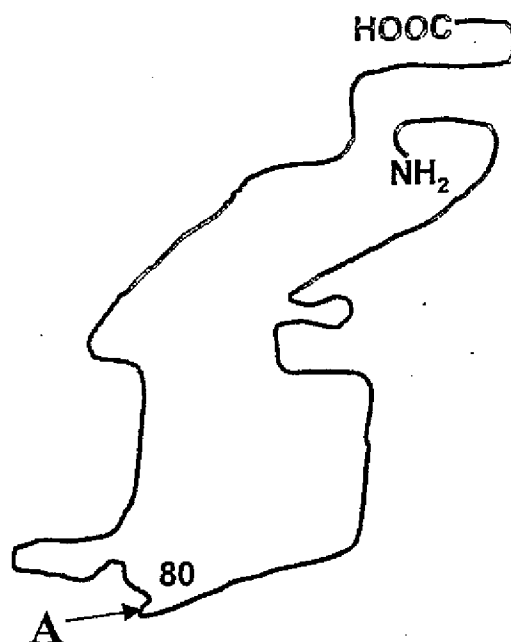


FIG. 31O

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a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

 $v-y=0$; R = modifying group;

R' = H, glycosyl group, modifying group,

glycoconjugate.

FIG. 31P

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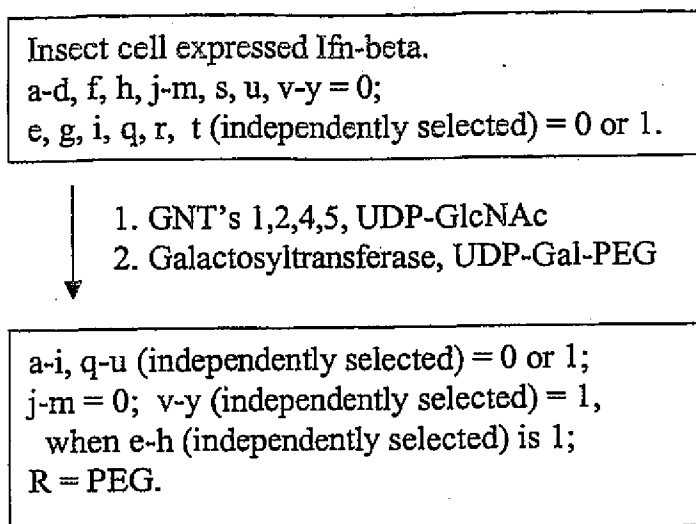


FIG. 31Q

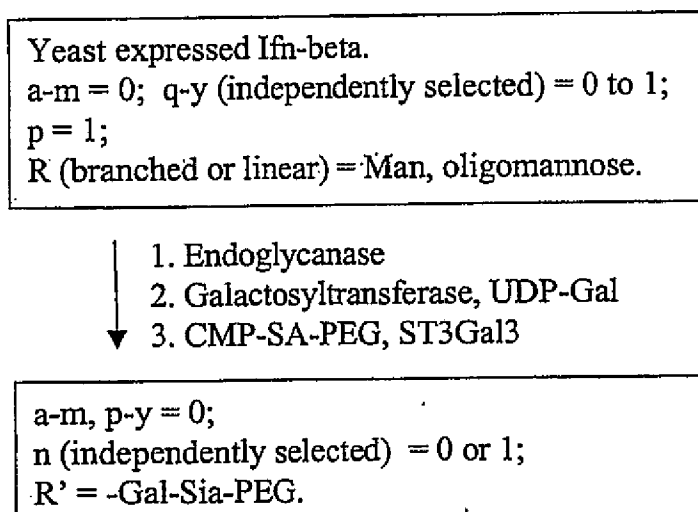


FIG. 31R

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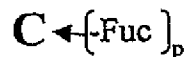
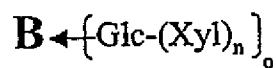
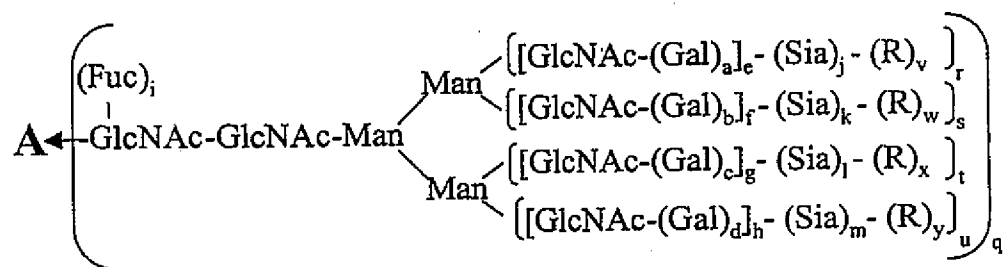
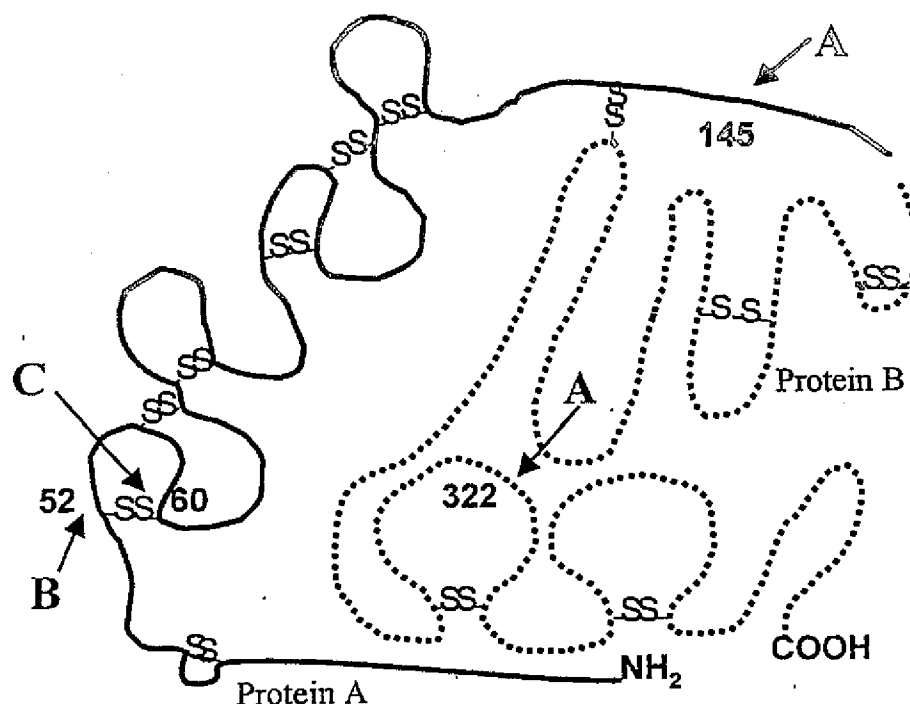
CHO, BHK, 293 cells, Vero expressed Ifn-beta.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 31S

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a-d, i, q-u (independently selected) = 0 or 1.

o, p (independently selected) = 0 or 1.

e-h, n (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-y = 0;

R = modifying group, mannose, oligo-mannose, Sia-Lewis X, Sia-Lewis A..

FIG. 32A

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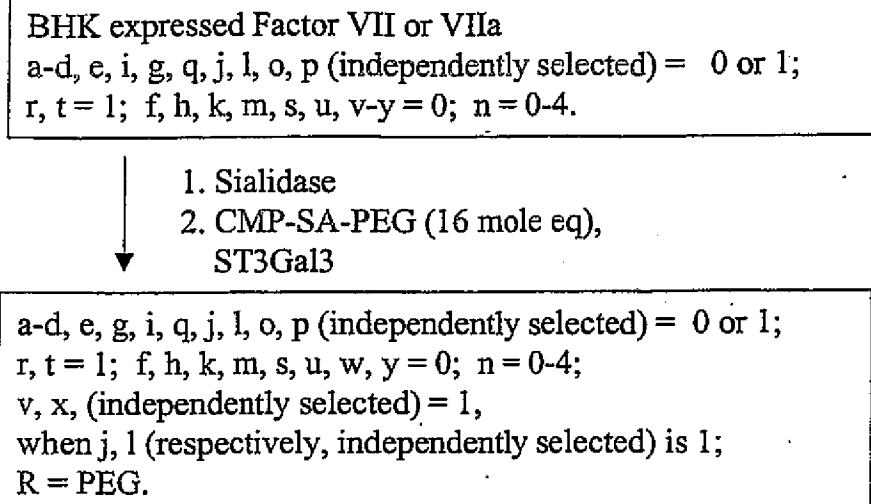


FIG. 32B

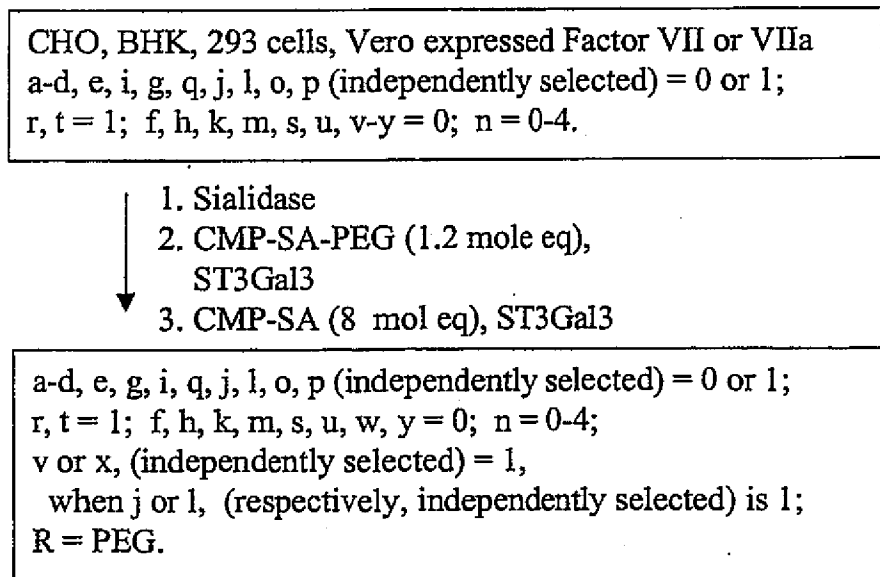


FIG. 32C

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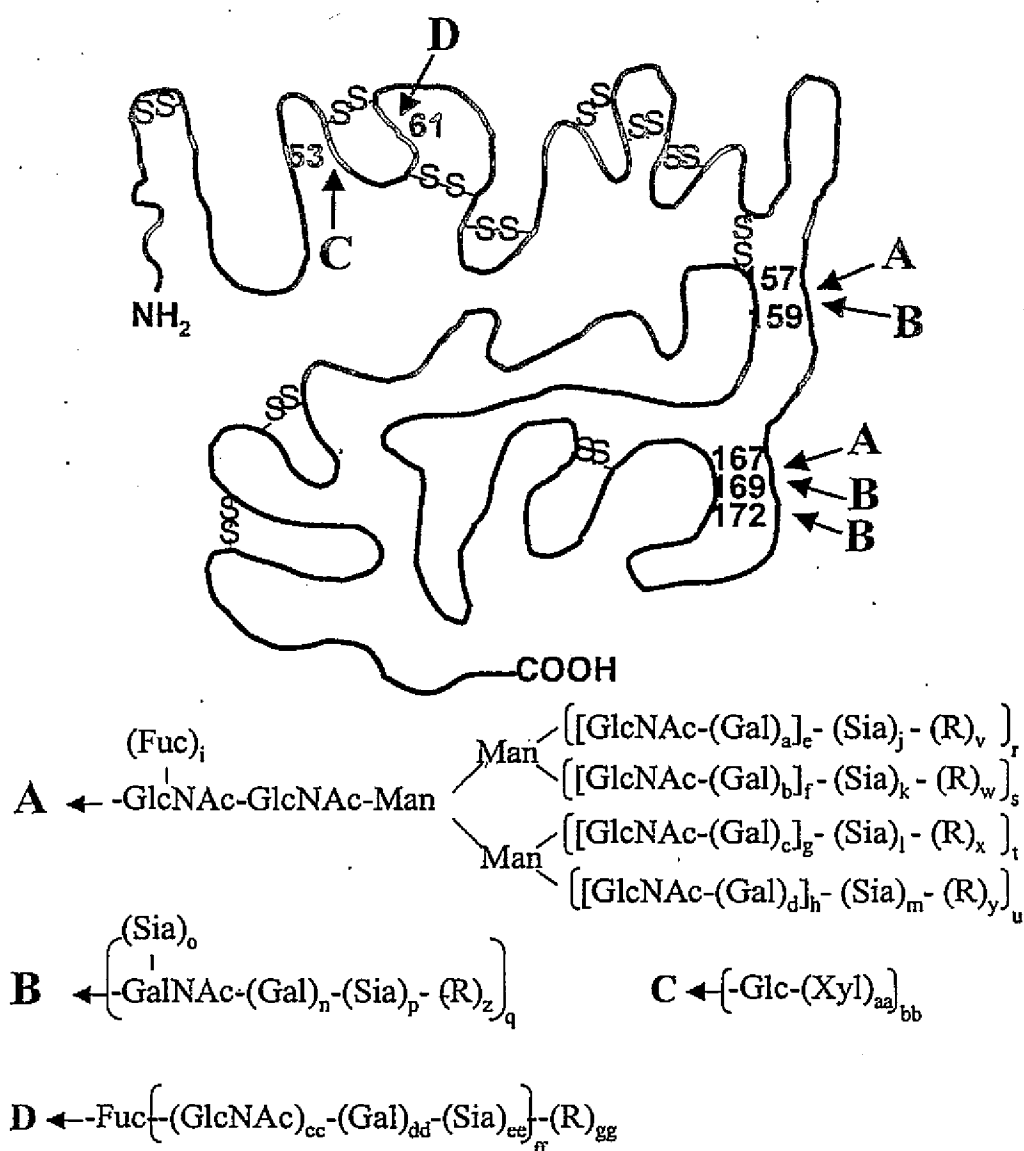
NSO expressed Factor VII or VIIa
a--u (independently selected) = 0 or 1;
v-y = 0; n = 0-4;
Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
2. Galactosyltransferase, UDP-Gal
▼ 3. CMP-SA-PEG, ST3Gal3

a-m, o-u (independently selected) = 0 or 1;
n = 0-4; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
Sia = Sia; R = PEG.

FIG. 32D

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a-d, i, n-u (independently selected) = 0 or 1.

bb, cc, dd, ee, ff, gg (independently selected) = 0 or 1.

e-h, aa (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

FIG. 33A

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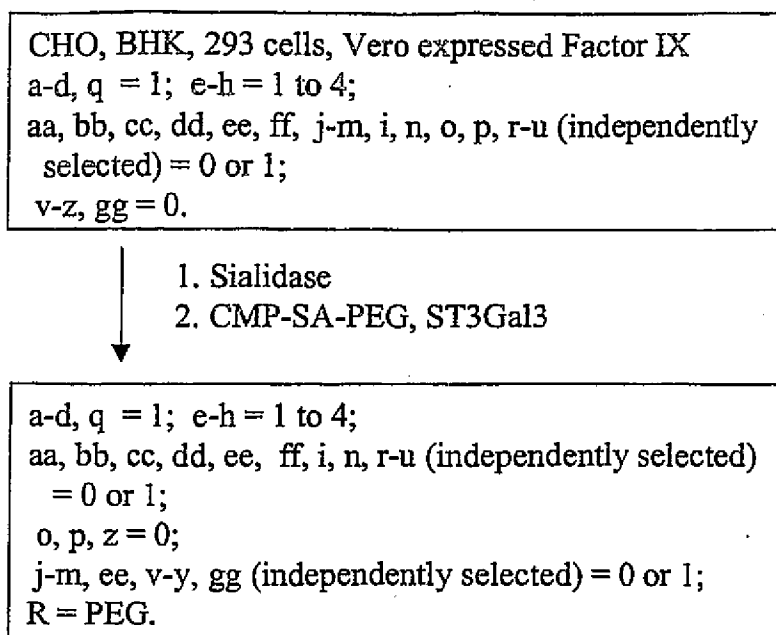


FIG. 33B

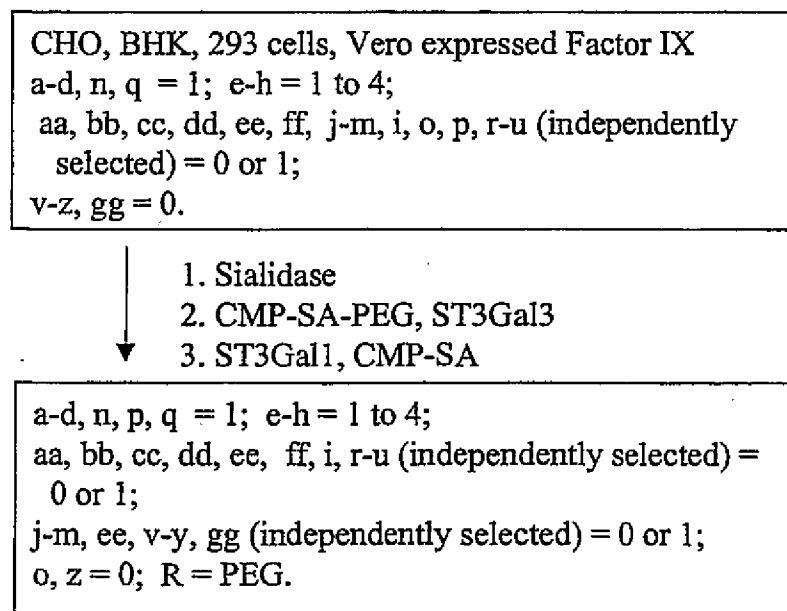


FIG. 33C

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CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1; e-h, aa = 1 to 4; ee, j-m, i,
 o, p, r-u (independently selected) = 0 or 1; v-z, gg = 0.

1. sialidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA, ST3Gal3
4. CMP-SA-PEG, ST3Gal1

a-d, n, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =
 0 or 1; R = PEG;
 o, v-y, gg = 0;
 j-m, p, ee (independently selected) = 0 or 1, but when
 p = 1, z = 1.

FIG. 33D

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1; R = PEG;
 o, p, z = 0; j-m, ee, v-y, gg (independently selected) =
 0 or 1.

FIG. 33E

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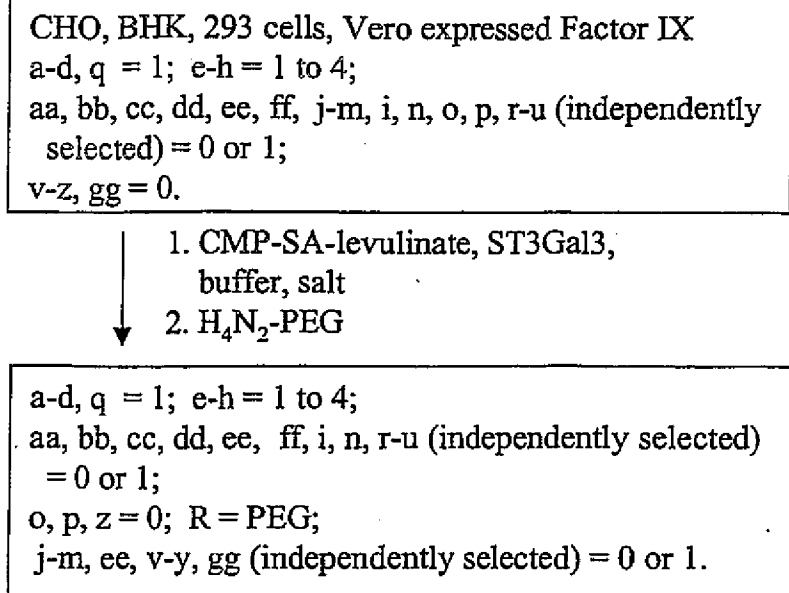


FIG. 33F

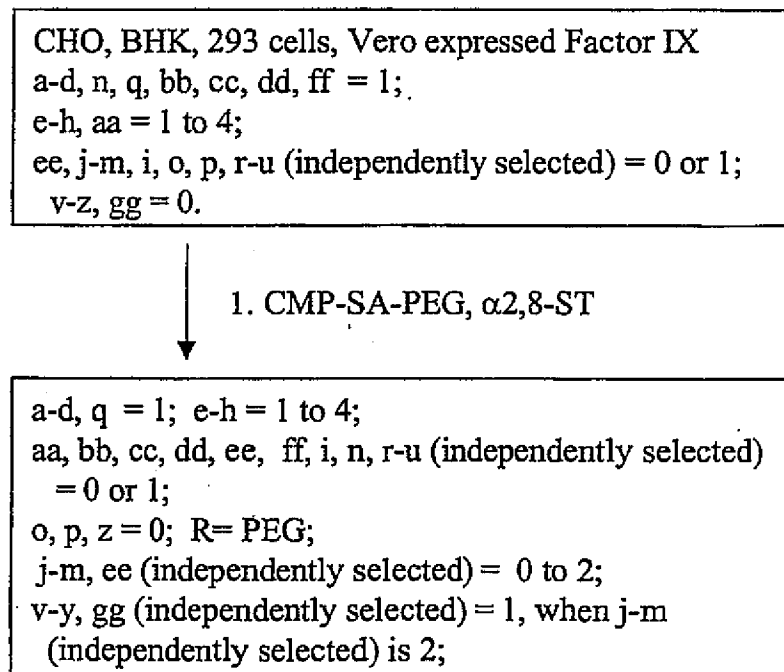
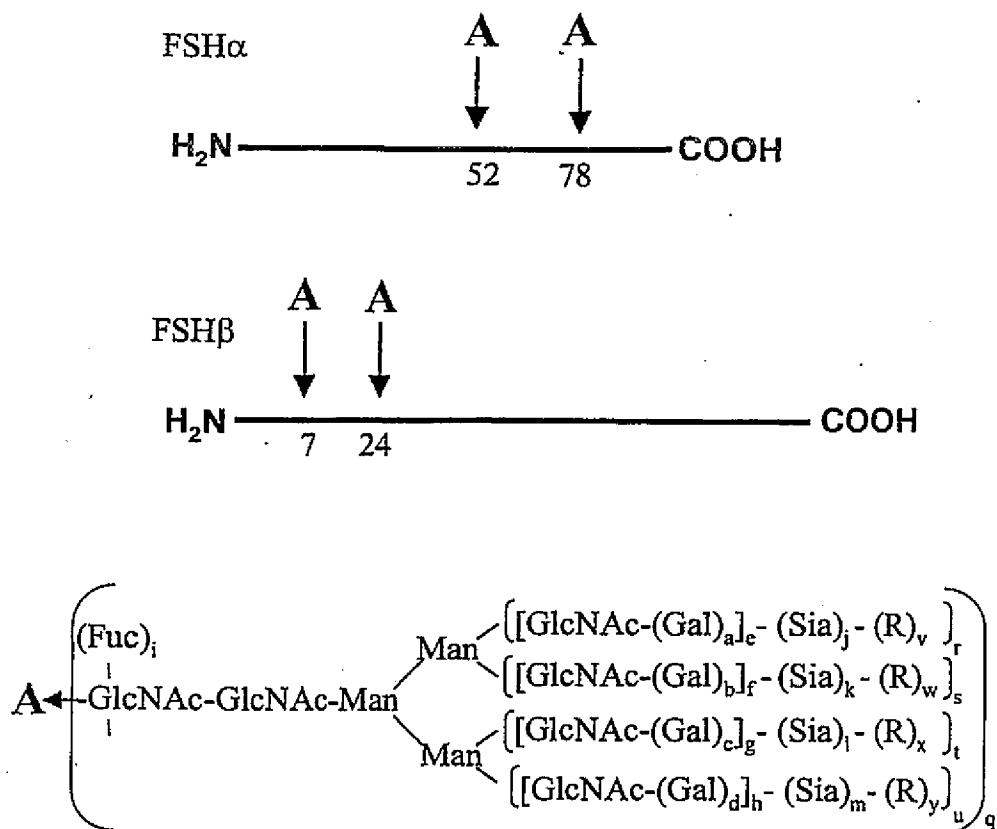


FIG. 33G

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 34A

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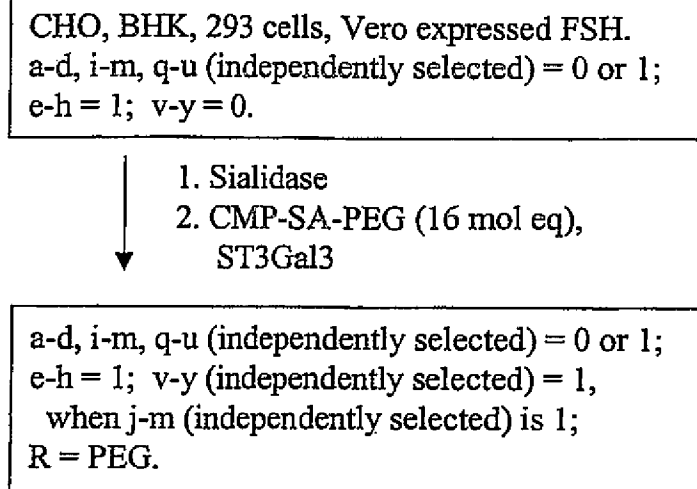


FIG. 34B

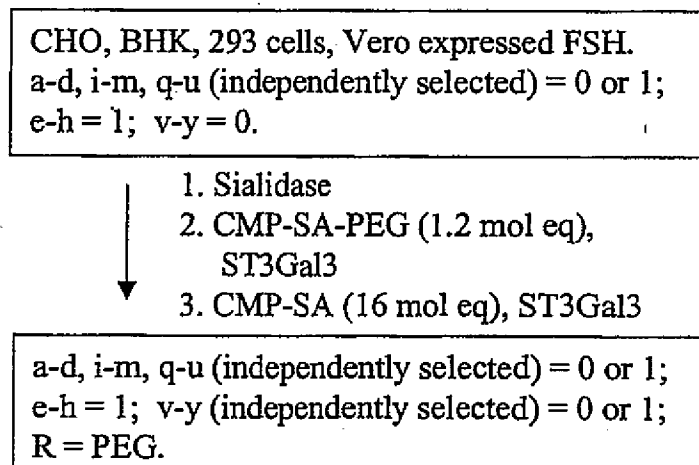


FIG. 34C

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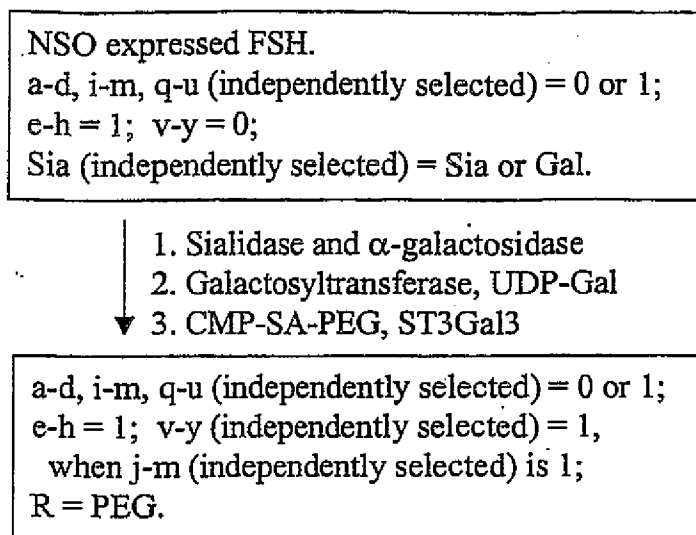


FIG. 34D

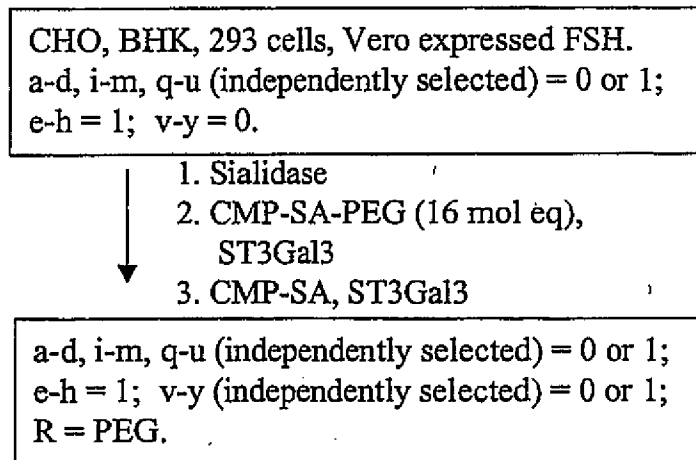


FIG. 34E

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CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 34F

CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, $\alpha 2,8$ -ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 34G

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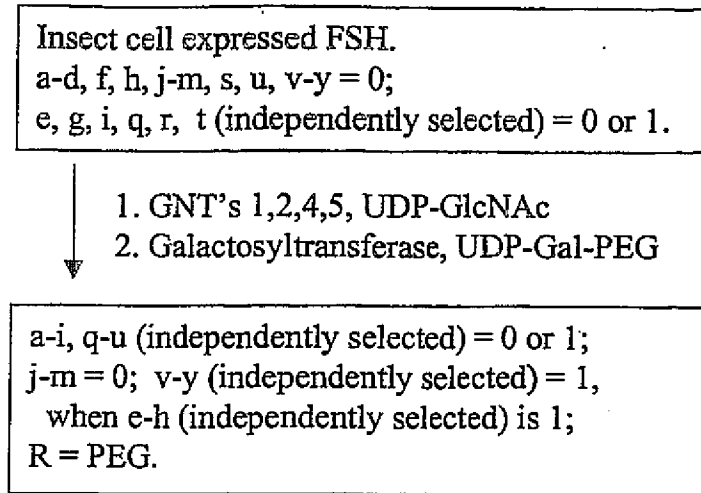


FIG. 34H

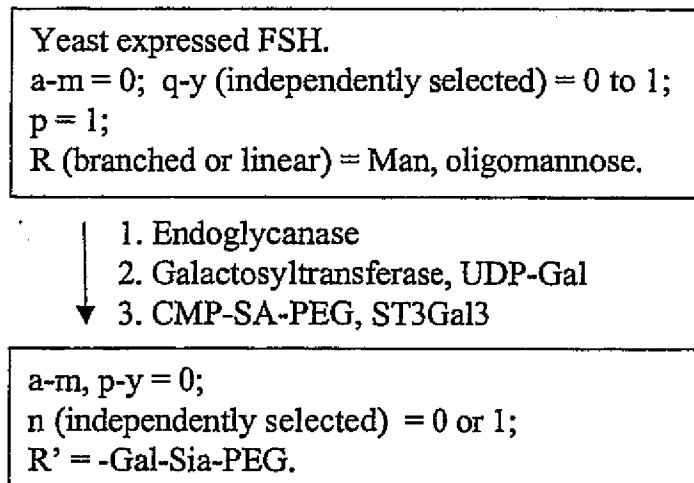


FIG. 34I

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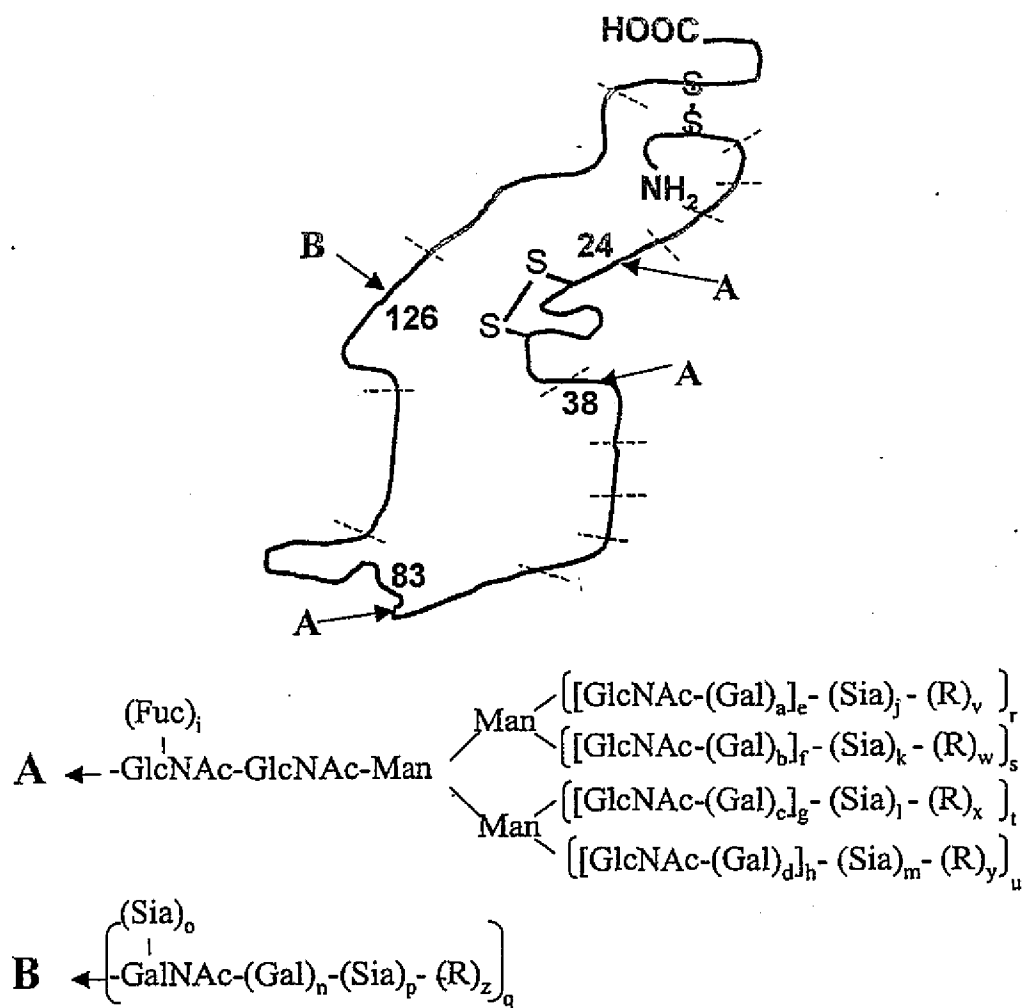
CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated chorionic gonadrophin (CG) produced in CHO.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-CG.

FIG. 34J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = polymer.

FIG. 35A

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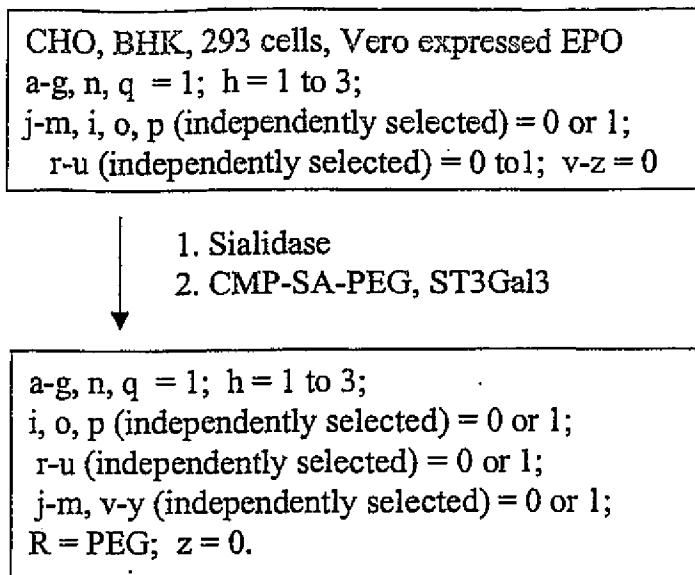


FIG. 35B

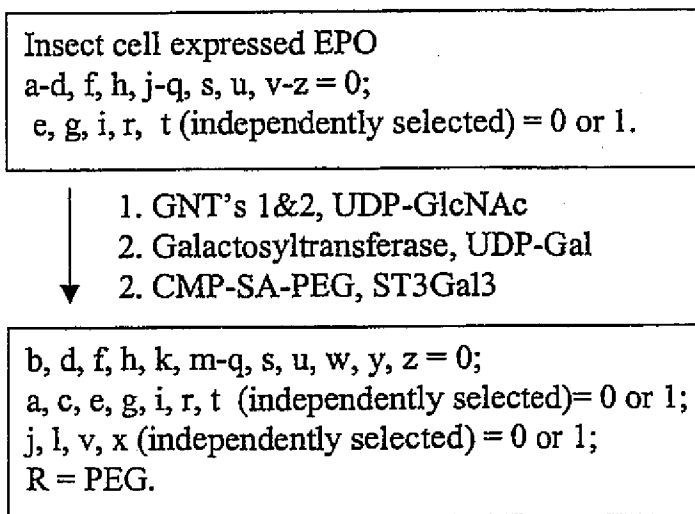


FIG. 35C

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CHO, BHK, 293 cells, Vero expressed EPO
 a-q, r-u (independently selected) = 0 or 1;
 v-z = 0.

1. sialidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA, ST3Gal3
4. CMP-SA-PEG, ST3Gal1

a-h, n, q = 1;
 i-m, o, r-u (independently selected) = 0 or 1;
 v-y = 0; p, z = 0 or 1; R = PEG.

FIG. 35D

CHO, BHK, 293 cells, Vero expressed EPO
 a-g, n, q = 1; h = 1 to 3;
 j-m, i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 v-z = 0

1. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;
 i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1;
 j-m, v-y (independently selected) = 0 or 1;
 R = PEG; z = 0.

FIG. 35E

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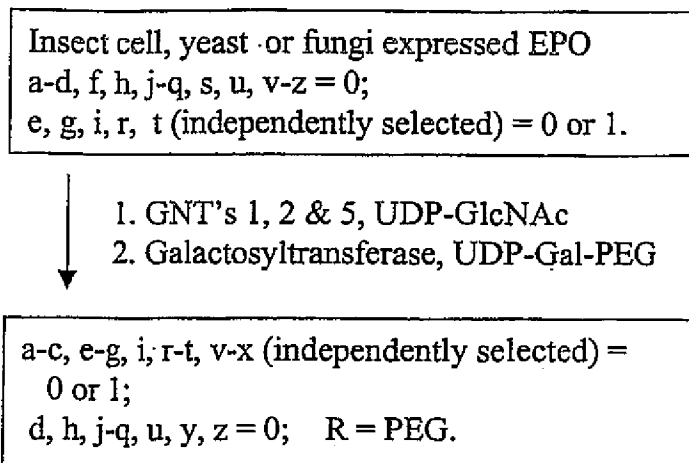


FIG. 35F

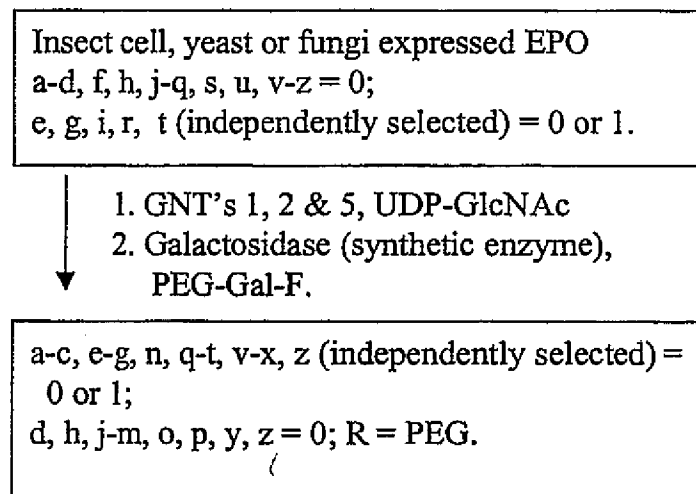


FIG. 35G

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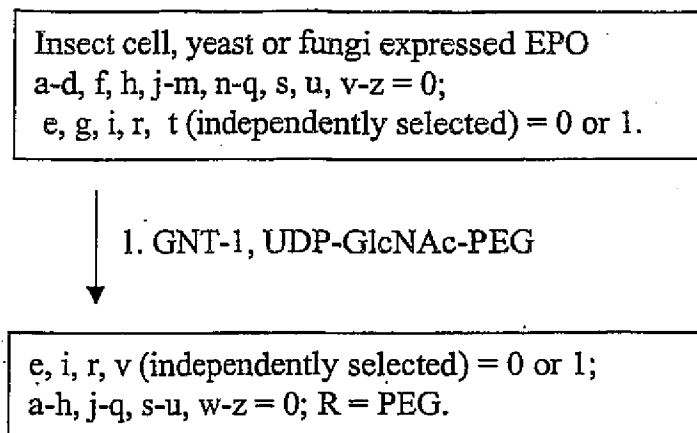


FIG. 35H

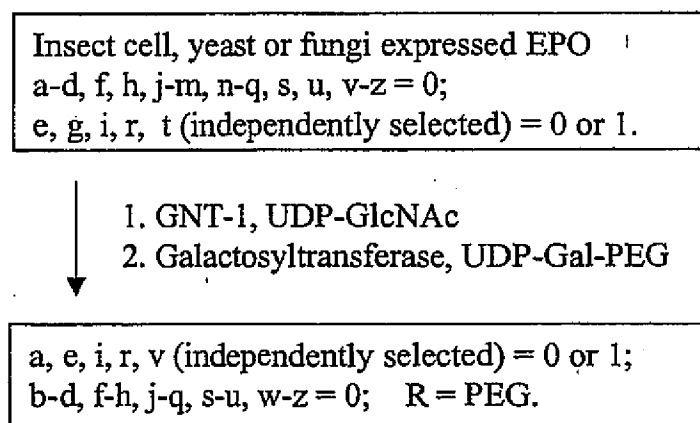


FIG. 35I

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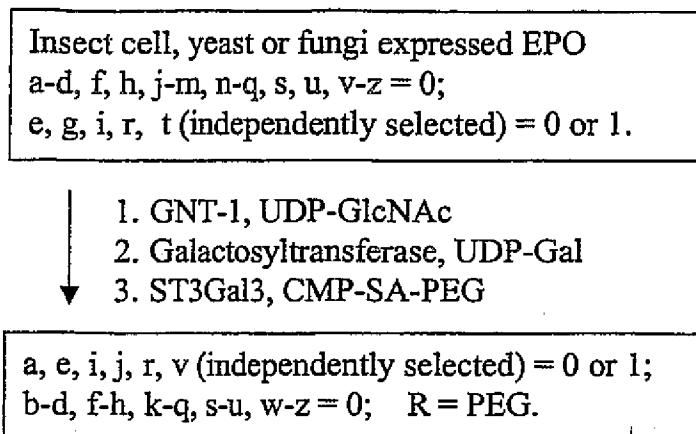


FIG. 35J

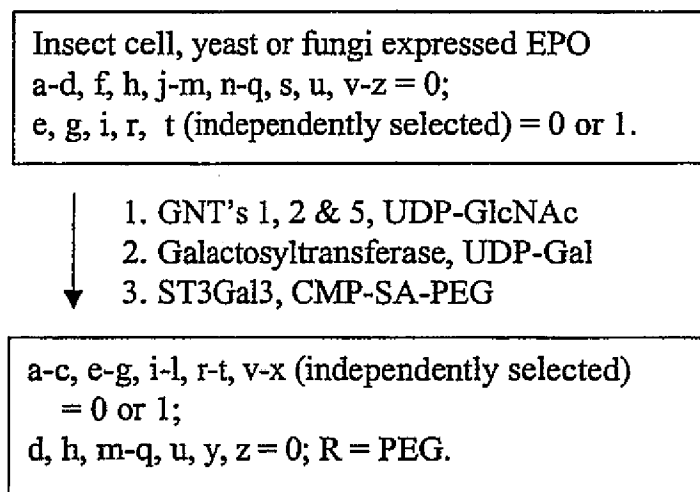


FIG. 35K

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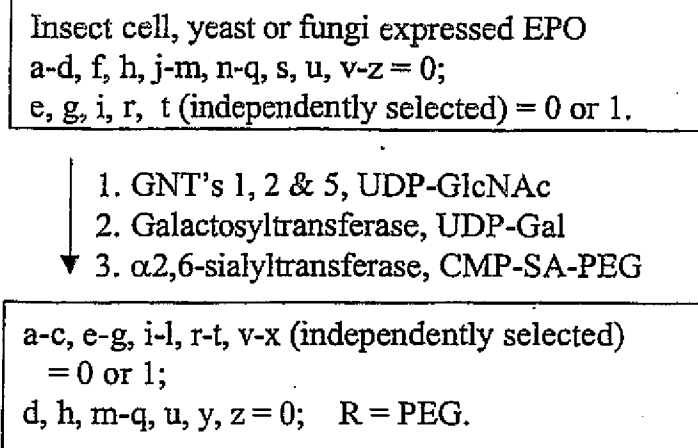


FIG. 35L

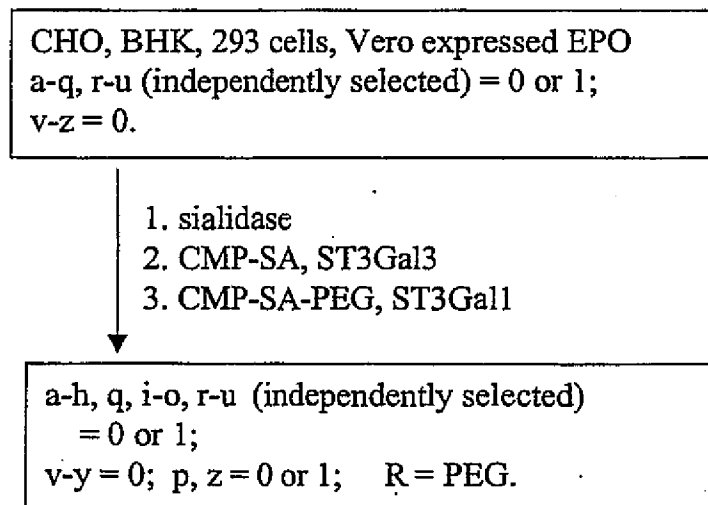


FIG. 35M

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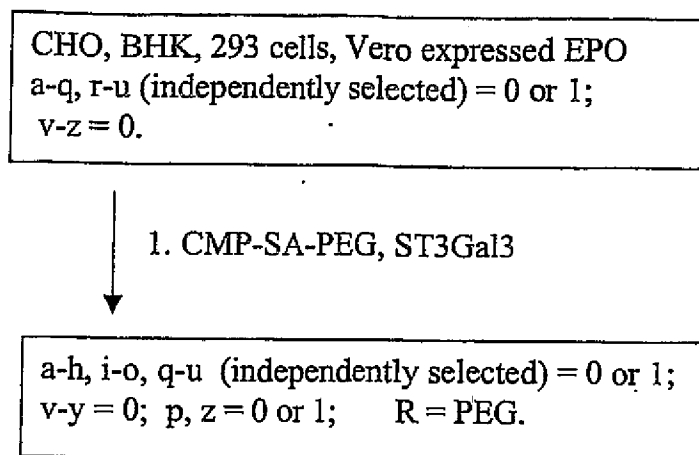


FIG. 35N

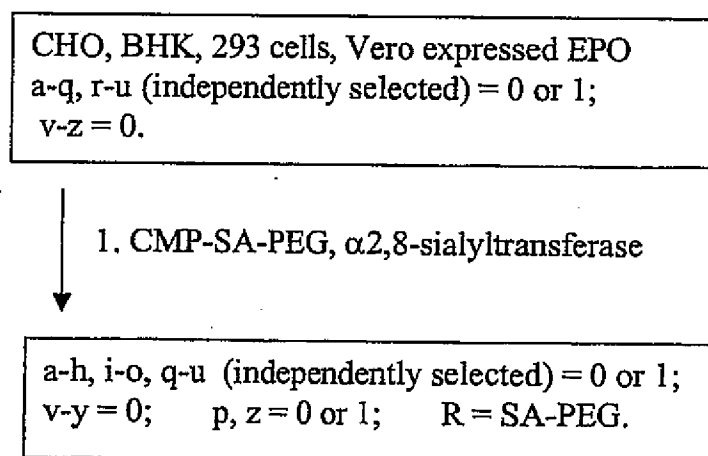


FIG. 35O

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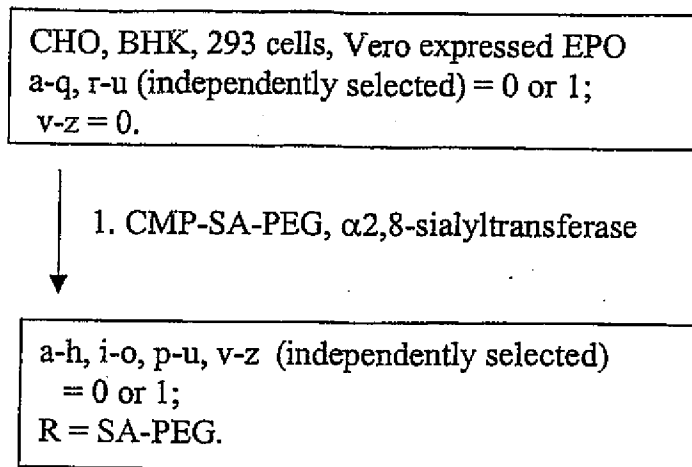


FIG. 35P

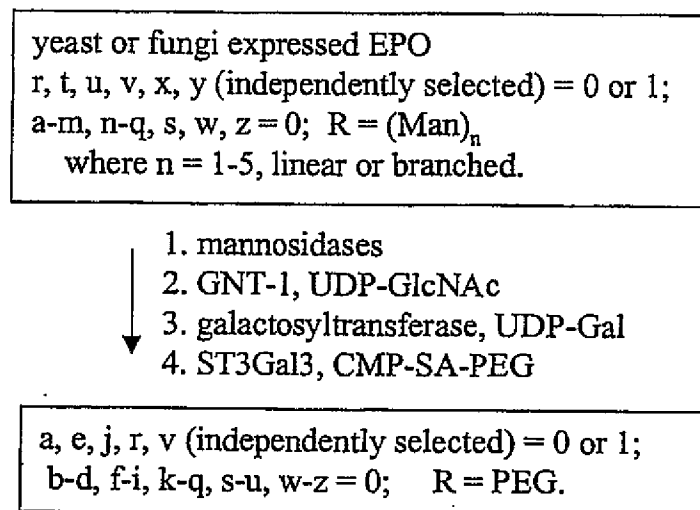


FIG. 35Q

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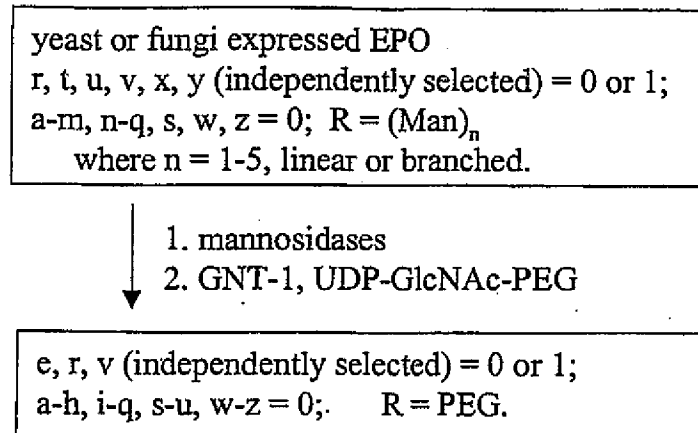


FIG. 35R

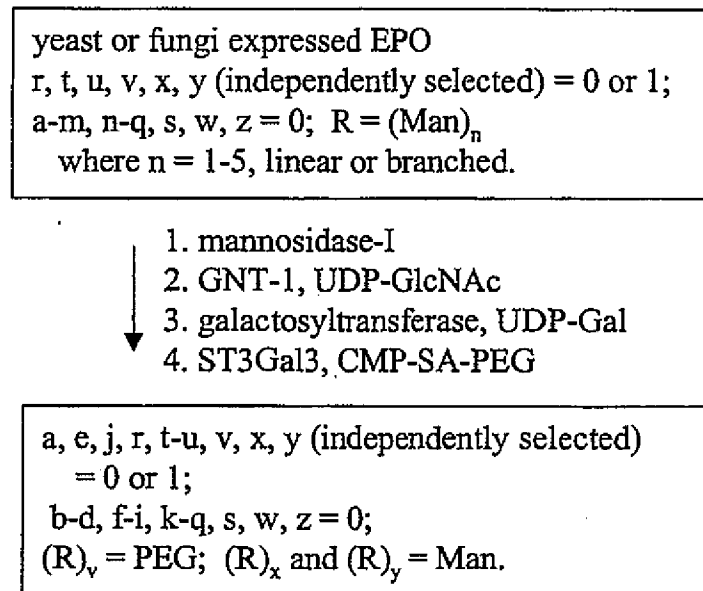
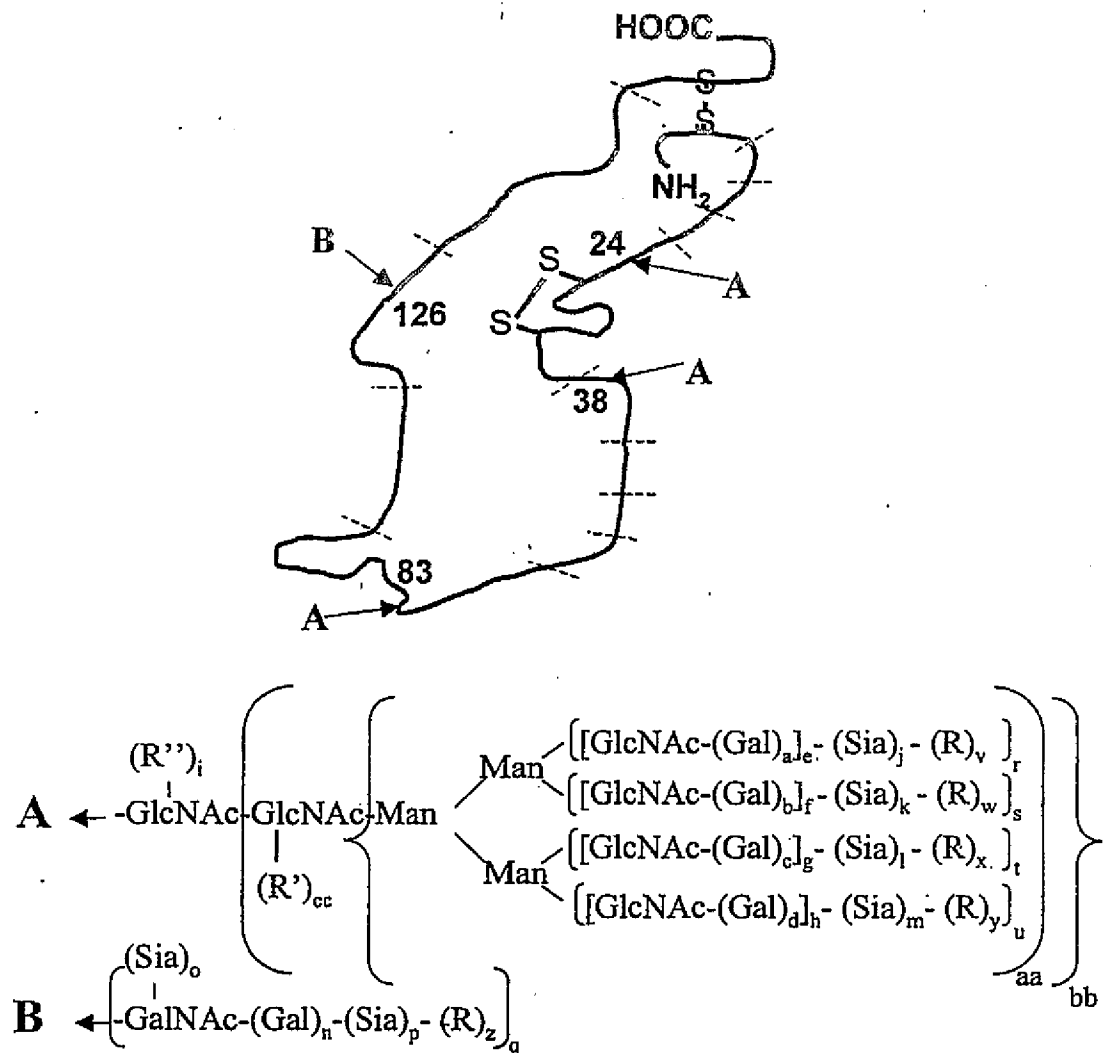


FIG. 35S

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; aa, bb = 1; cc = 0;

R = polymer; R'' and R' = sugar-polymer or Fuc.

FIG. 35T

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yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 cc, a-m, n-q, s, w, z = 0;
 aa, bb = 1;
 R = (Man)_n where n = 1-100, linear or branched.

- ↓
 1. endo-H
 ↓
 2. galactosyltransferase, UDP-Gal-PEG

i (independently selected) = 0 or 1;
 aa, bb, cc, a-h, j-z = 0; R'' = Gal-PEG.

FIG. 35U

yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 cc, a-m, n-q, s, w, z = 0; aa, bb = 1;
 R = (Man)_n where n = 1-100, linear or branched.

- ↓
 1. endo-H
 ↓
 2. galactosyltransferase, UDP-Gal
 ↓
 3. ST3Gal3, CMP-SA-PEG

i (independently selected) = 0 or 1;
 aa, bb, cc, a-h, j-z = 0; R'' = Gal-SA-PEG.

FIG. 35V

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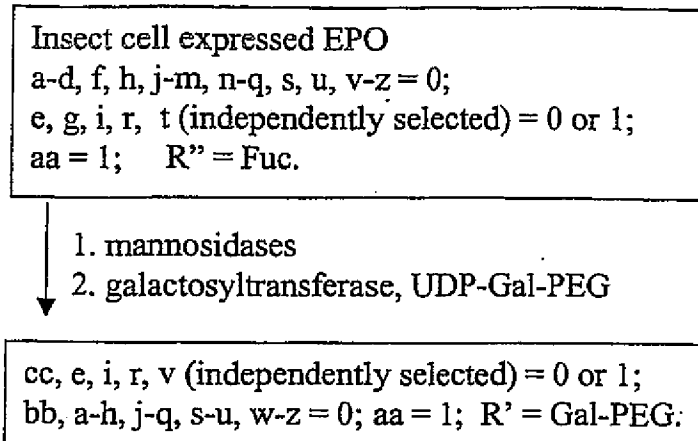
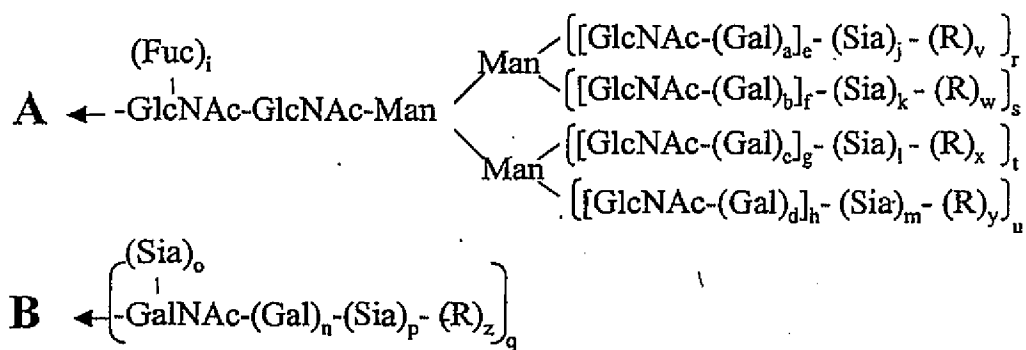
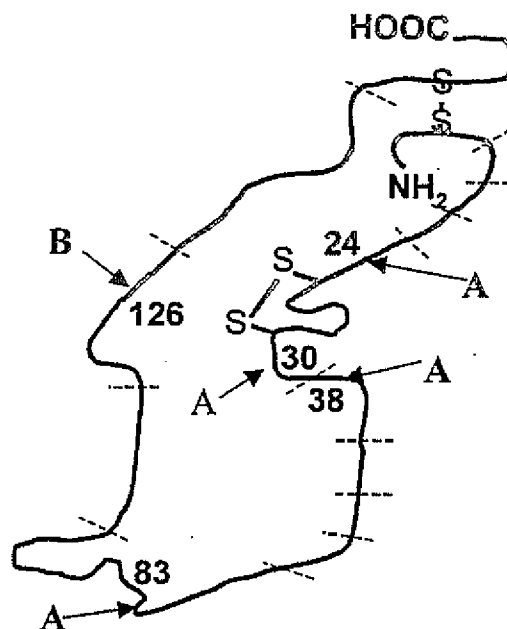


FIG. 35W

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = polymer.

FIG. 35X

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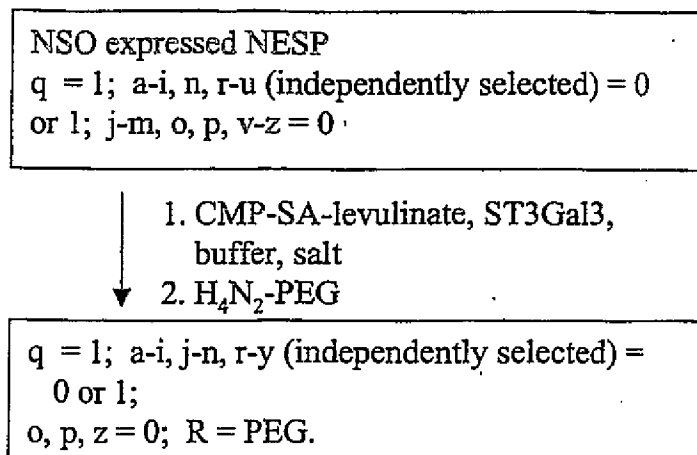


FIG. 35Y

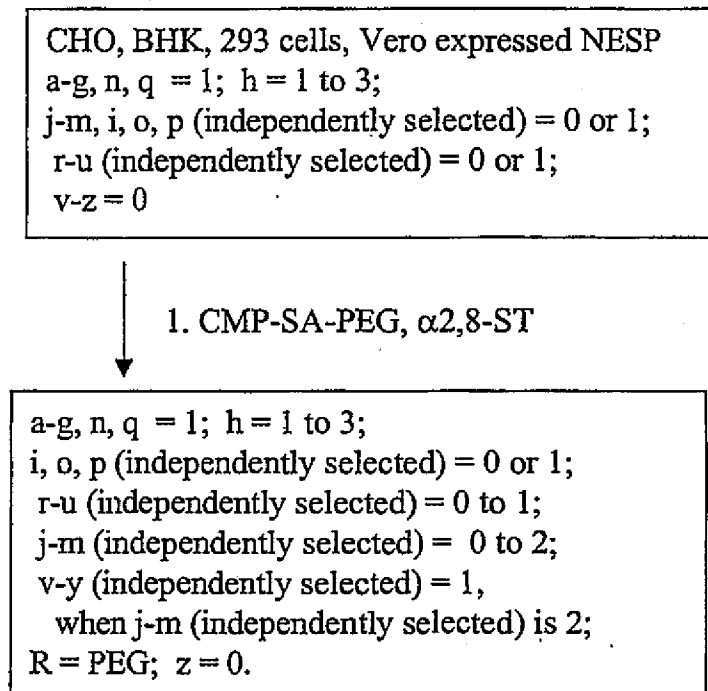


FIG. 35Z

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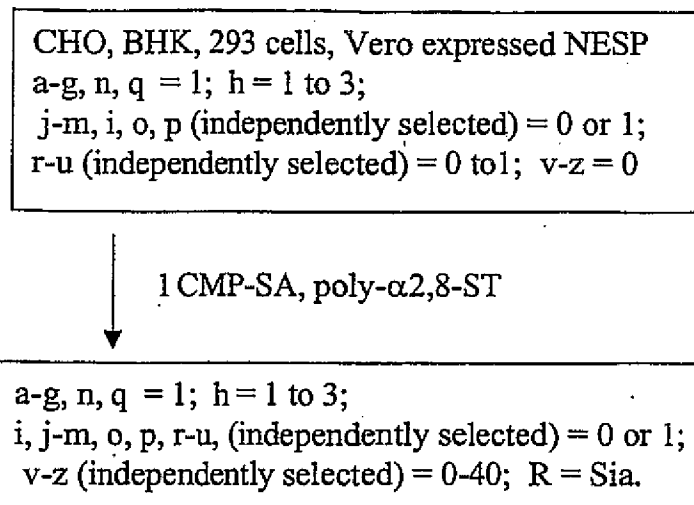
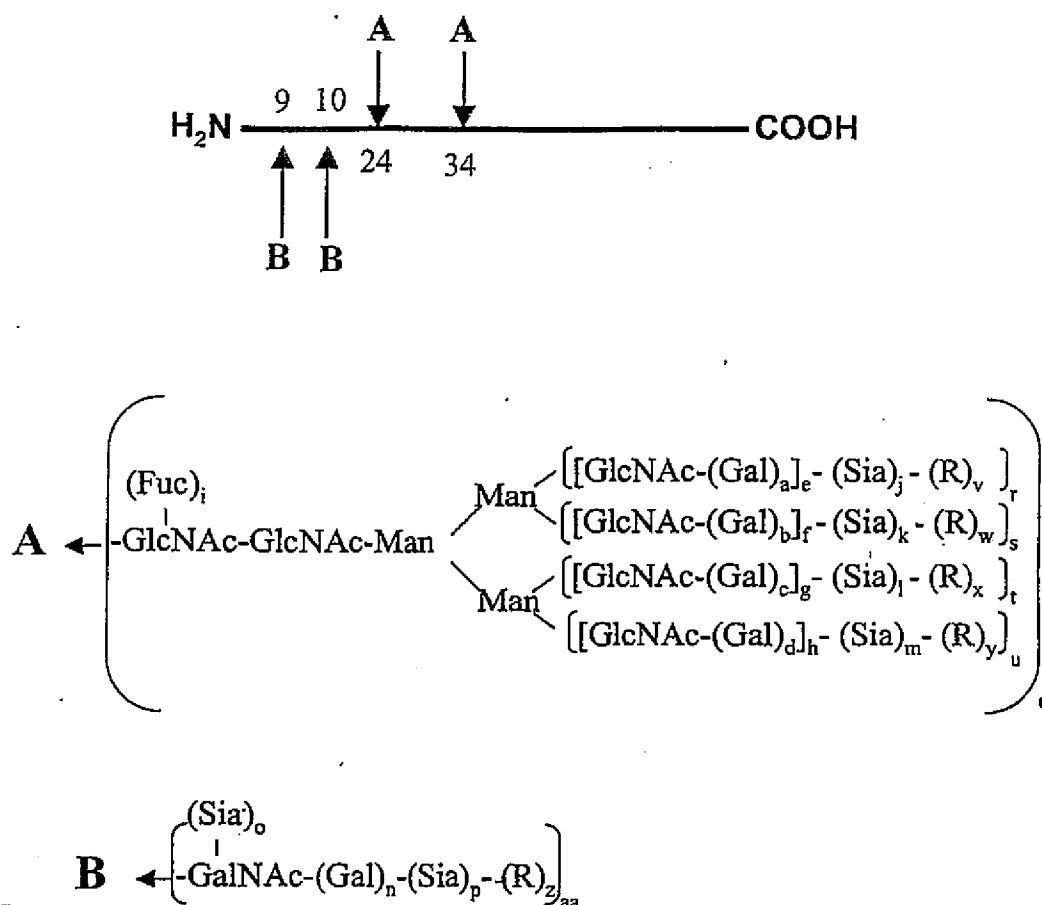


FIG. 35AA

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a-d, i, n-u, aa (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer, glycoconjugate.

FIG. 36A

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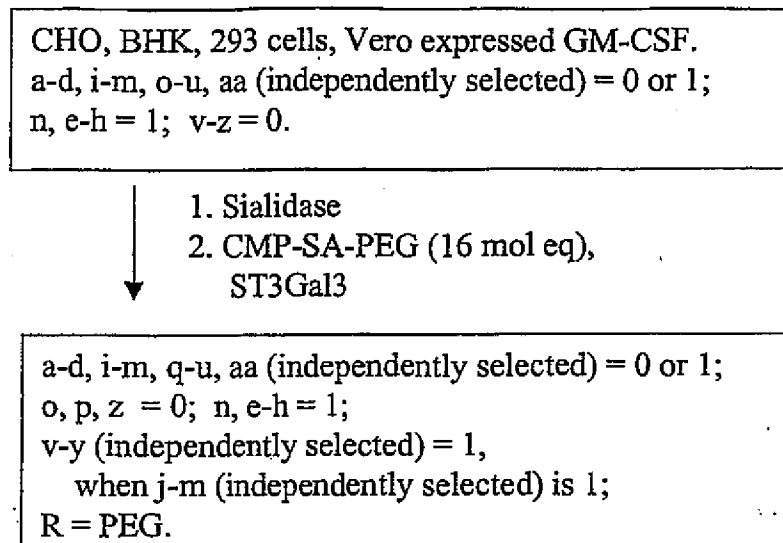


FIG. 36B

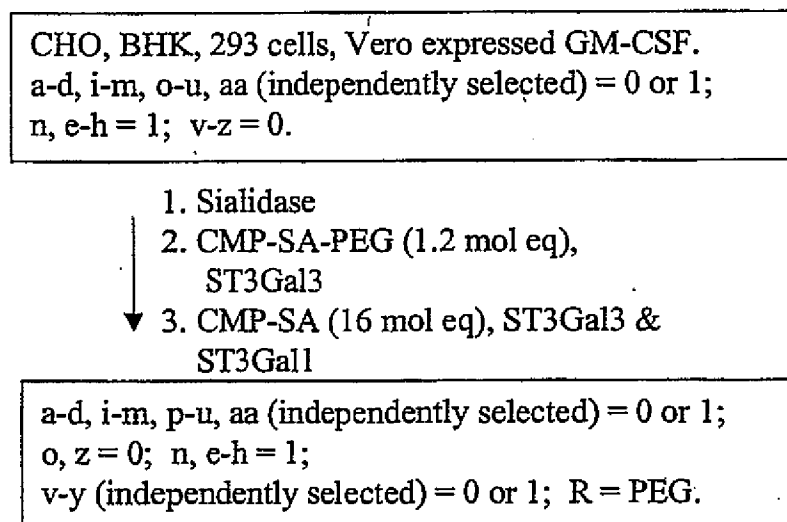


FIG. 36C

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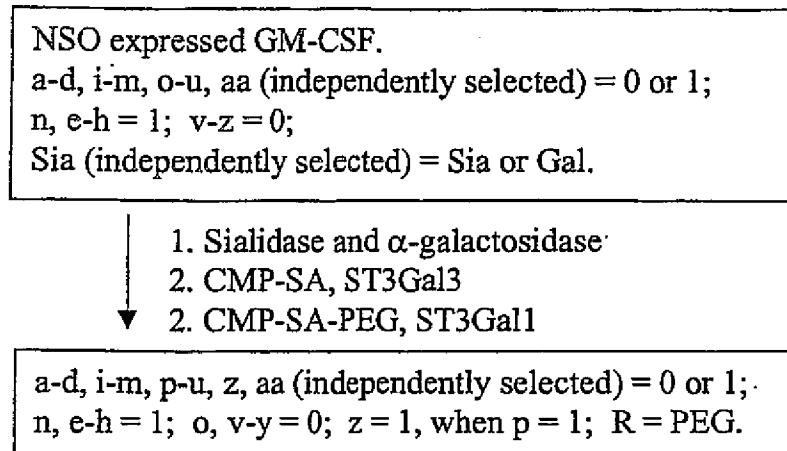


FIG. 36D

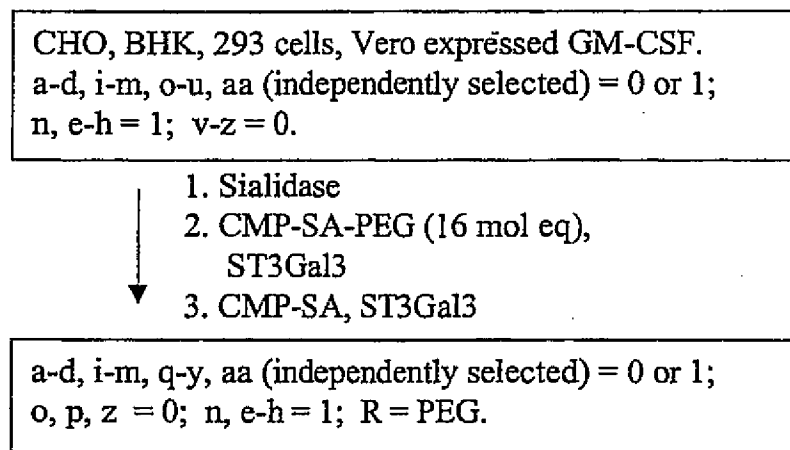


FIG. 36E

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CHO, BHK, 293 cells, Vero expressed GM-CSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.



1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
2. H₄N₂-PEG

a-d, i-m, o-y, aa (independently selected) = 0 or 1;
z = 0; n, e-h = 1; R = PEG.

FIG. 36F

CHO, BHK, 293 cells, Vero expressed GMCSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

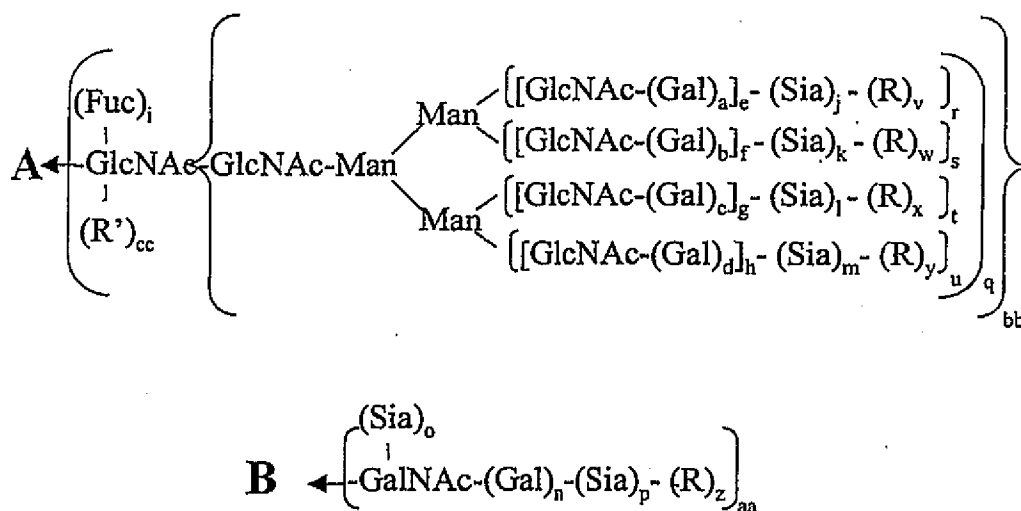
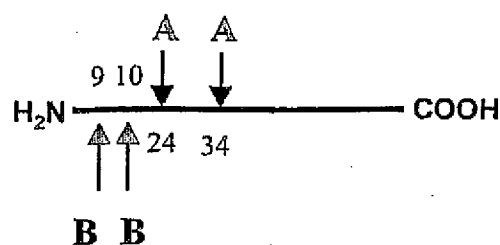


1. CMP-SA, α 2,8-ST

a-d, i, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; j-m (independently selected) = 0-20;
v-z (independently selected) = 0.

FIG. 36G

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a-d, i, n-u, aa, bb, cc (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 36H

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Insect cell expressed GM-CSF.

a-d, f, h, j-m, o, p, s, u, v-z = 0;

e, g, i, n, q, r, t, aa (independently selected) = 0 or 1.

1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, n, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 36I

Yeast expressed GM-CSF.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1;

bb = 1; R (branched or linear) = Man, oligomannose;

GalNAc = Man.

1. Endoglycanase

2. mannosidase (if aa = 1).

3. Galactosyltransferase, UDP-Gal-PEG

a-p, r-z, aa, bb = 0;

q, cc (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 36J

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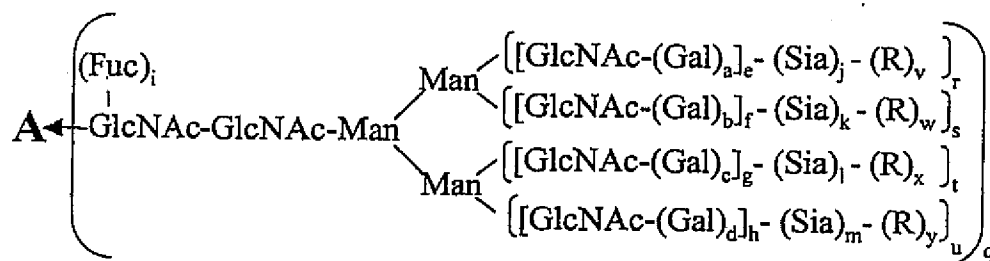
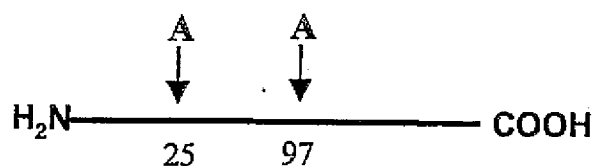
CHO, BHK, 293 cells, Vero expressed GM-CSF.
a--m, o-u, aa, bb (independently selected) = 0 or 1;
n, v-z, cc = 0.

- ↓
1. sialidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-linker-SA-CMP, ST3Gal1
 3. ST3Gal3, transferrin

a--m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y, cc = 0; bb, n = 1; R = transferrin.

FIG. 36K

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 37A

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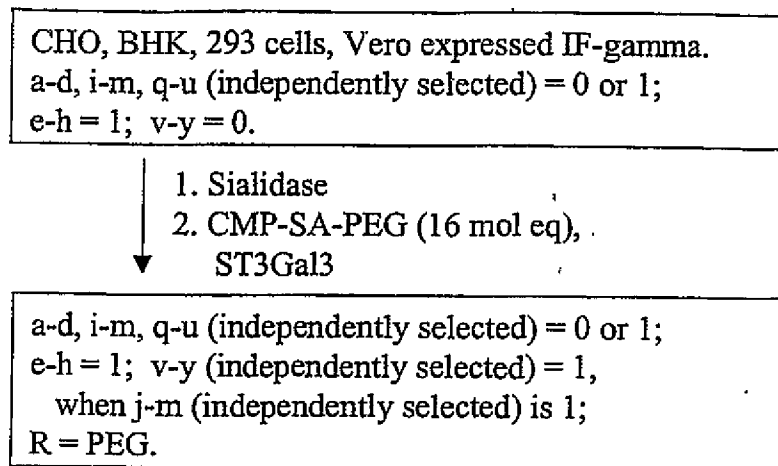


FIG. 37B

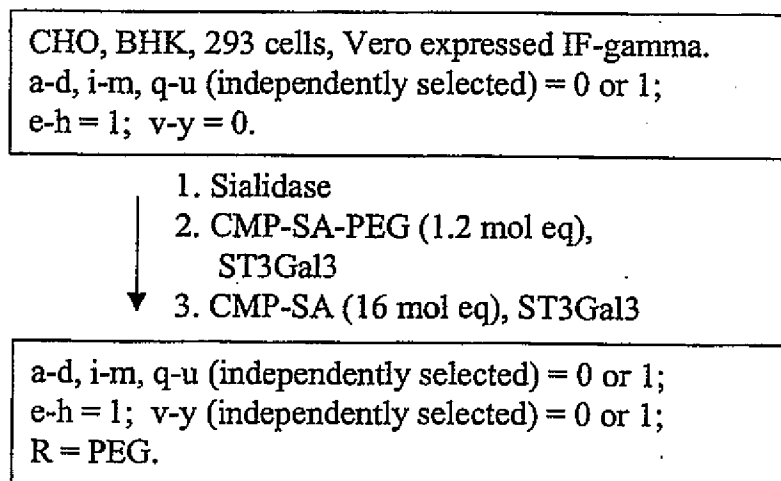


FIG. 37C

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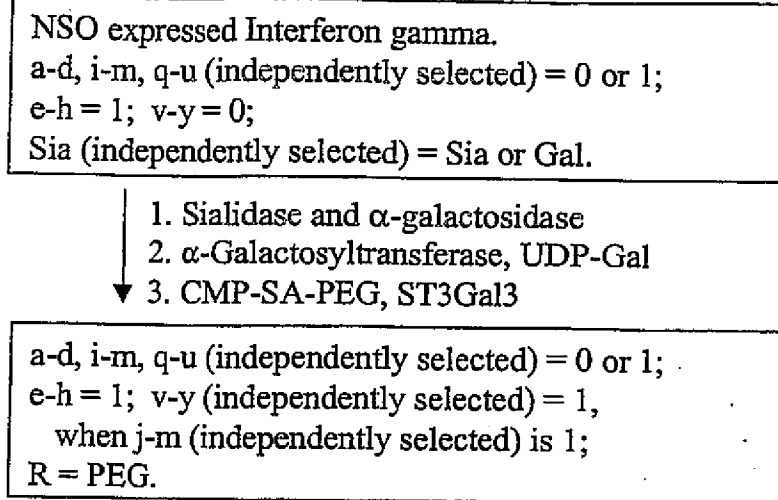


FIG. 37D

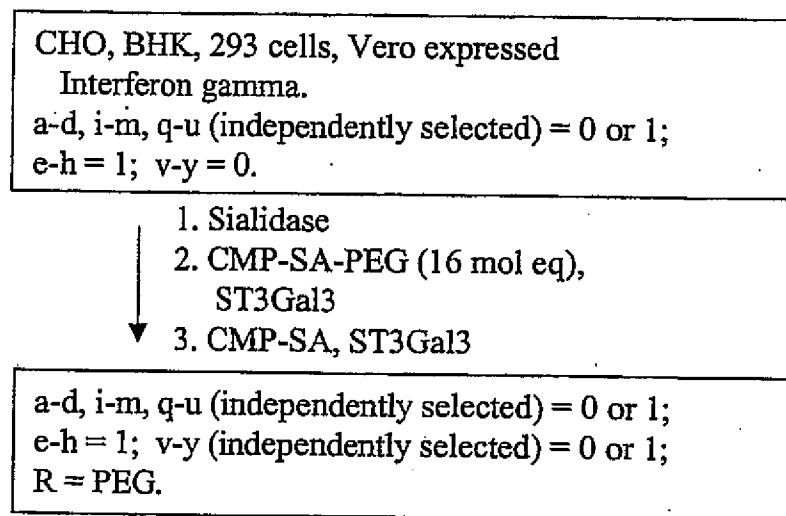


FIG. 37E

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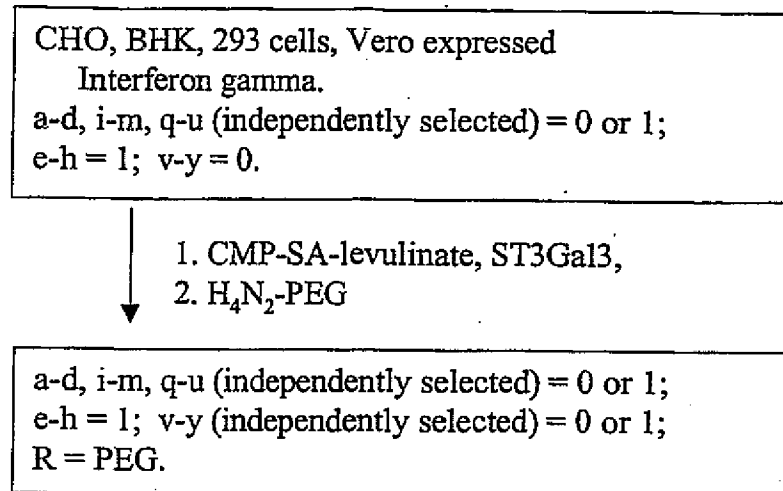


FIG. 37F

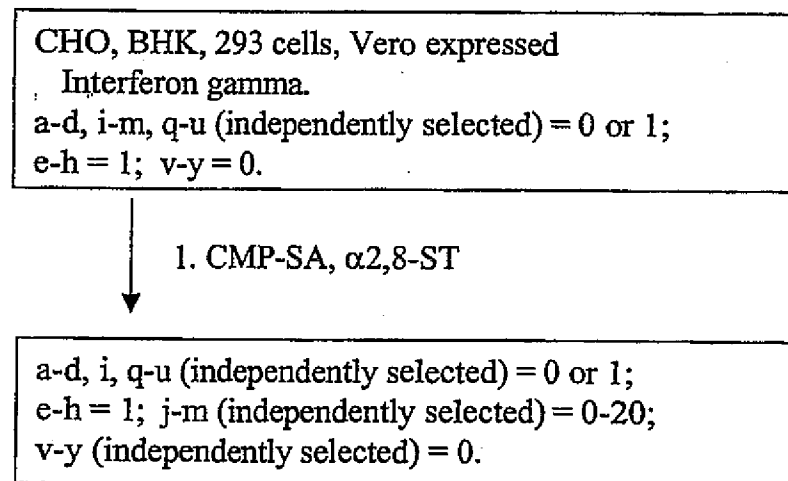
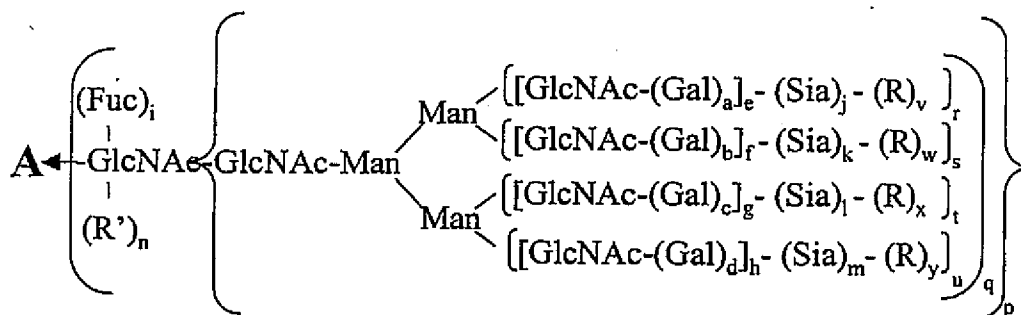
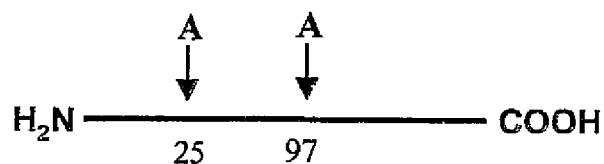


FIG. 37G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 37H

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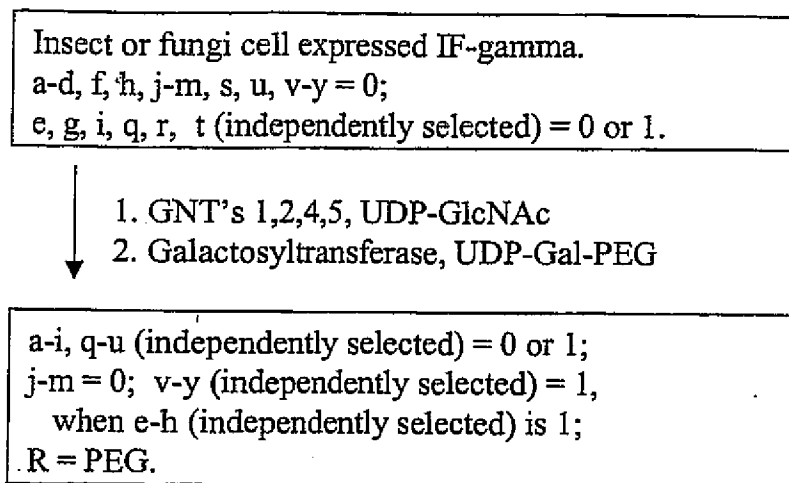


FIG. 37I

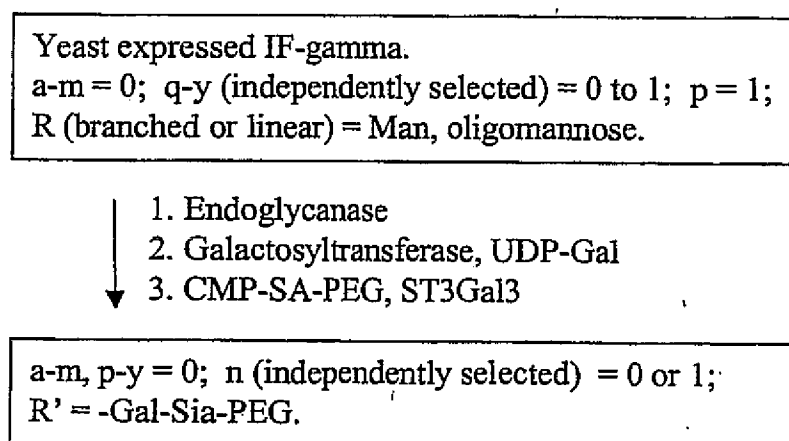


FIG. 37J

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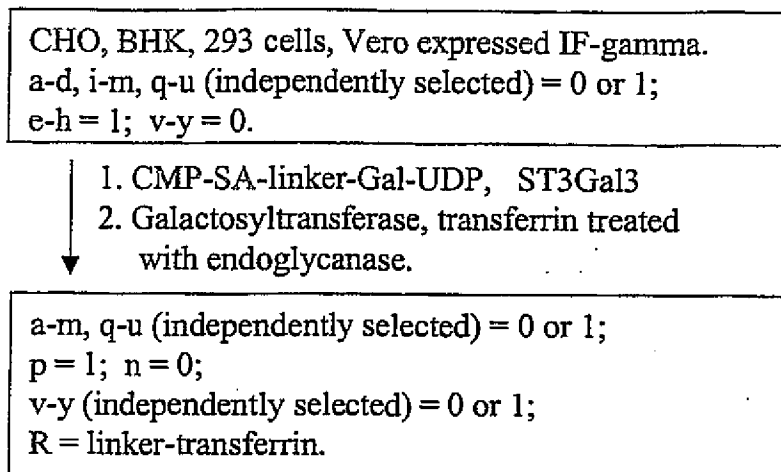


FIG. 37K

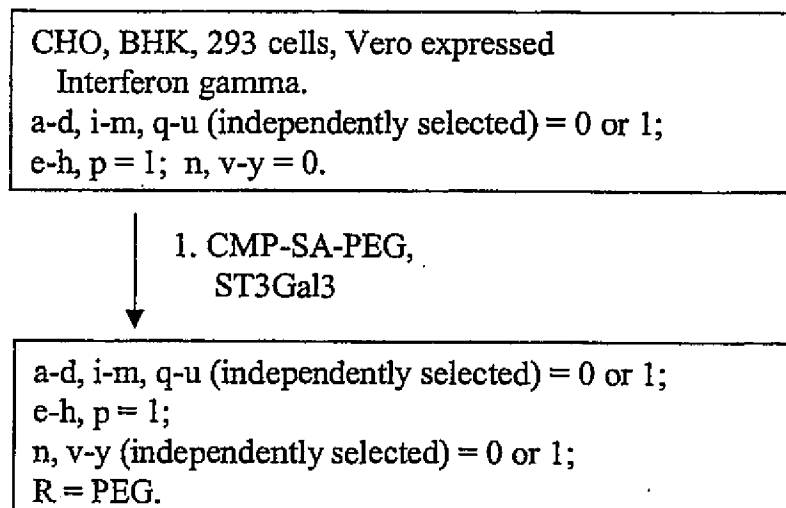


FIG. 37L

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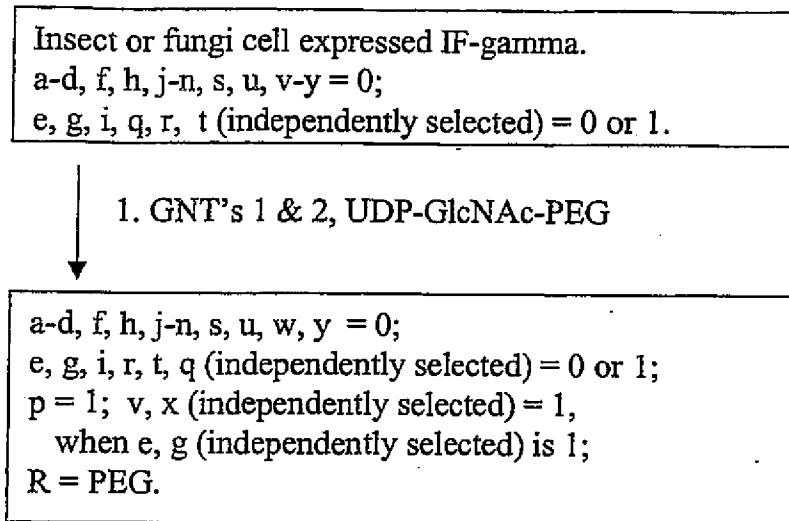


FIG. 37M

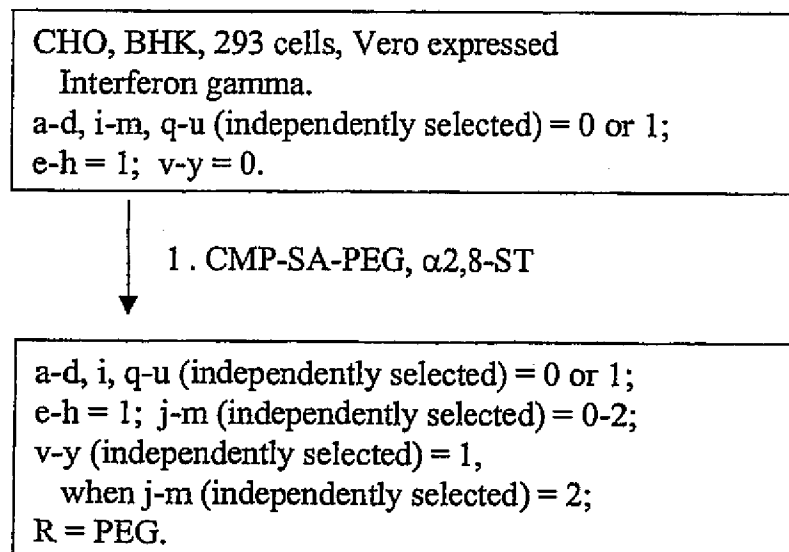
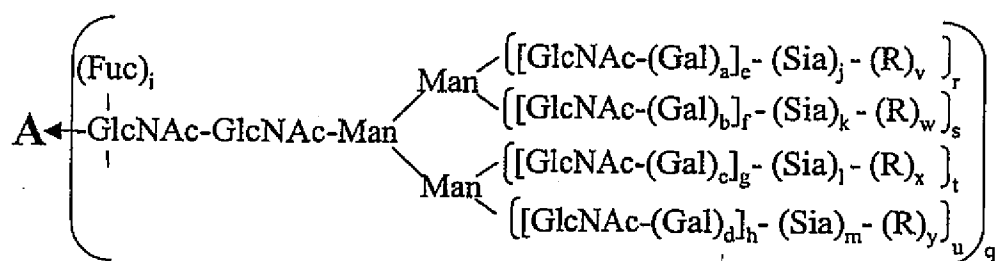
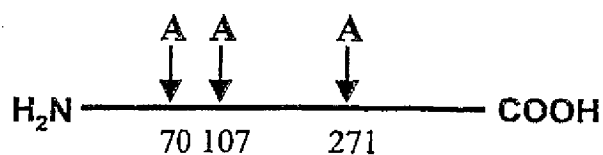


FIG. 37N

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a-d, i, q-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer.

FIG. 38A

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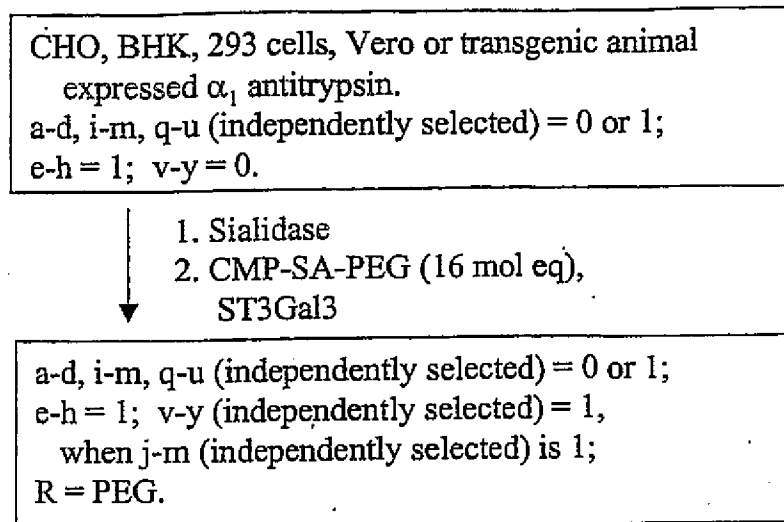


FIG. 38B

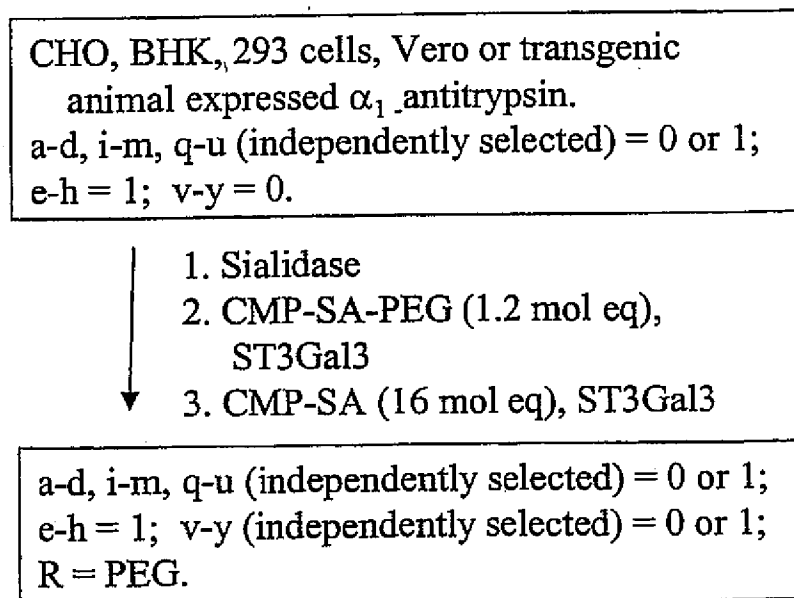


FIG. 38C

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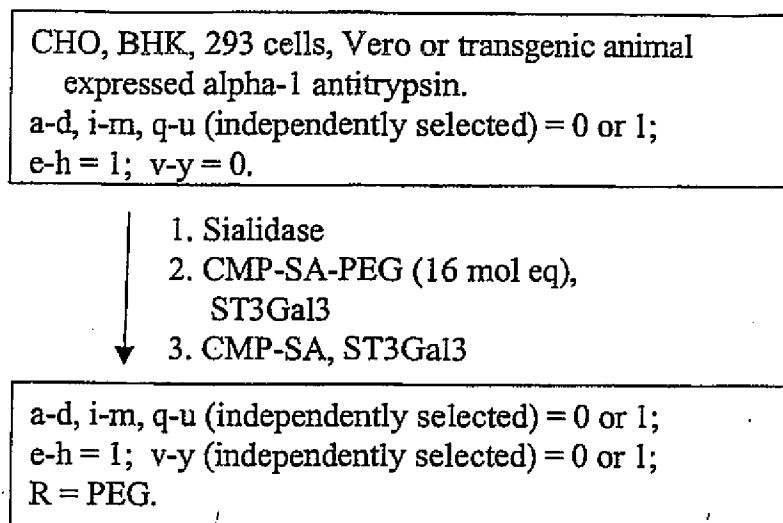


FIG. 38D

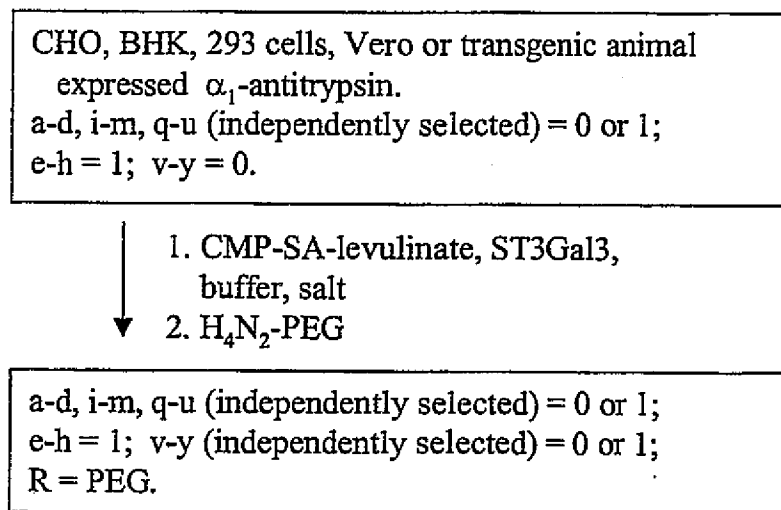


FIG. 38E

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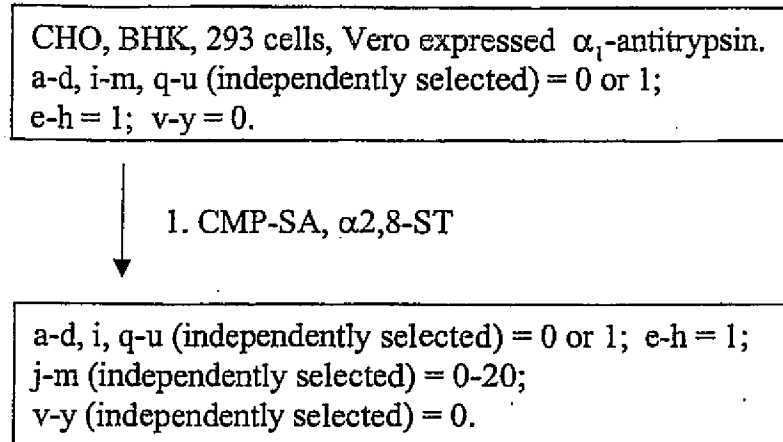
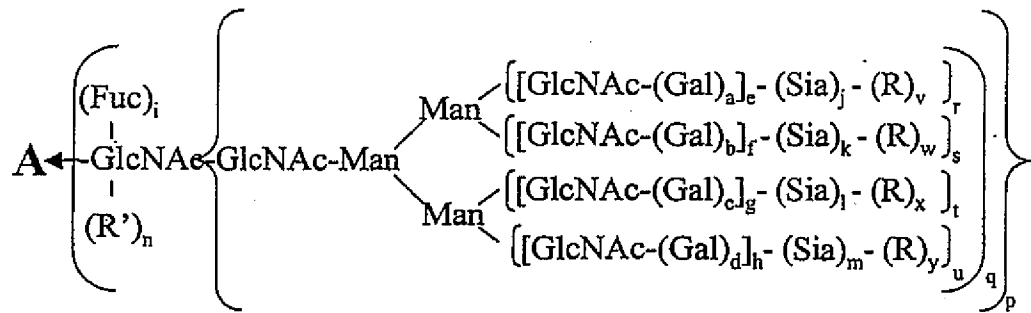
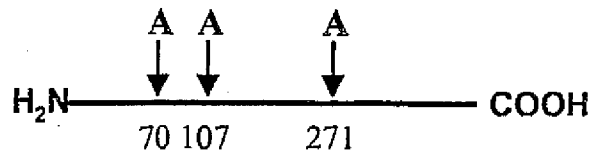


FIG. 38F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

$$v-y=0;$$

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 38G

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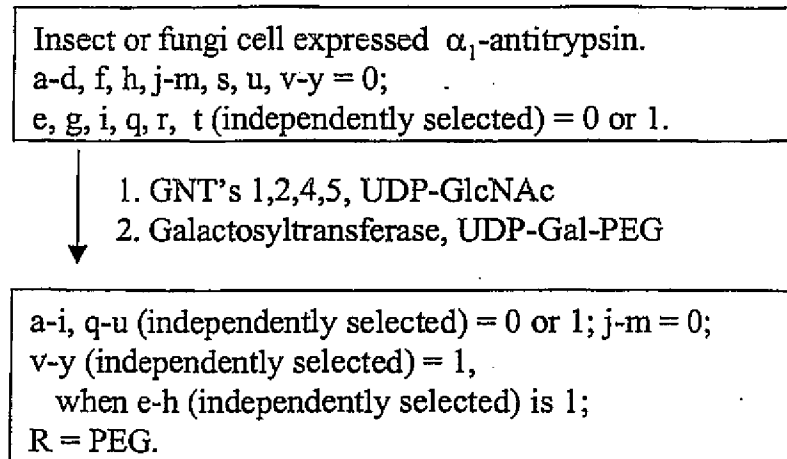


FIG. 38H

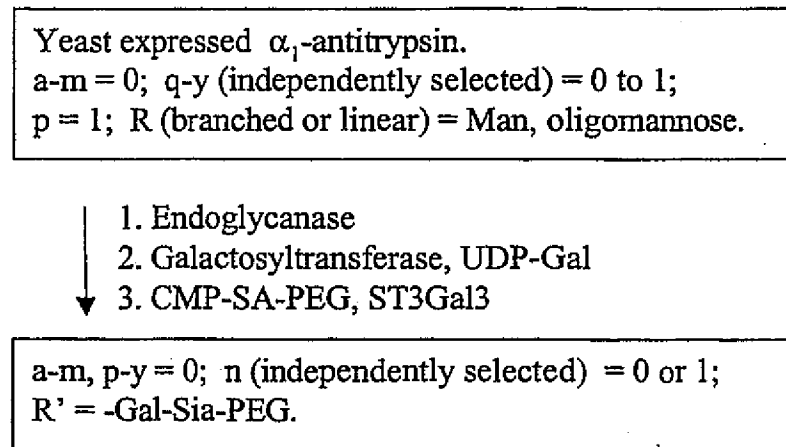


FIG. 38I

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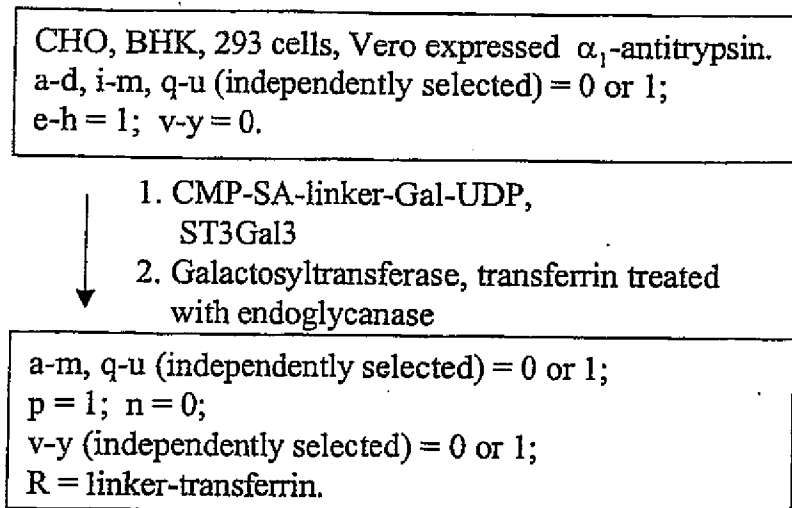
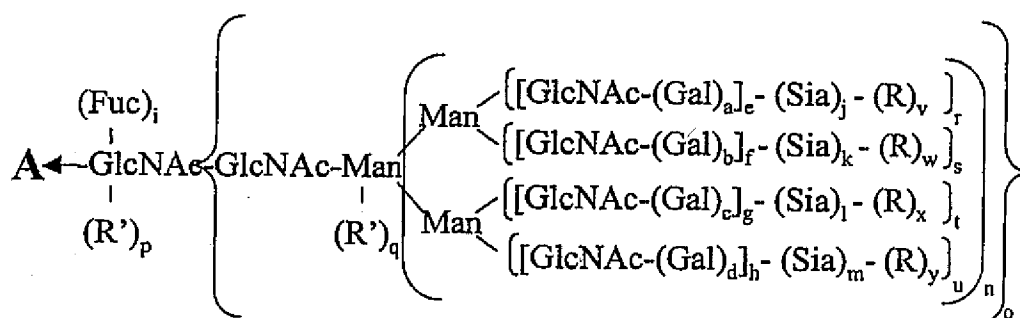
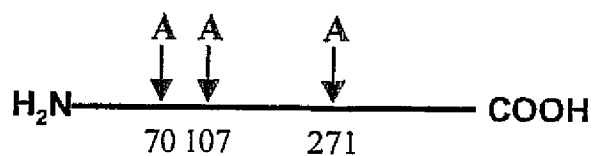


FIG. 38J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer;

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 38K

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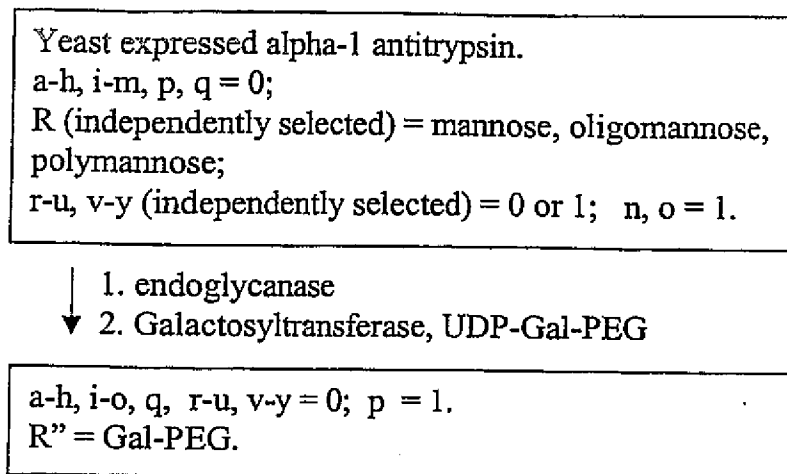


FIG. 38L

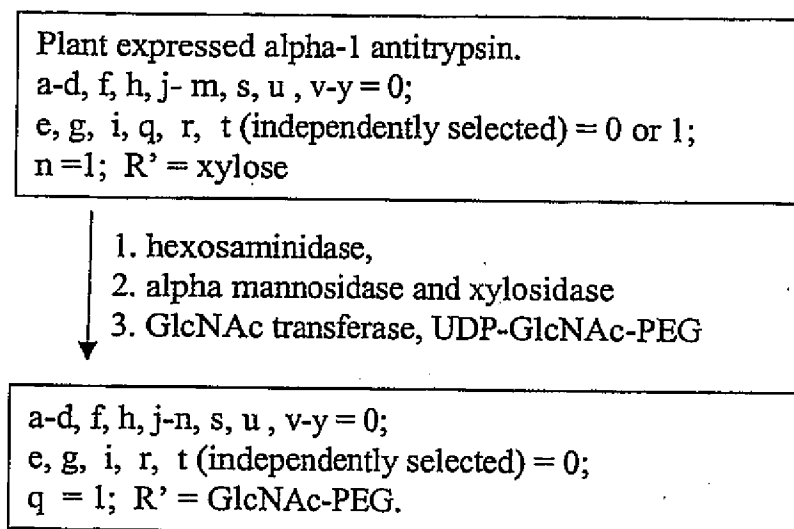


FIG. 38M

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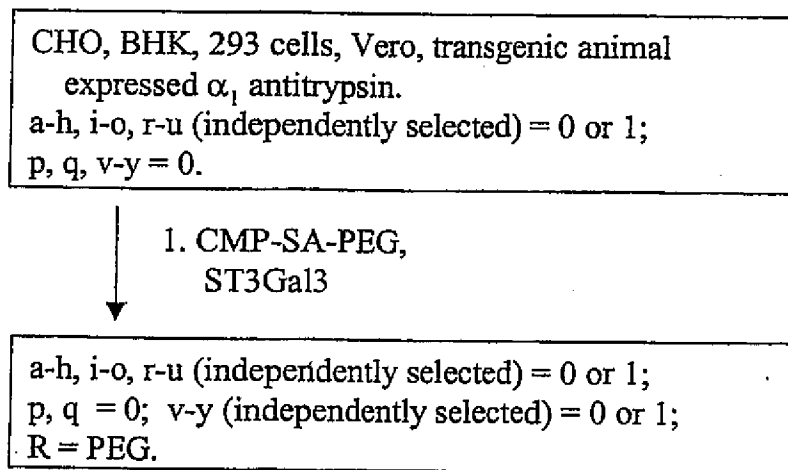
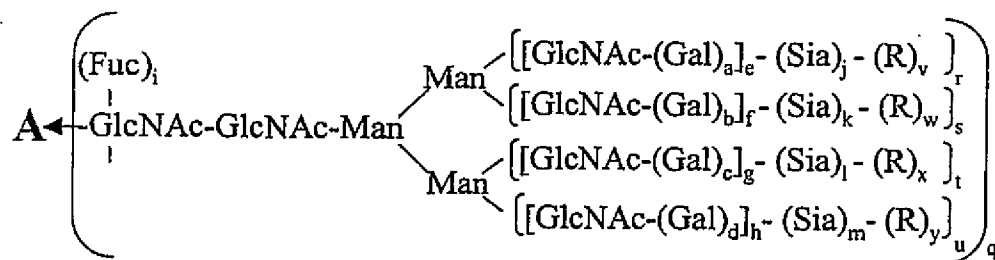
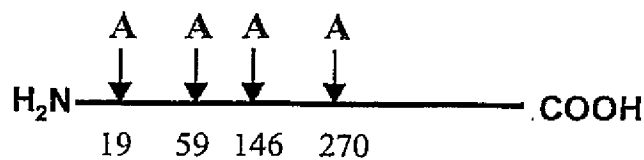


FIG. 38N

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 39A

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CHO, BHK, 293 cells, Vero expressed Cerezyme
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 39B

CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-M-6-P (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = mannose-6-phosphate

FIG. 39C

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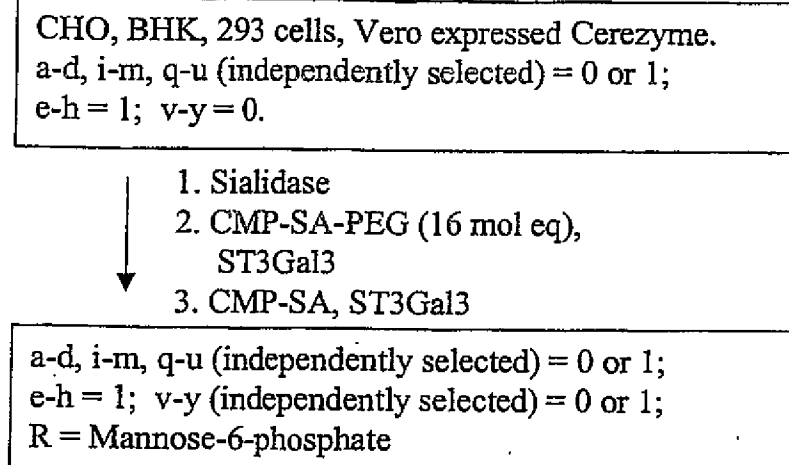


FIG. 39D

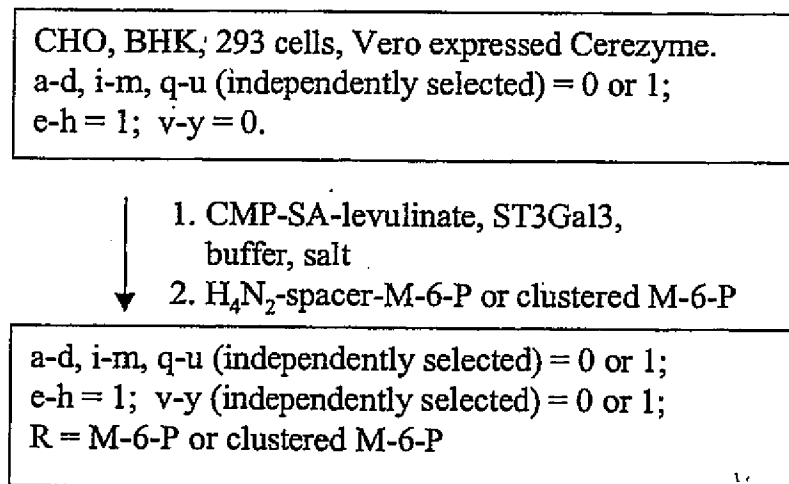


FIG. 39E

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CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

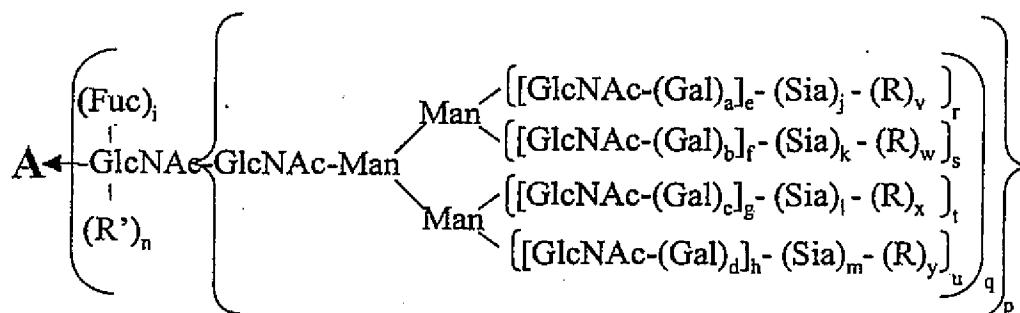
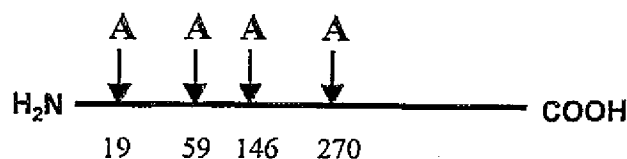


1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 39F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 39G

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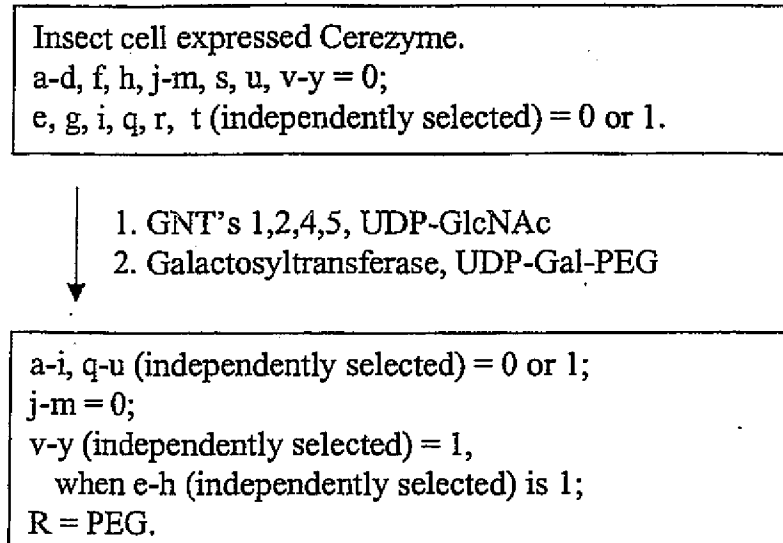


FIG. 39H

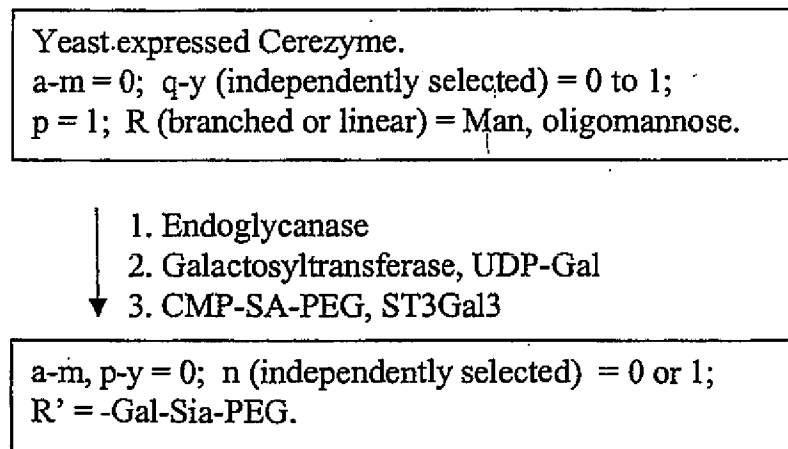


FIG. 39I

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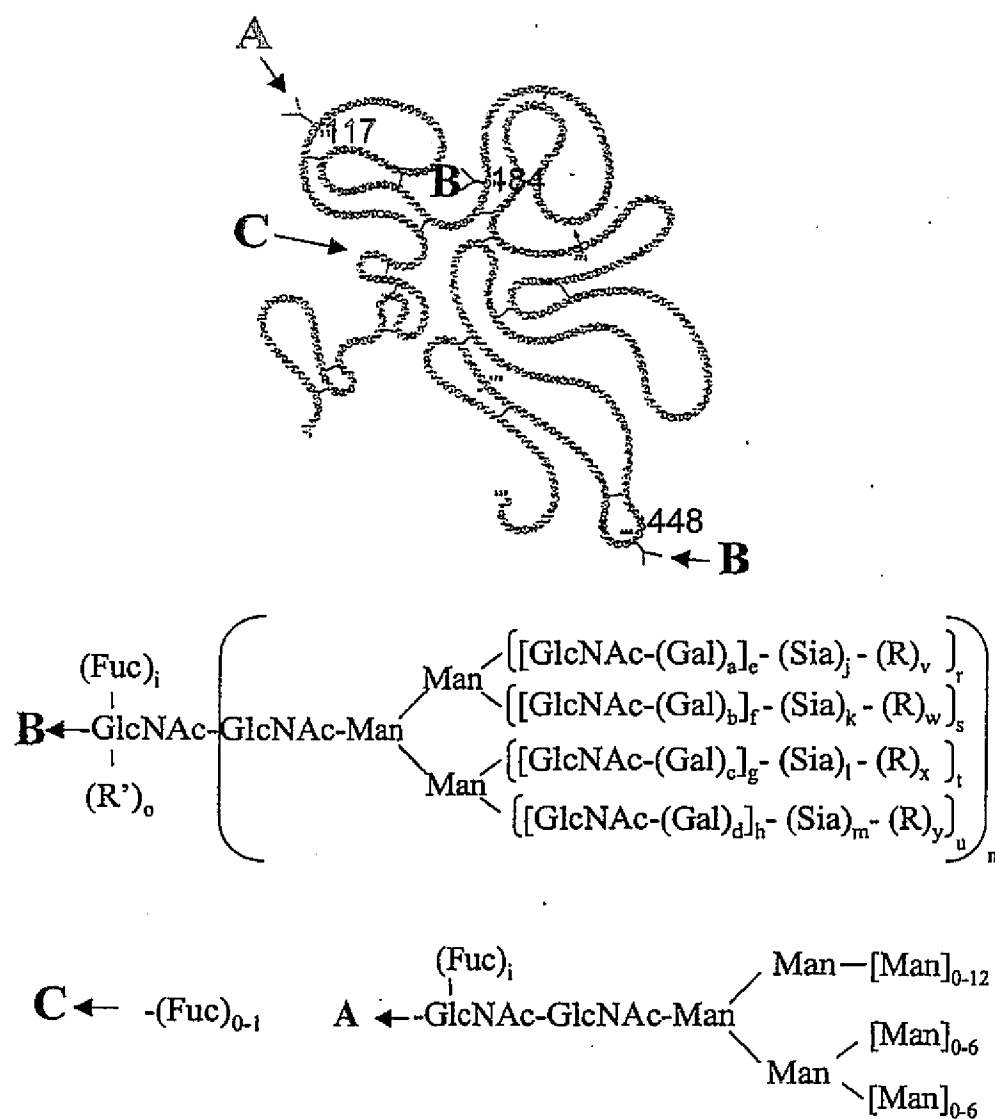
CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0; v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 39J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 40A

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CHO, BHK, 293 cells, Vero expressed tPA
 a-g, n = 1; h = 1 to 3;
 j-m, i, (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1; o, v-y = 0.

1. Mannosidase(s), sialidase
2. GNT1,2 (4 and/or 5) UDP-GlcNAc
3. Gal transferase, UDP-Gal
4. CMP-SA-PEG, ST3Gal3

A = B; a-g, n = 1; h = 1 to 3;
 i, r-u (independently selected) = 0 or 1;
 o = 0; j-m, v-y (independently selected) = 0 or 1;
 R = PEG

FIG. 40B

Insect or fungi cell expressed tPA
 A = B; a-d, f, h, j-o, s, u, v-y = 0;
 e, g, i, n, r, t (independently selected) = 0 or 1.

1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

A = B; b, d, f, h, k, m, o, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 n = 1; j, l, v, x (independently selected) = 0 or 1;
 R = PEG.

FIG. 40C

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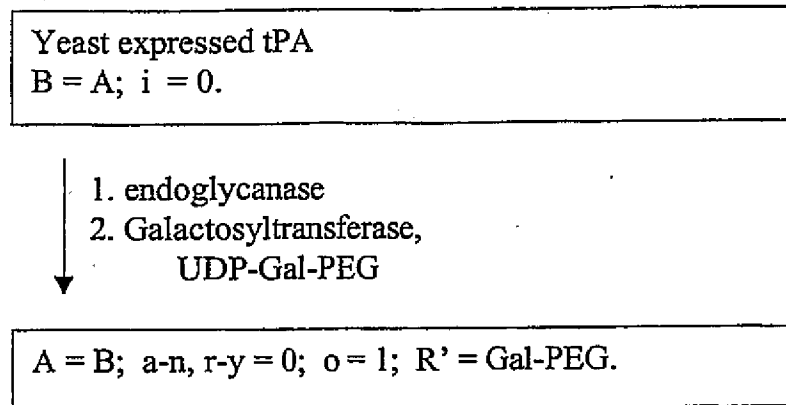


FIG. 40D

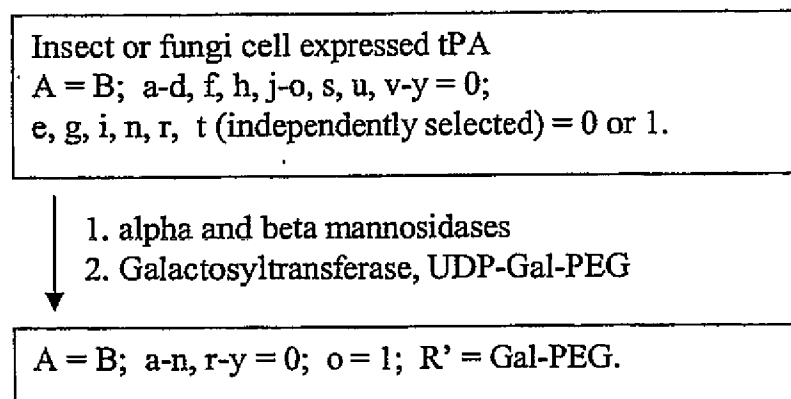


FIG. 40E

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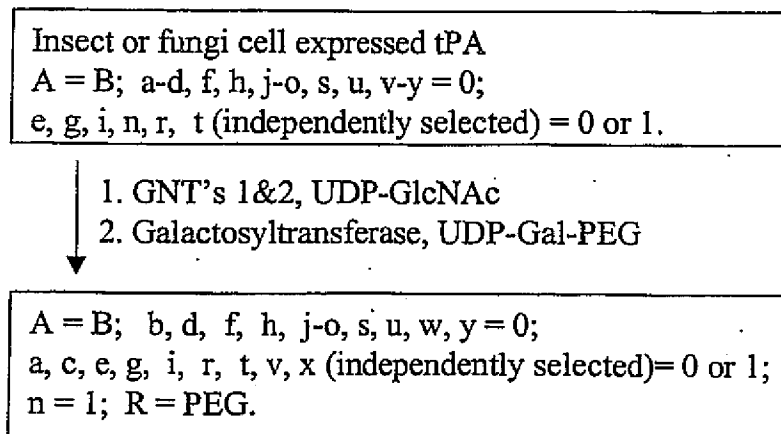


FIG. 40F

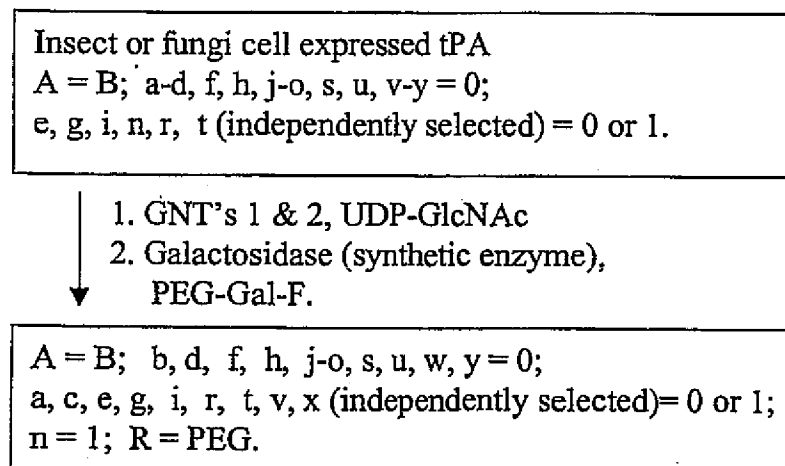
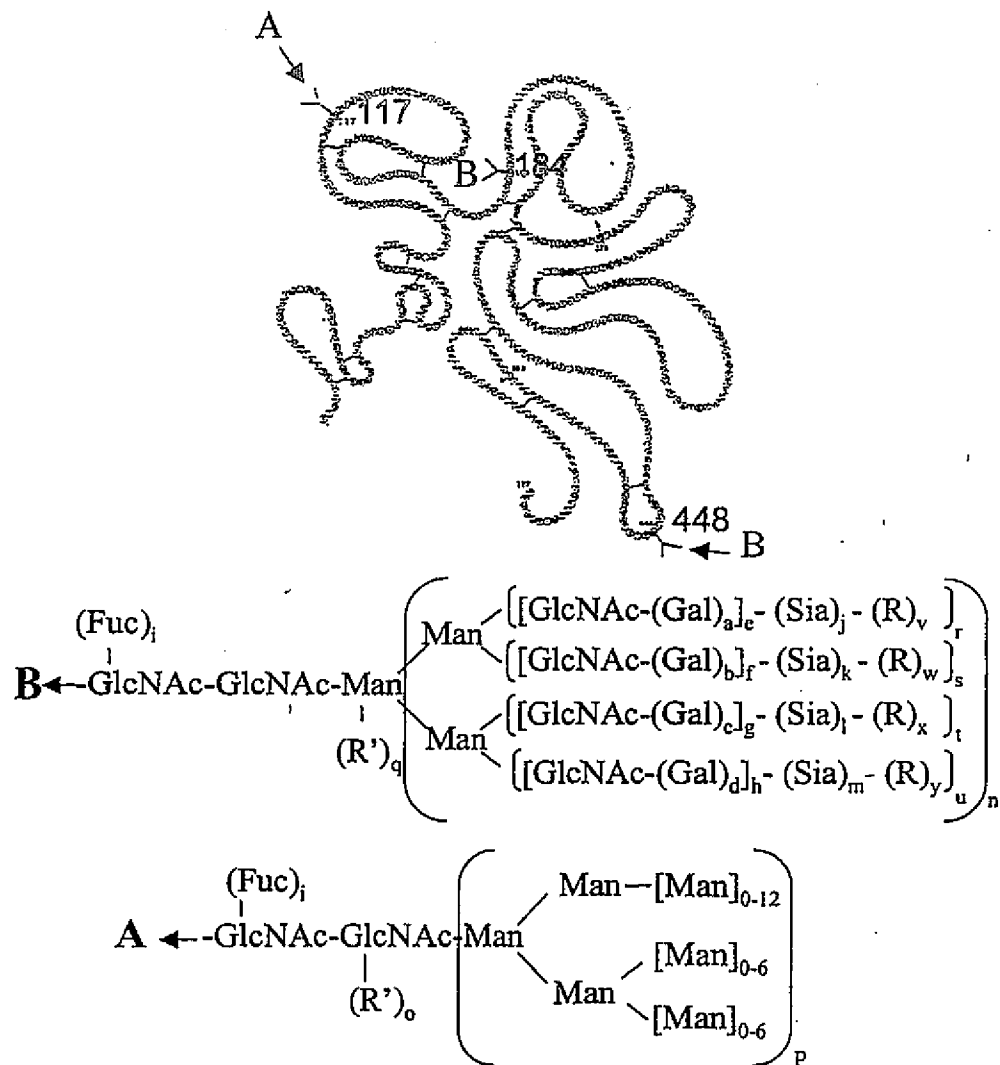


FIG. 40G

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 40H

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NSO expressed tPA

A = B; a-m, r-u (independently selected) = 0 or 1;
n = 1; o, p, q, v-y = 0

- ↓
1. sialidase, alpha-galactosidase
 2. CMP-SA-levulinate, ST3Gal3,
 3. H₄N₂-PEG

A = B; a-m, r-y (independently selected) = 0 or 1;
n = 1; o, p, q = 0;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 40I

CHO, BHK, 293 cells, Vero expressed tPA

a-g, n, p = 1; h = 1 to 3;
j-m, i, (independently selected) = 0 or 1;
r-u (independently selected) = 0 to 1; q, o, v-y = 0.

- ↓
1. alpha and beta Mannosidases
 2. CMP-SA, ST3Gal3
 3. Galactosyltransferase, UDP-Gal-PEG

a-g, n = 1; h = 1 to 3;
i, r-u (independently selected) = 0 or 1; o = 1;
q, p, v-y = 0; j-m (independently selected) = 0 or 1;
R' = Gal-PEG

FIG. 40J

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Plant expressed tPA

A = B; a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1;

n=1; R' = xylose

- ↓
1. hexosaminidase,
 2. alpha mannosidase and xylosidase
 3. GlcNAc transferase, UDP-GlcNAc-PEG

A = B; a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0;

q = 1; R' = GlcNAc-PEG.

FIG. 40K

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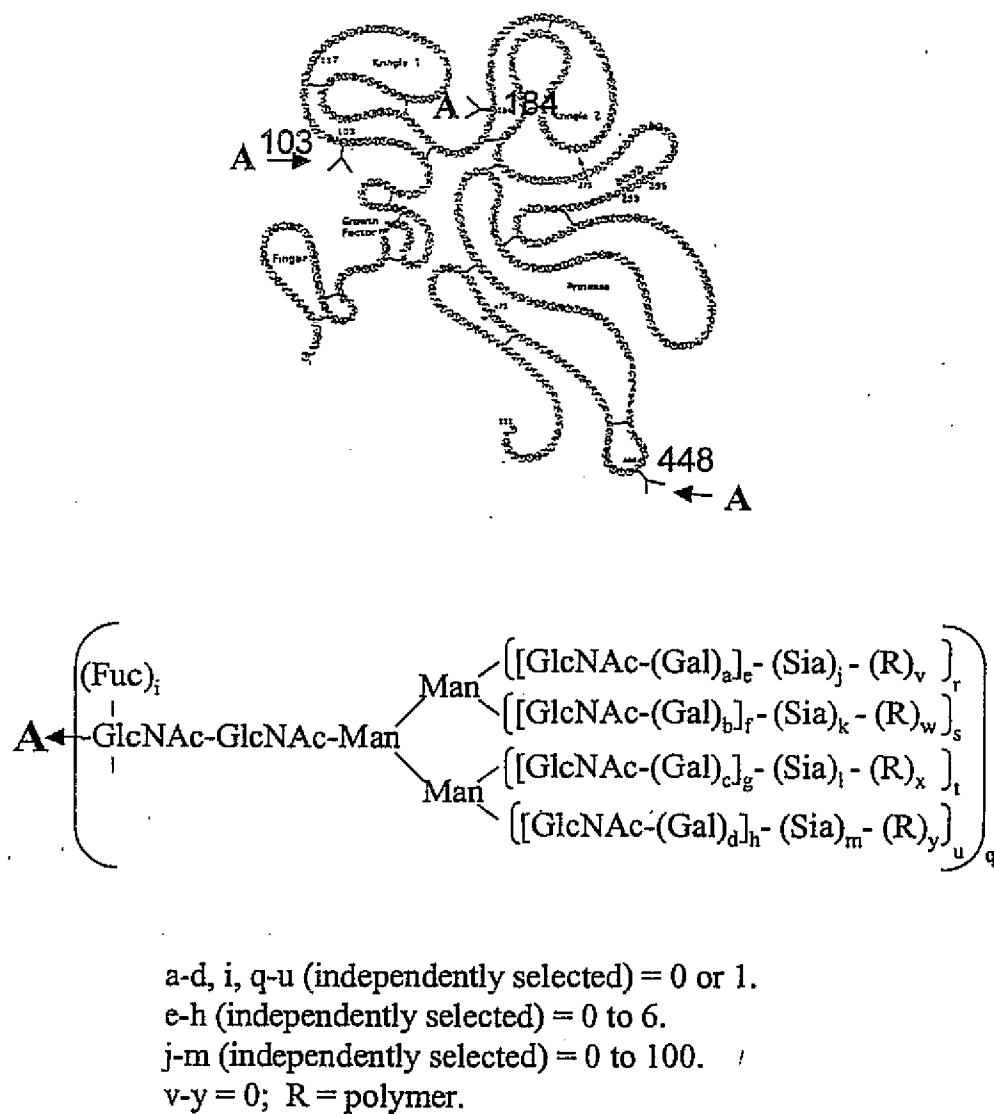


FIG. 40L

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CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 40M

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40N

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NSO expressed TNK tPA

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

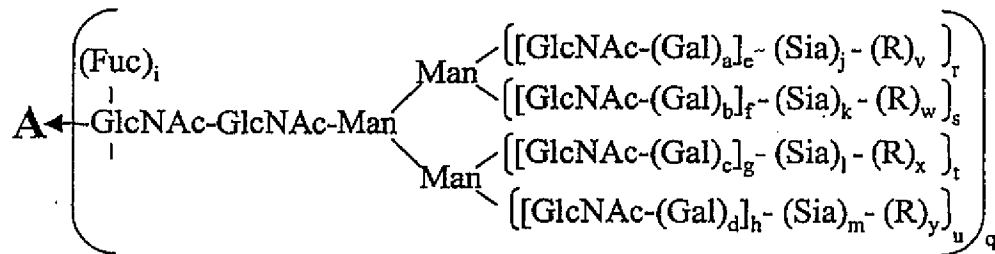
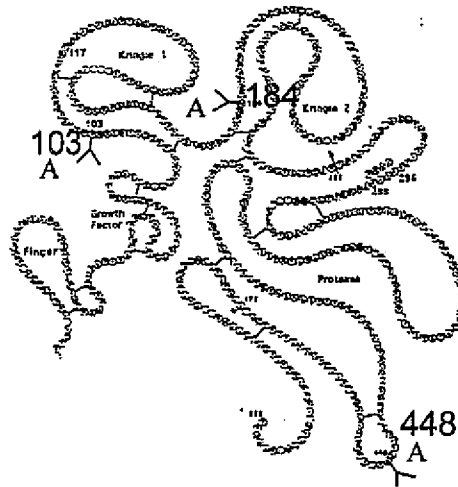
e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 400

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 40P

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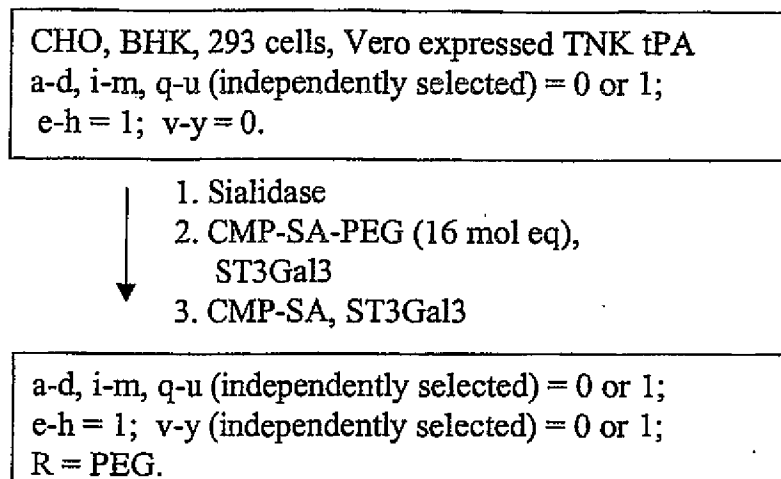


FIG. 40Q

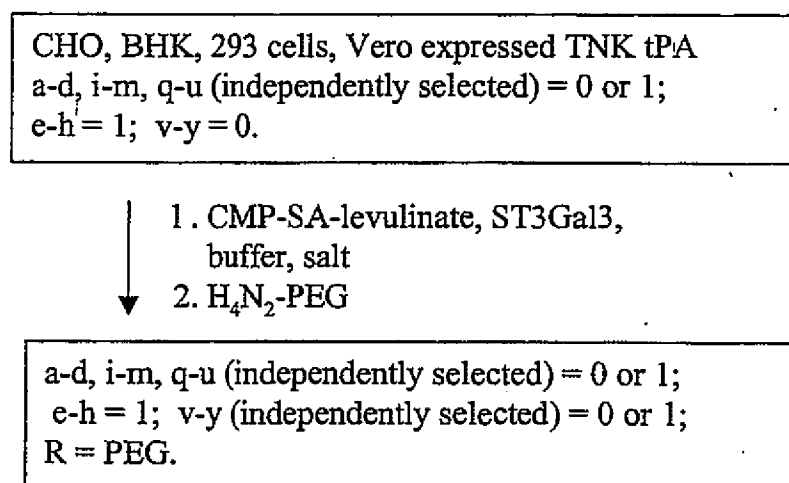


FIG. 40R

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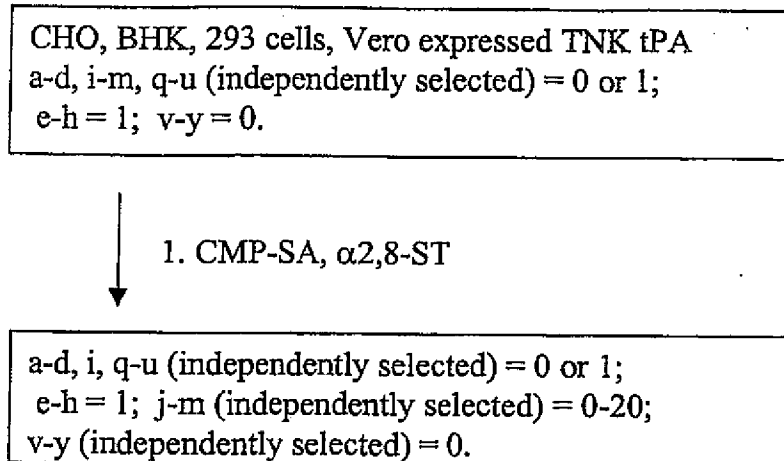
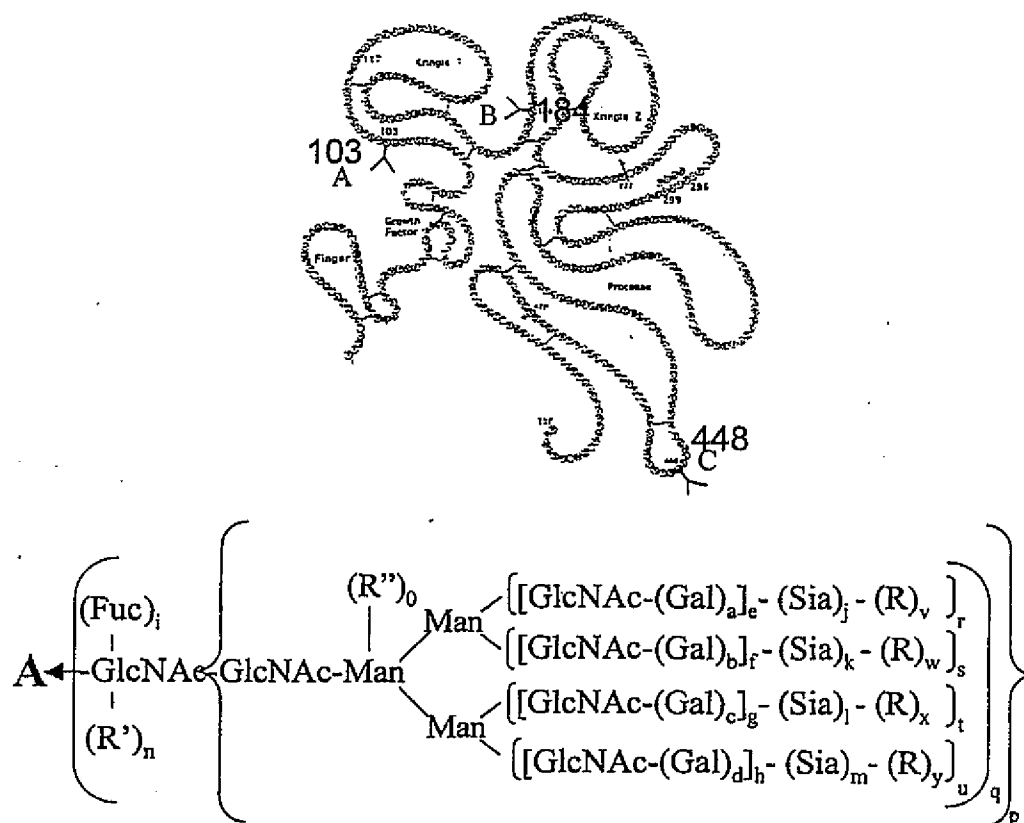


FIG. 40S

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a-d, i, n-y (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

R'' = glycosyl residue.

FIG. 40T

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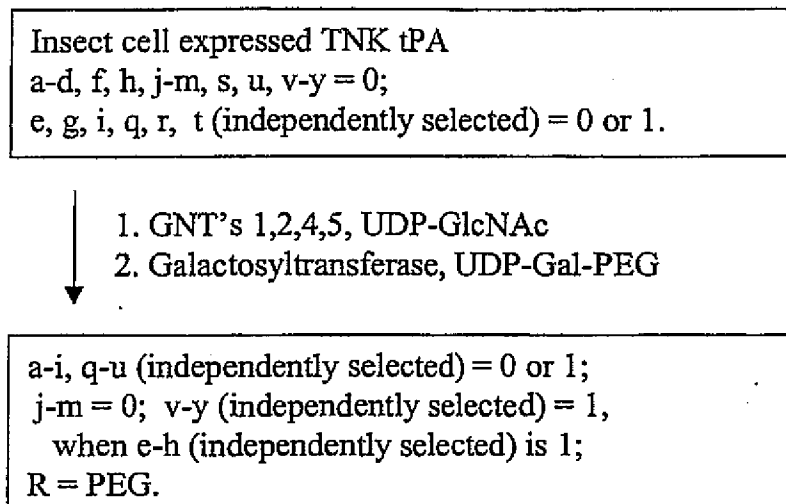


FIG. 40U

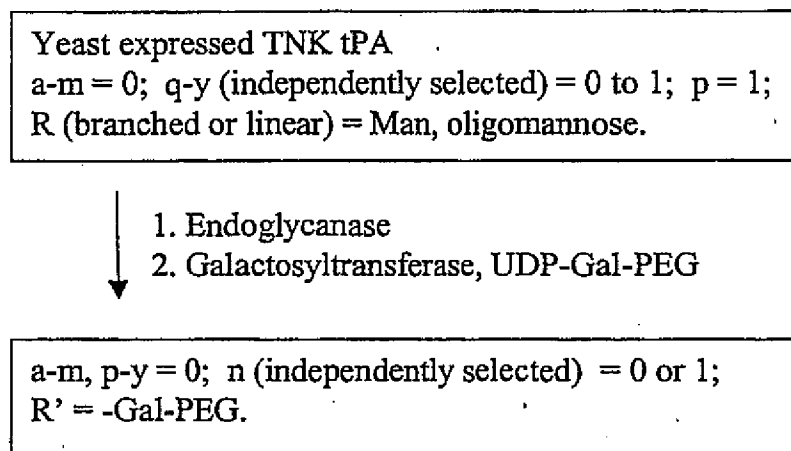


FIG. 40V

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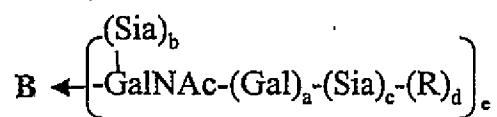
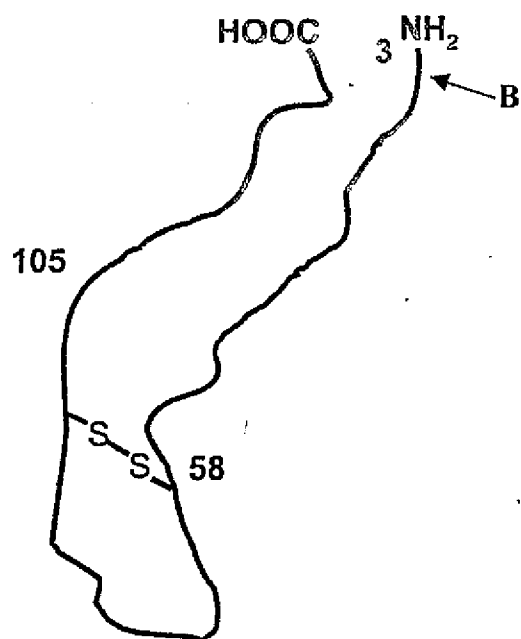
CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, anti-TNF
IG chimera produced in CHO.

a-m, r-u (independently selected) = 0 or 1; p, q = 1;
n = 0; v-y (independently selected) = 0 or 1;
R = linker-anti-TNF IG chimera protein.

FIG. 40W

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a-c, e (independently selected) = 0 or 1;
d = 0;
R = modifying group, mannose, oligo-
mannose.

FIG. 41A

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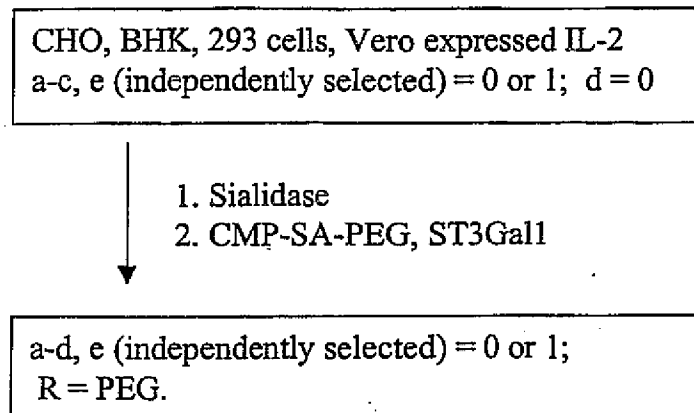


FIG. 41B

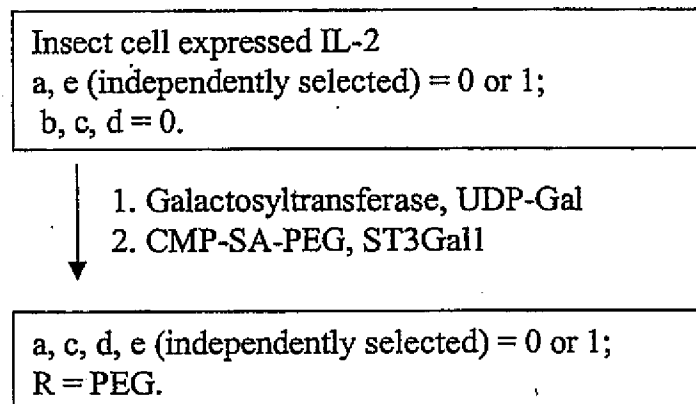


FIG. 41C

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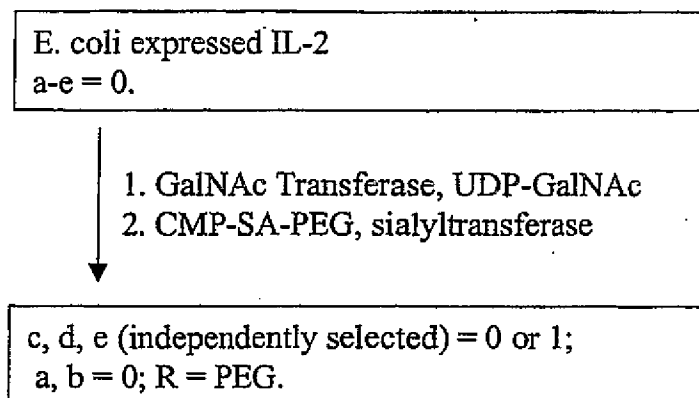


FIG. 41D

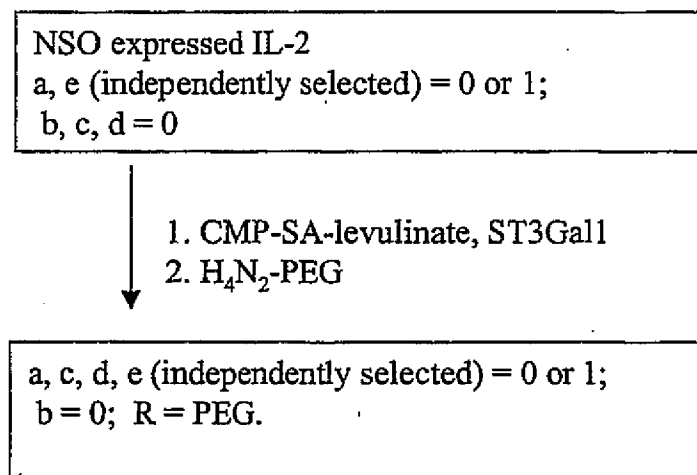


FIG. 41E

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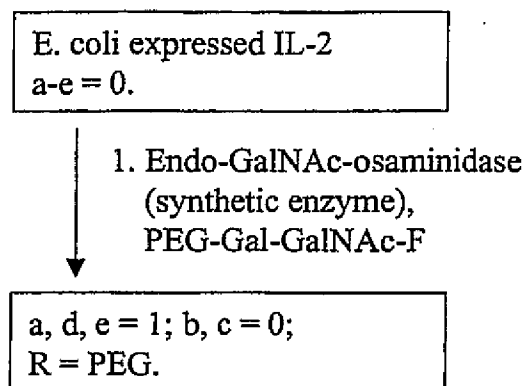


FIG. 41F

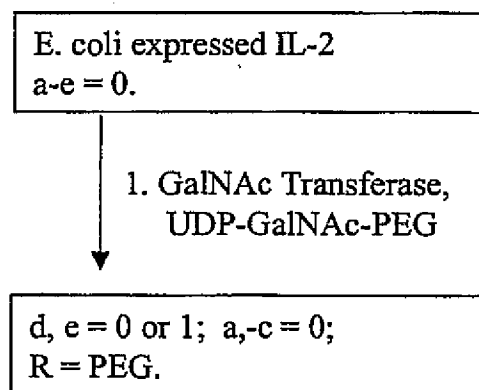
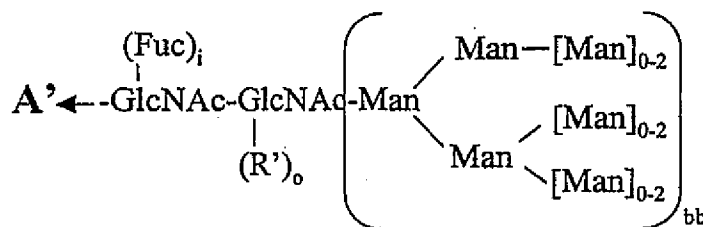
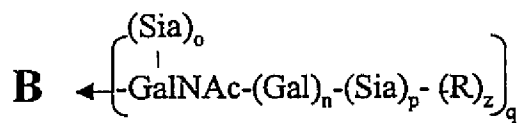
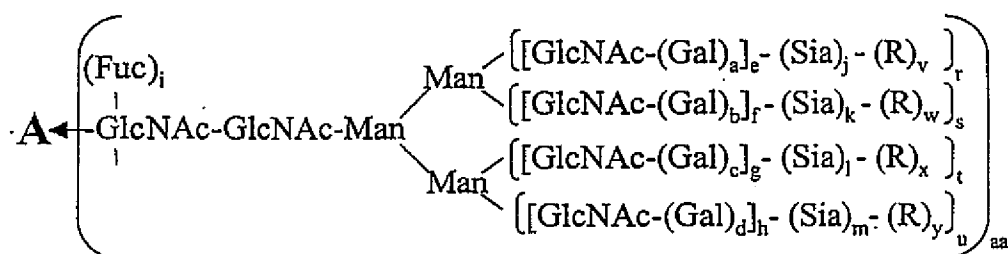


FIG. 41G

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2 peptides
 A and A' - N-linked sites
 B - O-linked sites



Alternate structure
 for some N-linked
 structures of A.

- a-d, i, n-u (independently selected) = 0 or 1.
 aa, bb (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 20.
 v-z = 0; R = polymer, glycoconjugate.

FIG. 42A

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CHO, BHK, 293s cells, Vero, MDCK, HEKC expressed
Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.



1. Sialidase

2. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n, q-u (independently selected) = 0 or 1;

o, p, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42B

CHO, BHK, 293S cells, Vero, MDCK, 293S, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.



1. Sialidase

2. CMP-SA-PEG, ST3Gal3

3. ST3Gal1, CMP-SA

e-h = 1 to 4;

aa, bb, a-d, i, n, p-u (independently selected) = 0 or 1;

o, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42C

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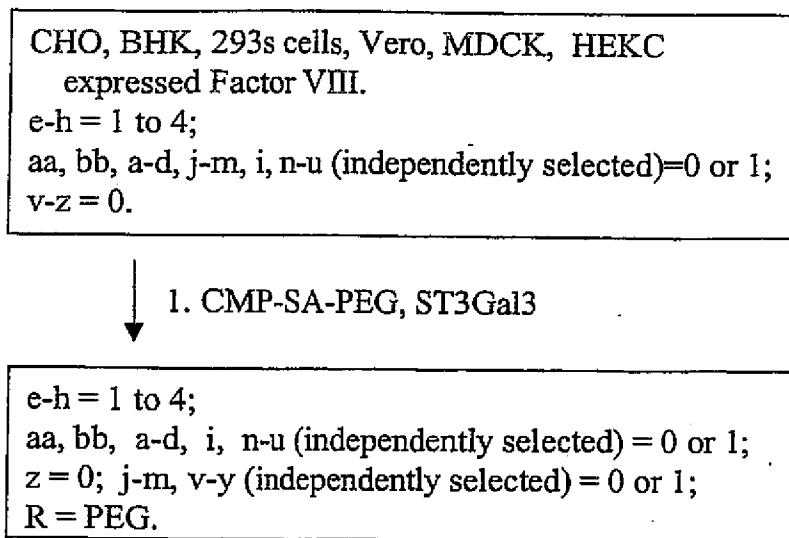


FIG. 42D

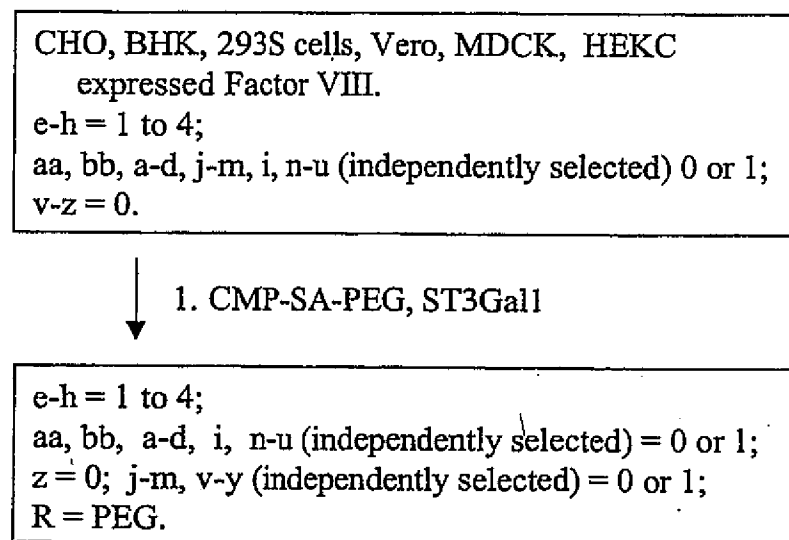


FIG. 42E

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;

v-z = 0.



1. CMP-SA-PEG, α 2,8-ST

e-h = 1 to 4;

aa, bb, a-d, i, n-y (independently selected) = 0 or 1;

z = 0; j-m (independently selected) = 0 to 2;

v-y (independently selected) = 1,

when j-m (independently selected) is 2;

R = PEG.

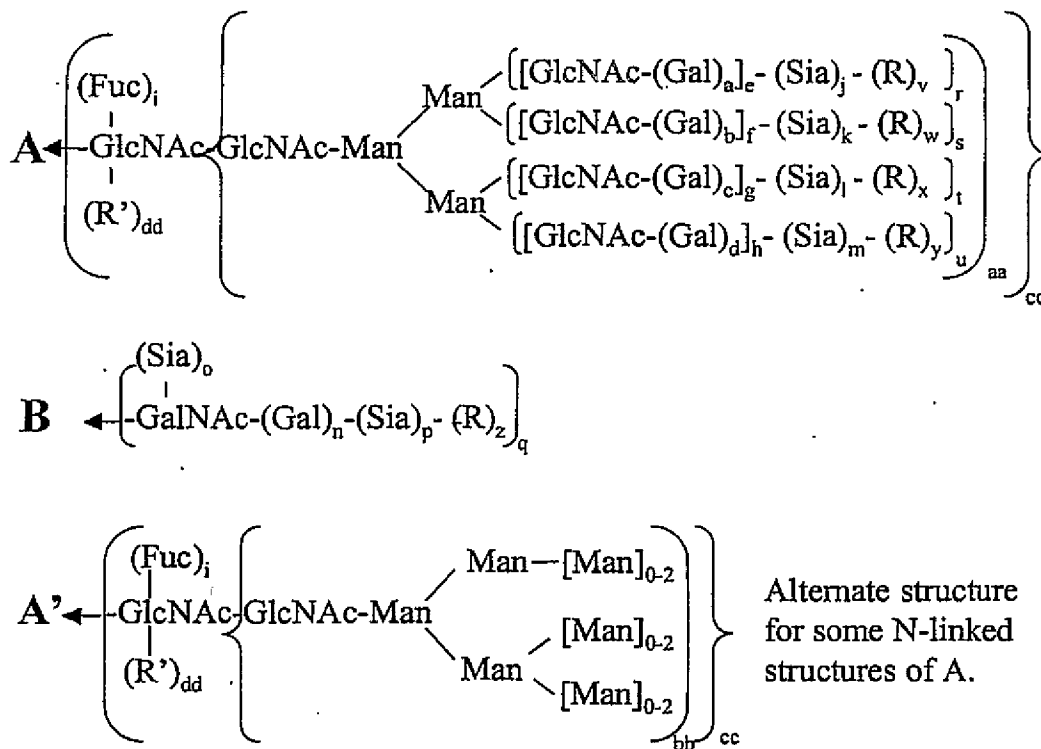
FIG. 42F

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2 peptides

A or A' - N-linked sites

B - O-linked sites



a-d, i, n-u, (independently selected) = 0 or 1.

aa, bb, cc, dd (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 42G

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

↓ 1. CMP-SA-levulinate, ST3Gal3,
2. H₄N₂-PEG

e-h = 1 to 4;

aa, bb, cc, a-d, i, n-u (independently selected) = 0 or 1;

dd, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42H

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

↓ 1. endo-H
2. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 42I

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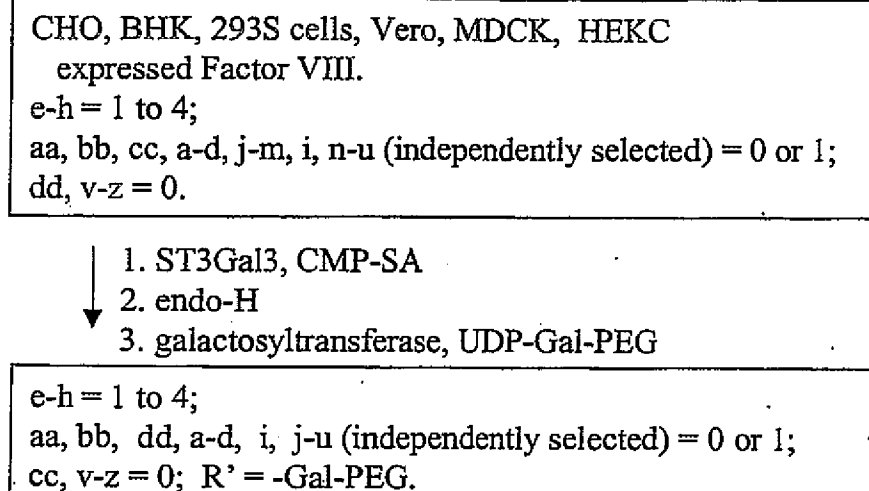


FIG. 42J

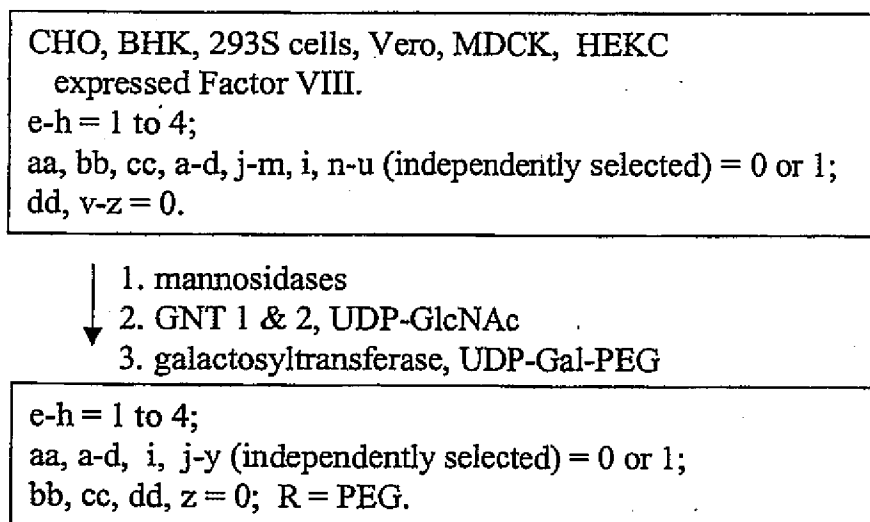


FIG. 42K

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

1. mannosidases
- ↓
2. GNT-1, 2, 4 & 5; UDP-GlcNAc
- ↓
3. galactosyltransferase, UDP-Gal
- ↓
4. ST3Gal3, CMP-SA

e-h = 1 to 4;

aa, bb, cc, a-d, i, j-q (independently selected) = 0 or 1;
dd, v-z = 0.

FIG. 42L

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

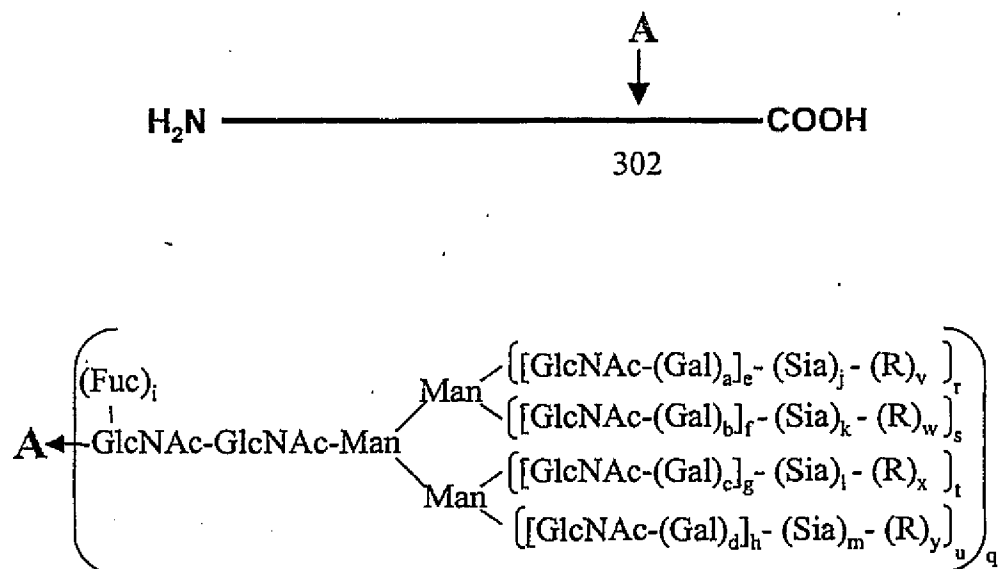
- ↓
1. mannosidases
- ↓
2. GNT-1, UDP-GlcNAc-PEG

e-h = 0 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;
bb, cc, dd, z = 0.

FIG. 42M

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a-d, i, q-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer.

FIG. 43A

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CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 43B

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 43C

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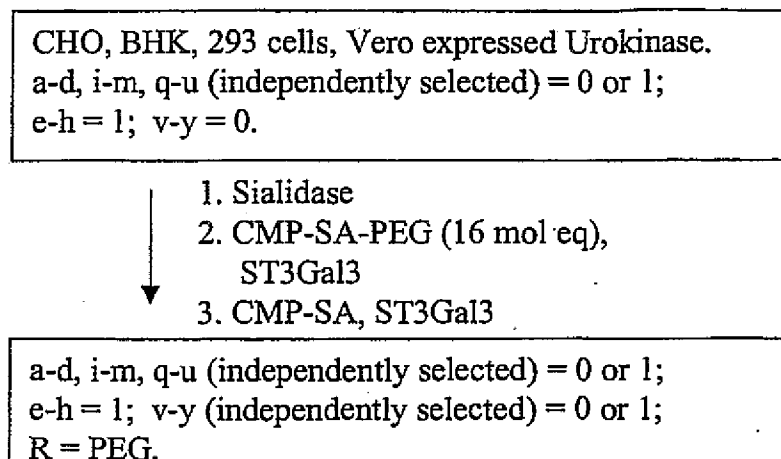


FIG. 43D

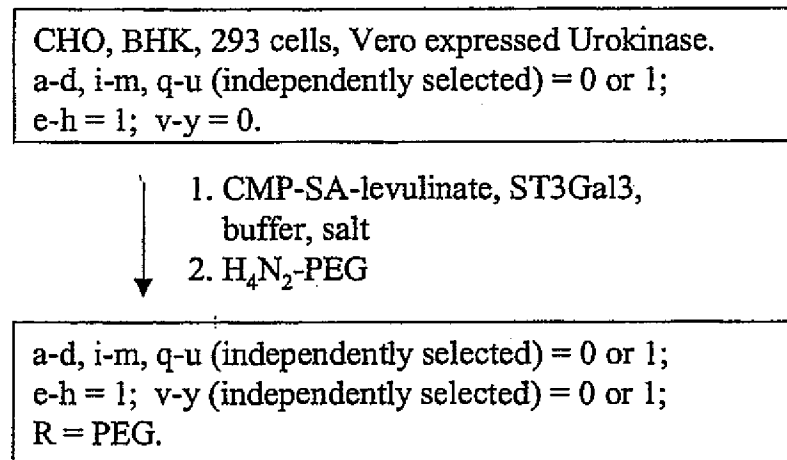


FIG. 43E

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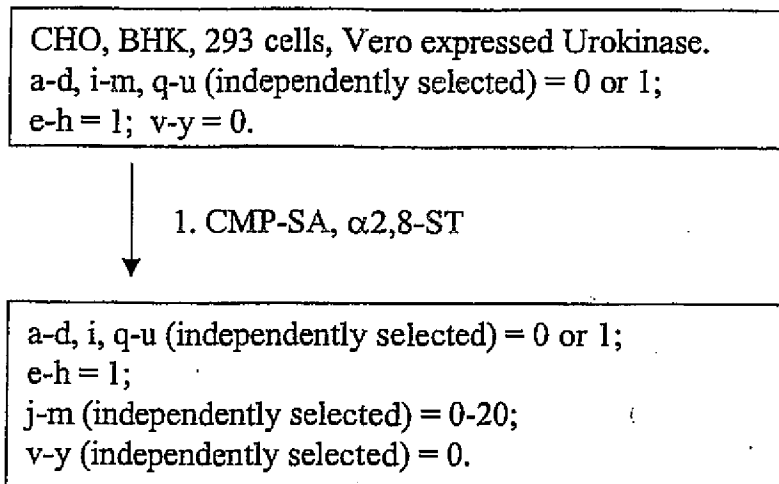
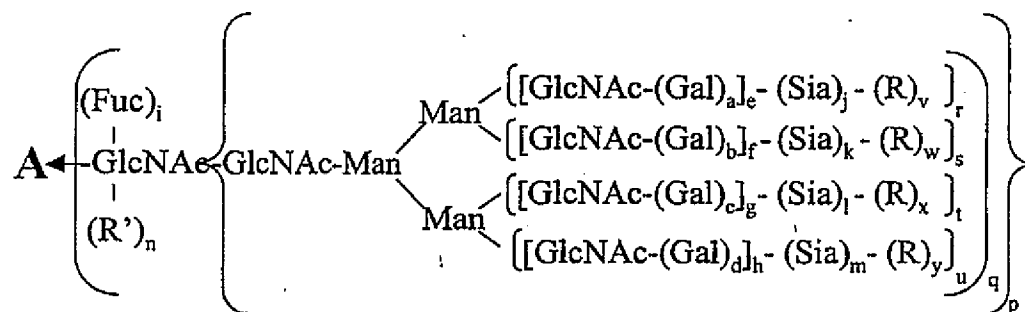


FIG. 43F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

$$v-y=0;$$

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 43G

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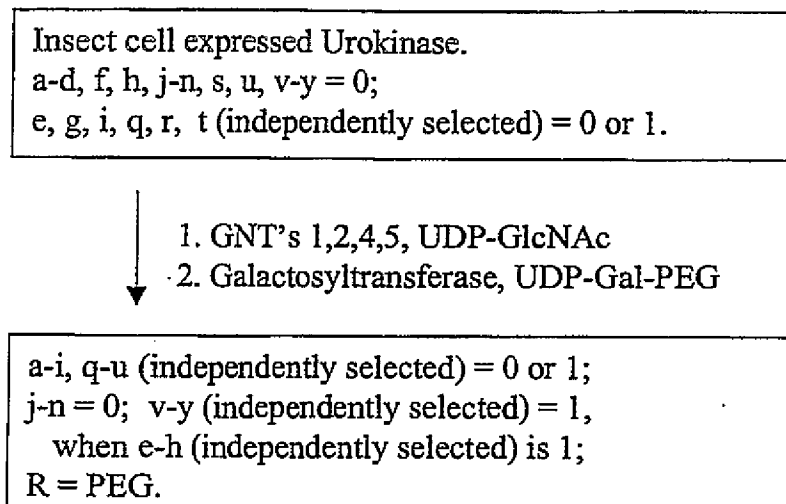


FIG. 43H

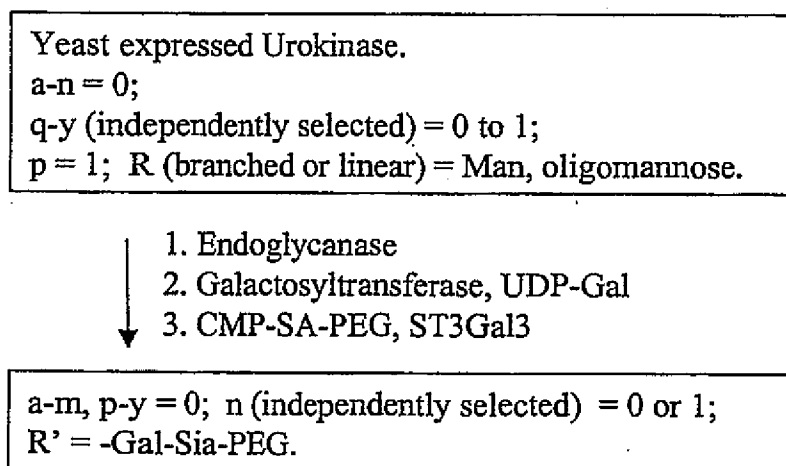


FIG. 43I

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CHO, BHK, 293 cells, Vero expressed Urokinase.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; n, v-y = 0.

1. CMP-SA-linker-SA-CMP, ST3Gal3
2. ST3Gal1, desialylated Urokinase produced in CHO.
3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
 p = 1; n = 0;
 v-y (independently selected) = 0 or 1;
 R = linker-Urokinase.

FIG. 43J

Isolated Urokinase.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0; n = 0;
 Sia (independently selected) = Sia or SO₄;
 Gal (independently selected) = Gal or GalNAc;
 GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

1. sulfohydrolase
2. CMP-SA-PEG, sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;
 n = 0; e-h = 1; Sia = Sia;
 Gal (independently selected) = Gal or GalNAc;
 GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.
 v-y (independently selected) = 0 or 1;
 R = PEG.

FIG. 43K

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Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n = 0; v-y = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.



1. sulfohydrolase, hexosaminidase

2. UDP-Gal-PEG, galactosyltransferase

a-d, i, q-u (independently selected) = 0 or 1;

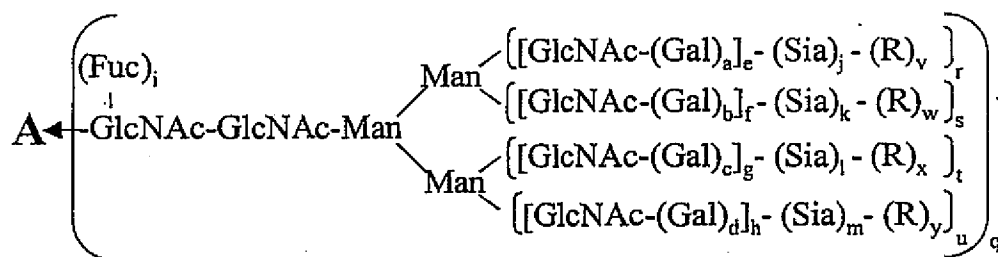
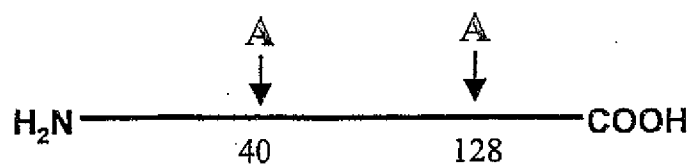
e-h = 1; j-n = 0; Gal (independently selected) = Gal;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 43L

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 44A

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CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 44B

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq), ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 44C

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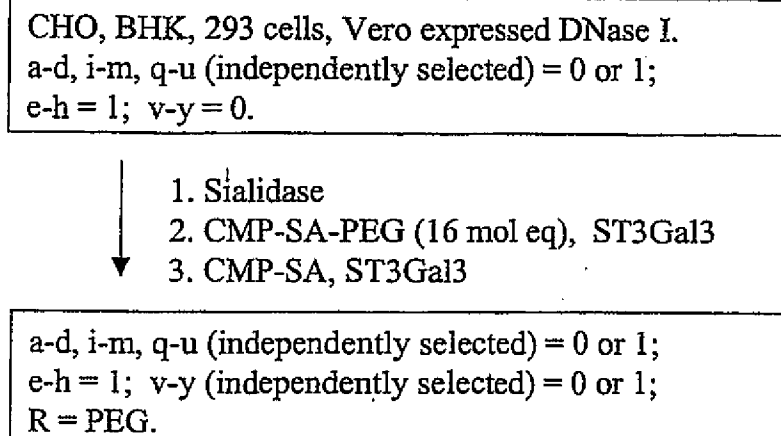


FIG. 44D

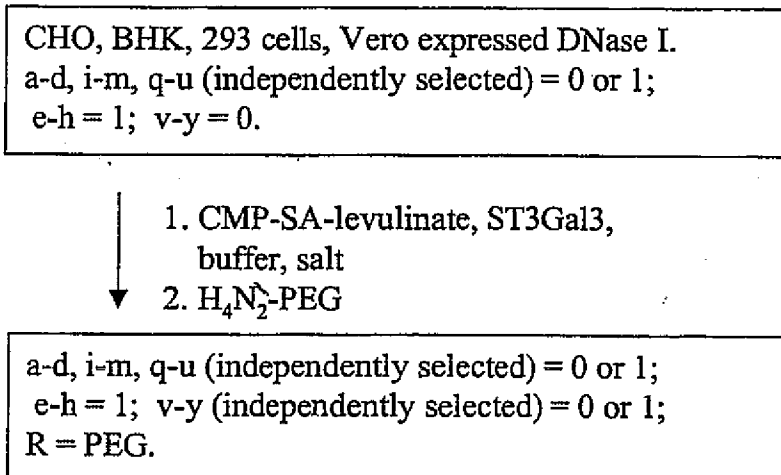


FIG. 44E

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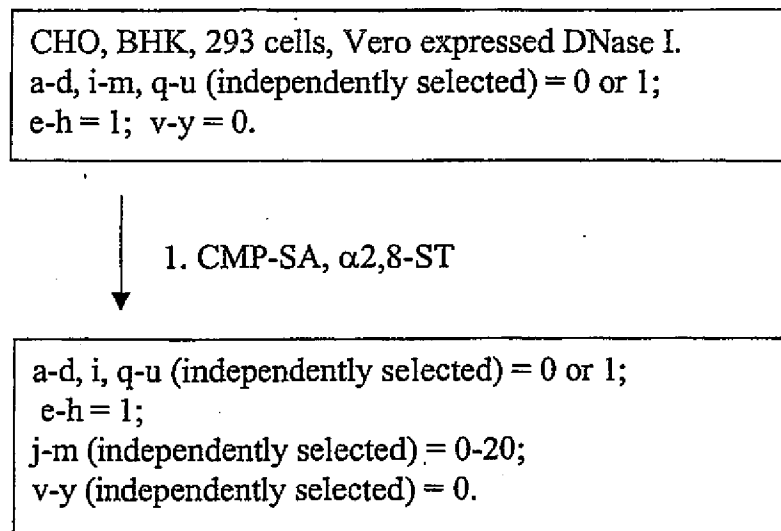
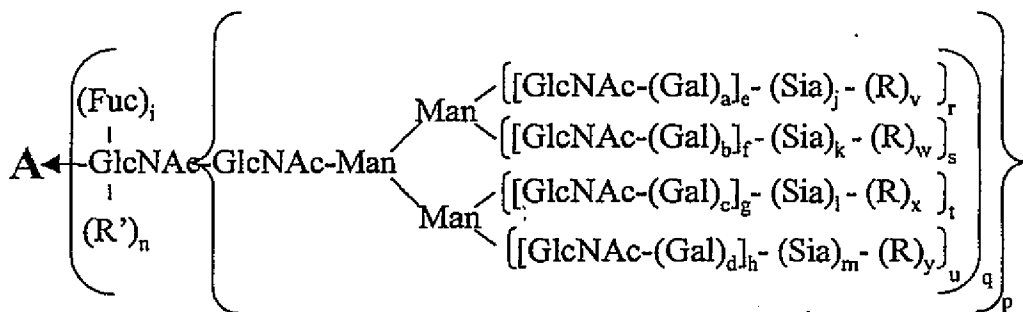
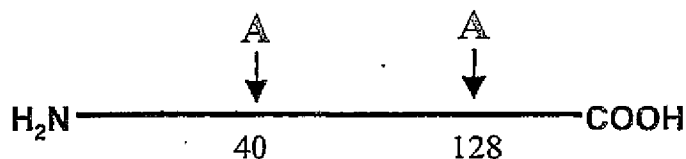


FIG. 44F

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a-d, i, n, p-u (independently selected) = 0 or 1.
e-h (independently selected) = 0 to 6.
j-m (independently selected) = 0 to 100.
v-y = 0;
R = modifying group, mannose, oligo-mannose;
R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 44G

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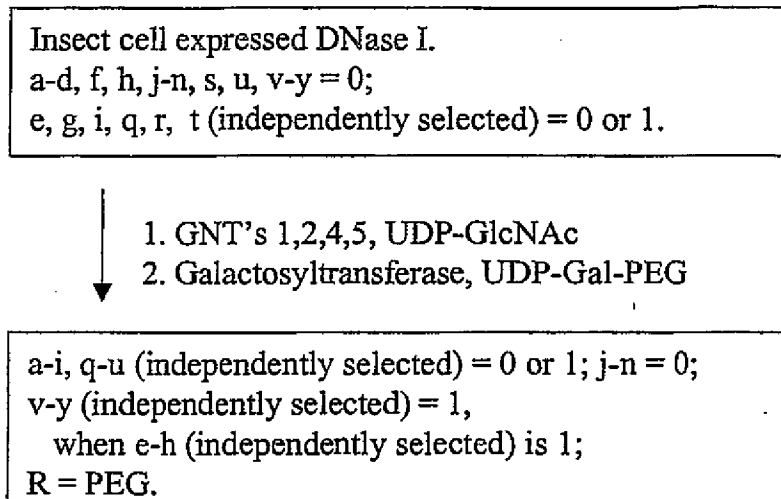


FIG. 44H

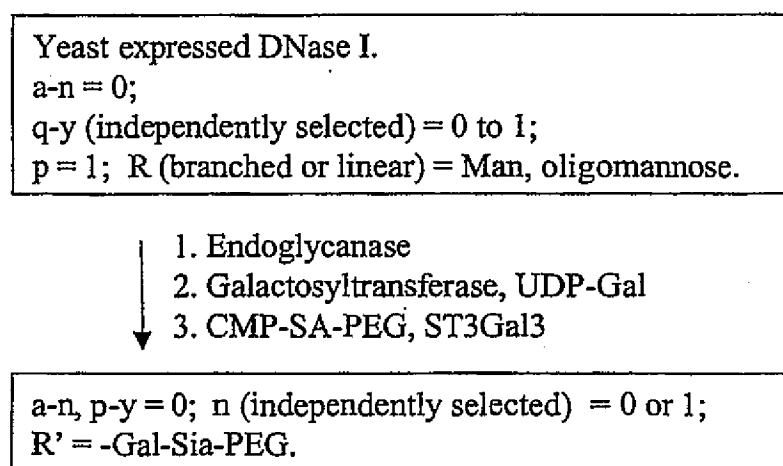


FIG. 44I

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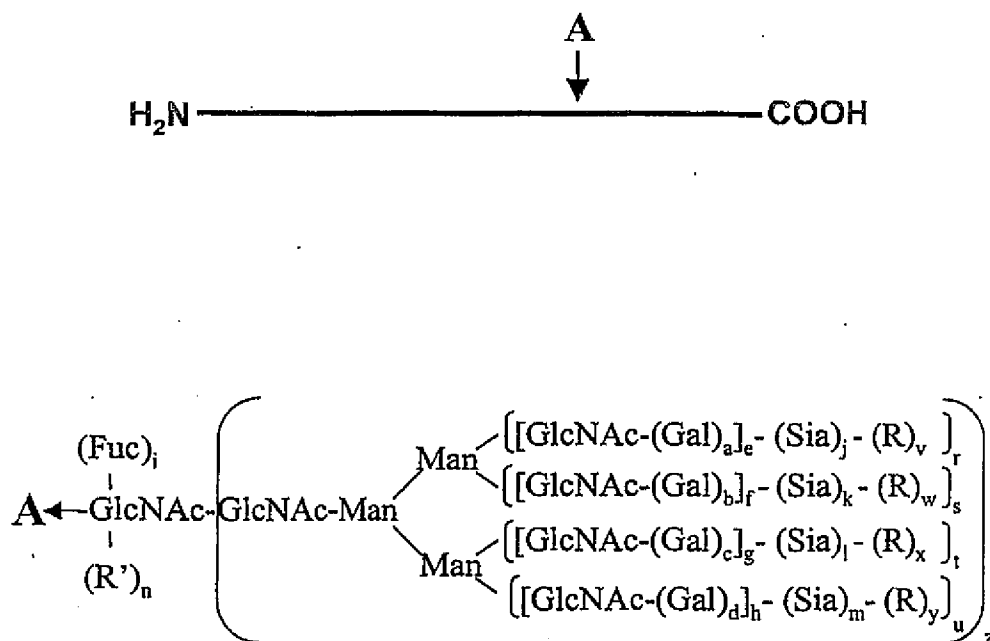
CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated alpha-1-
Proteinase inhibitor.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker- alpha-1-Proteinase inhibitor.

FIG. 44J

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 45A

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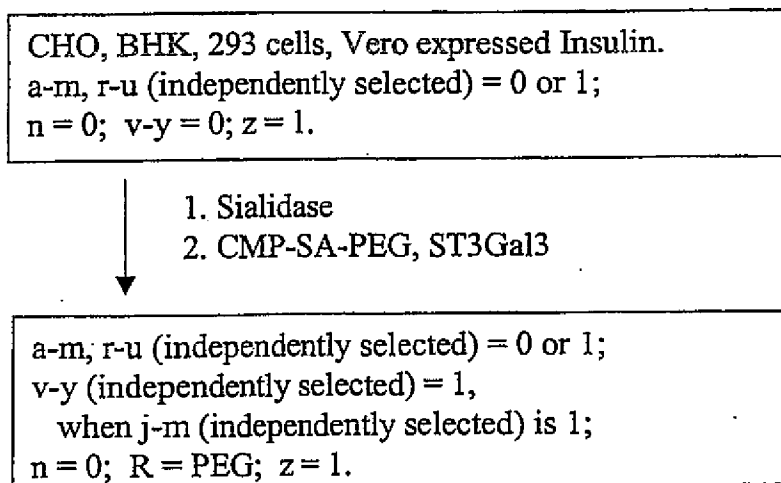


FIG. 45B

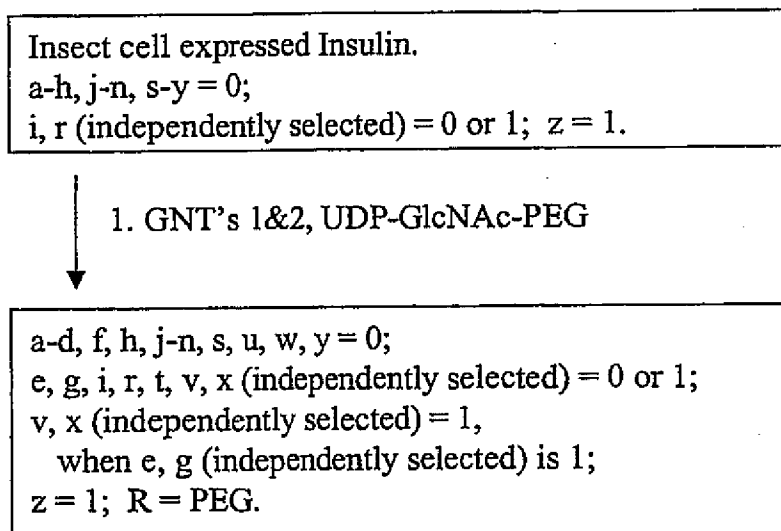


FIG. 45C

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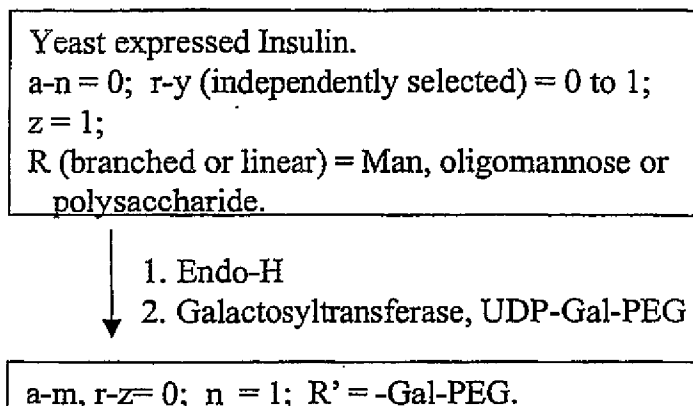
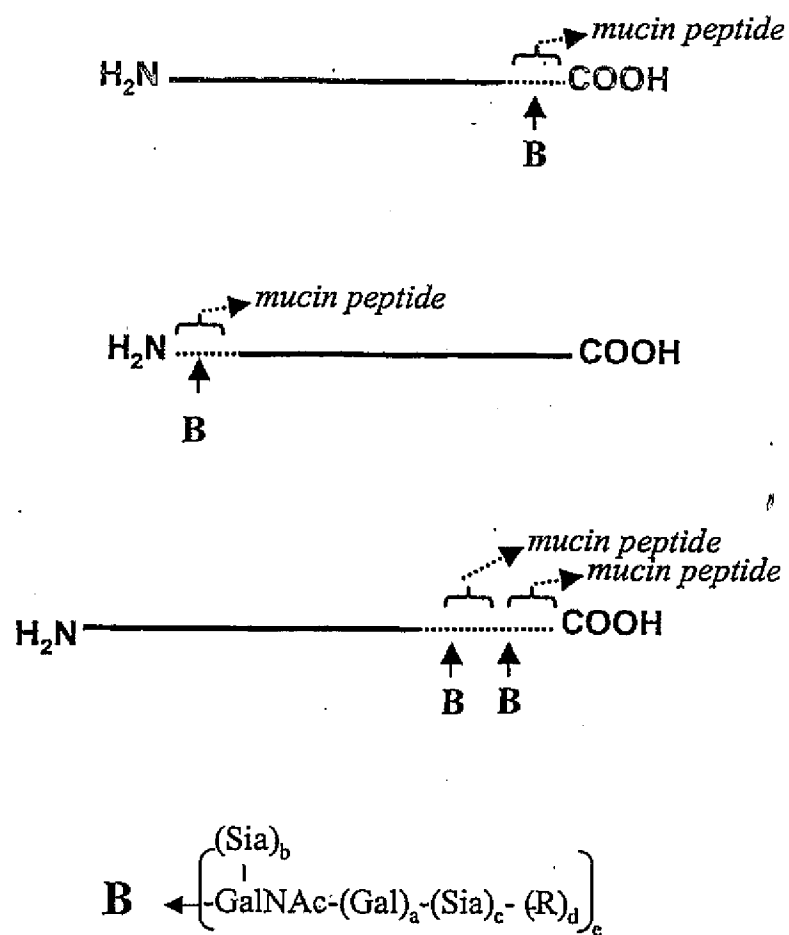


FIG. 45D

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer

FIG. 45E

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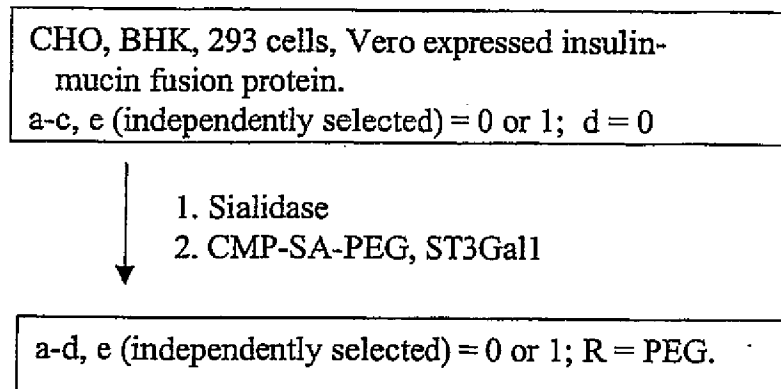


FIG. 45F

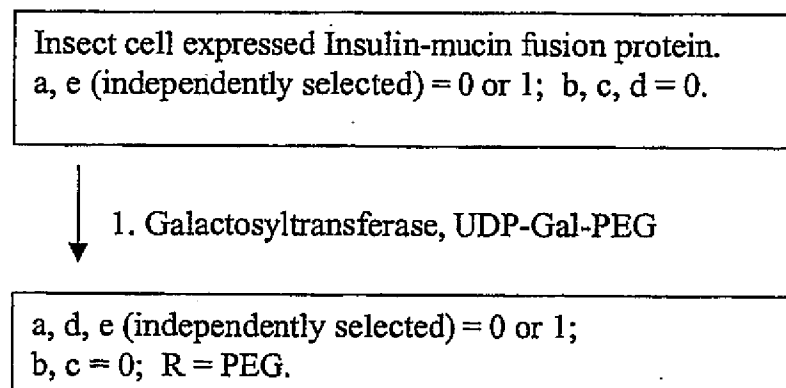


FIG. 45G

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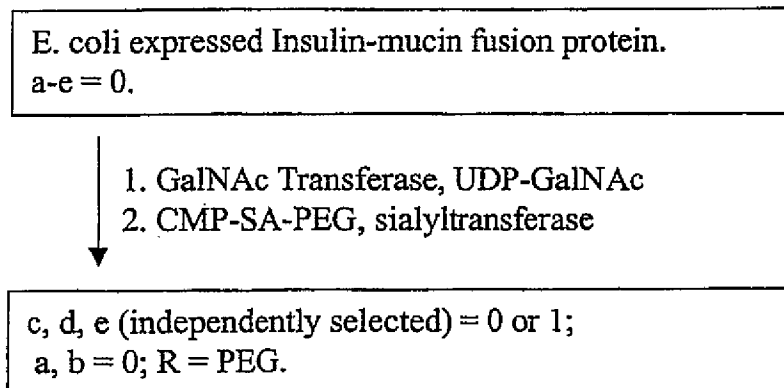
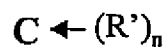
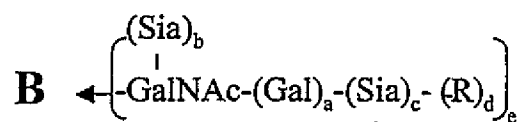
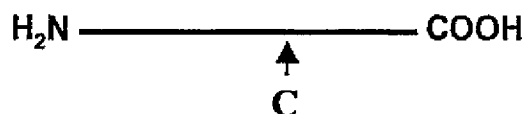
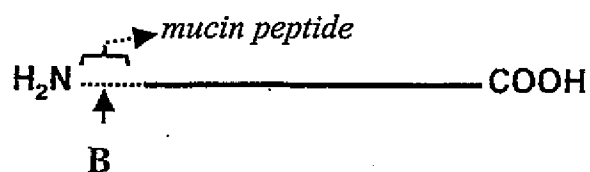


FIG. 45H

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = modifying group, mannose,
 oligo-mannose.

FIG. 45I

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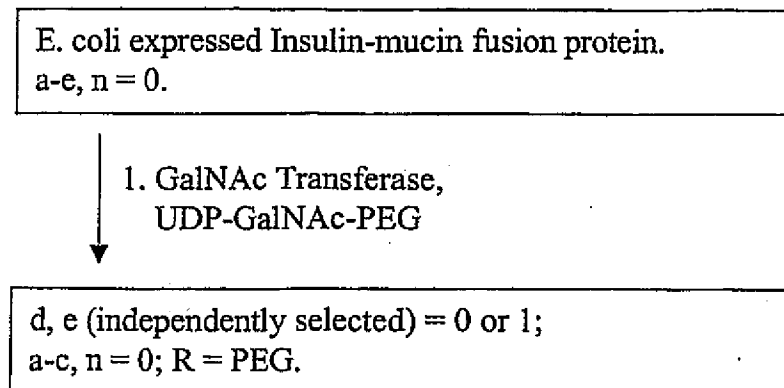


FIG. 45J

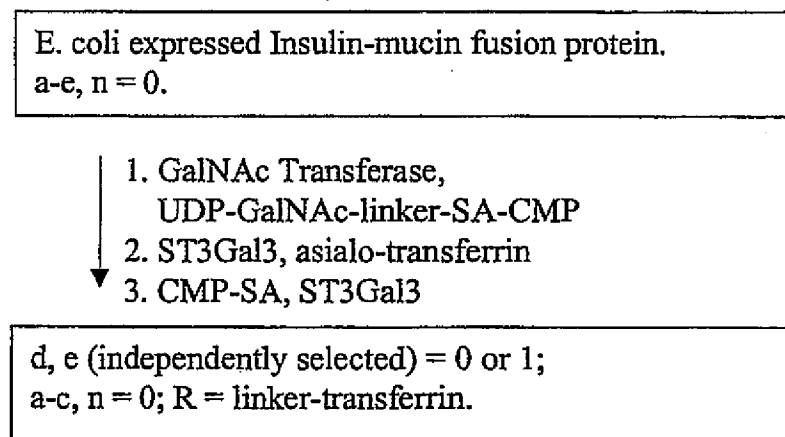


FIG. 45K

207/497

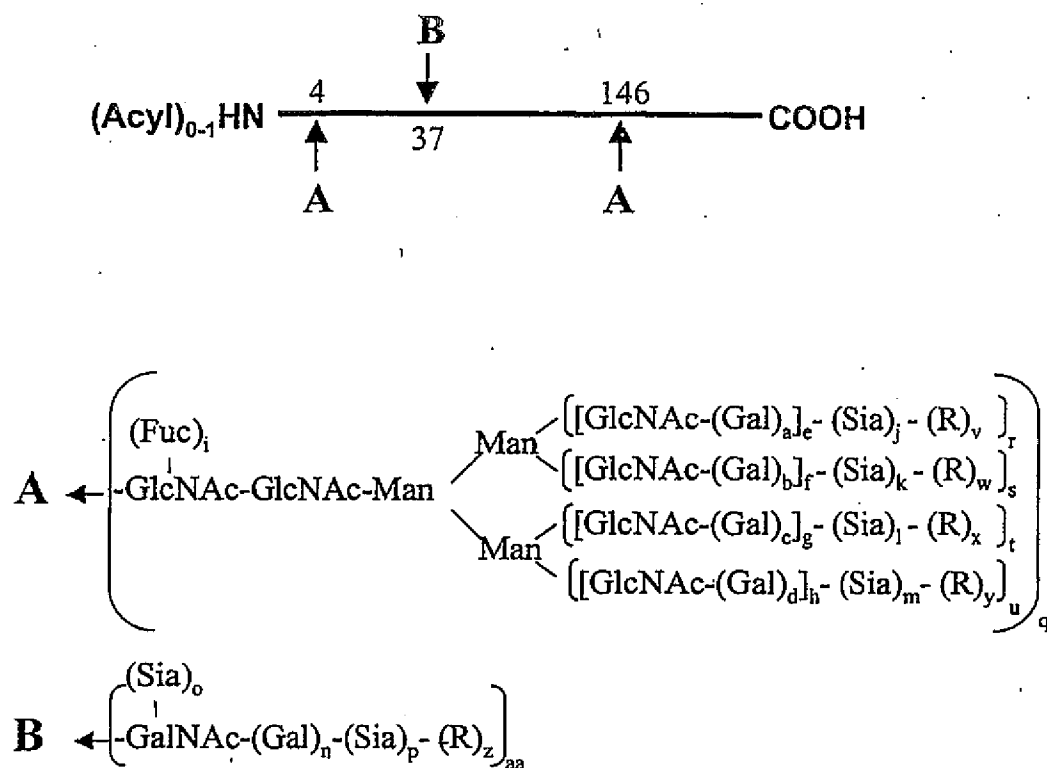
E. coli expressed Insulin (N)—no mucin peptide.
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
 2. ST3Gal3, asialo-transferrin
 3. CMP-SA, ST3Gal3

a-e = 0; n = 1;
R' = linker-transferrin.

FIG. 45L

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a-d, i, n-u, aa (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 46A

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CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-linker-lipid-A,
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
o, p, z = 0; n, e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = linker-lipid-A.

FIG. 46B

CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-linker-tetanus toxin, ST3Gal1
 3. CMP-SA, ST3Gal3

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y = 0; n, e-h = 1; R = tetanus toxin.

FIG. 46C

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NSO expressed M-antigen.

a-d, i-n, o-u, aa (independently selected) = 0 or 1;

e-h = 1; v-z = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. α -galactosidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-KLH, ST3Gal1

a-d, i-n, p-u, z, aa (independently selected) = 0 or 1;

e-h = 1; o, v-y = 0;

z = 1, when p = 1;

R = KLH.

FIG. 46D

Yeast expressed M-antigen.

a-p, z = 0; q-y, aa (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

- ↓
1. α 1,2-mannosidase
 2. GNT 1,
- UDP-GlcNAc-linker-diphtheria toxin.

e, q, l, m, r, t, u, v, aa (independently selected) = 0 or 1;

a-d, f-h, j, k, n-p, s, w-z = 0;

Sia = Man; R = linker-diphtheria toxin.

FIG. 46E

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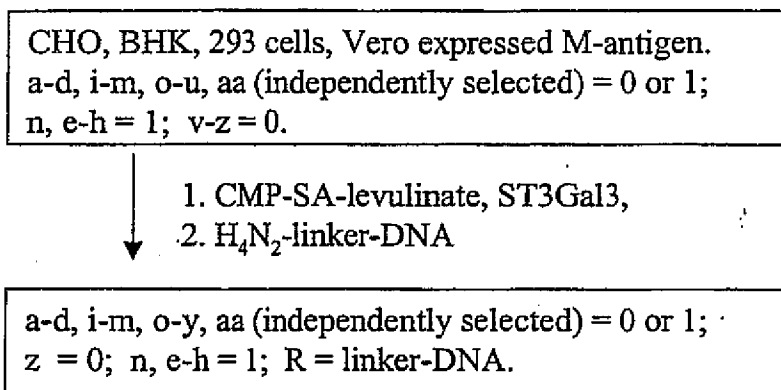


FIG. 46F

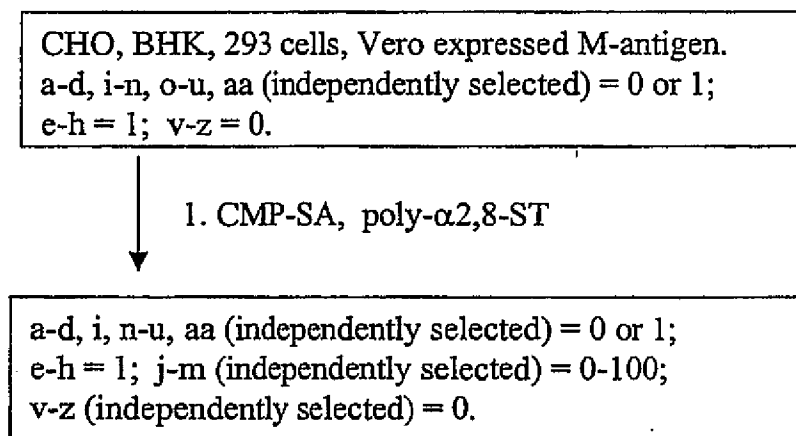
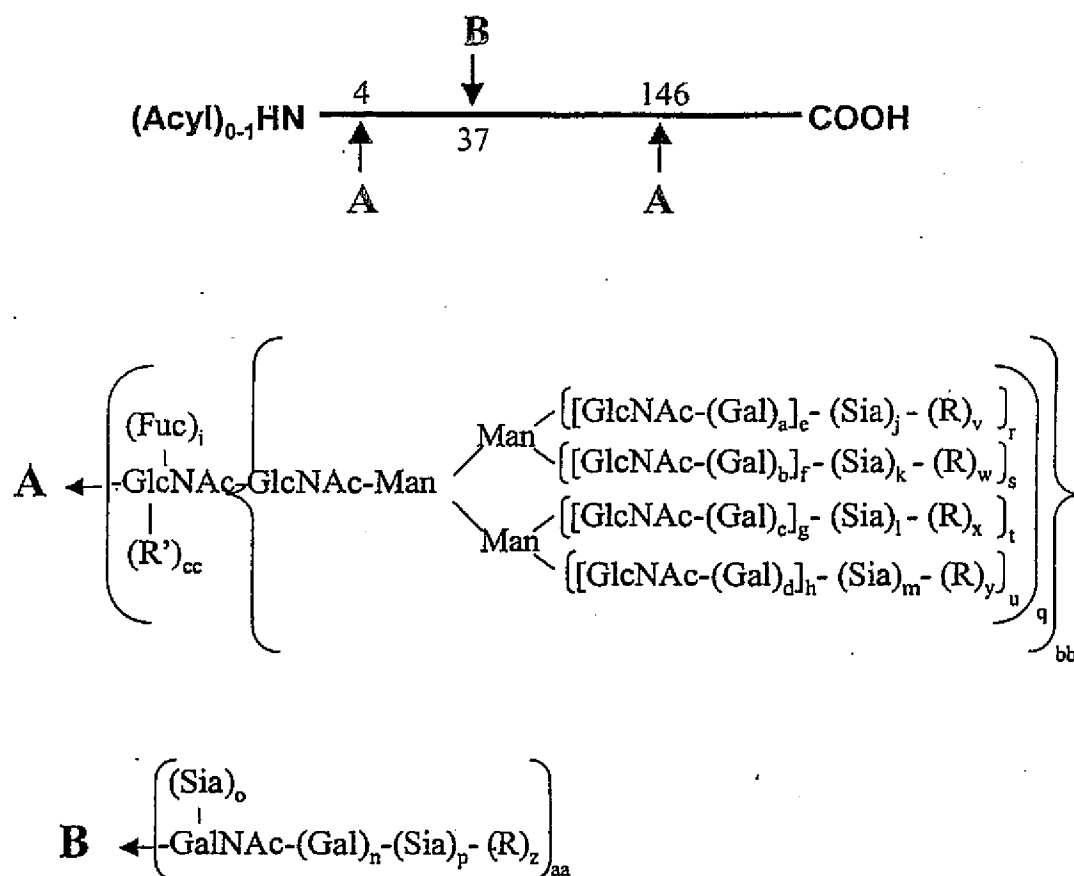


FIG. 46G

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a-d, i, n, q-u, aa, bb, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-p (independently selected) = 0 to 100.

Cc, v-y = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 46H

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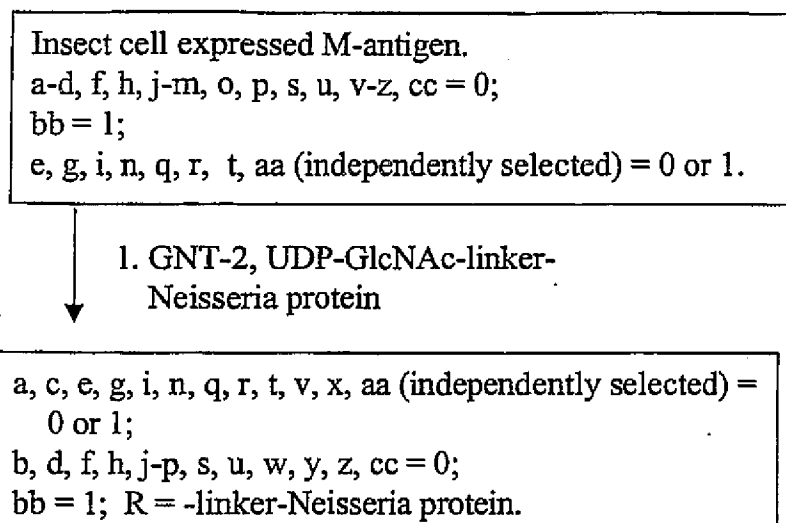


FIG. 46I

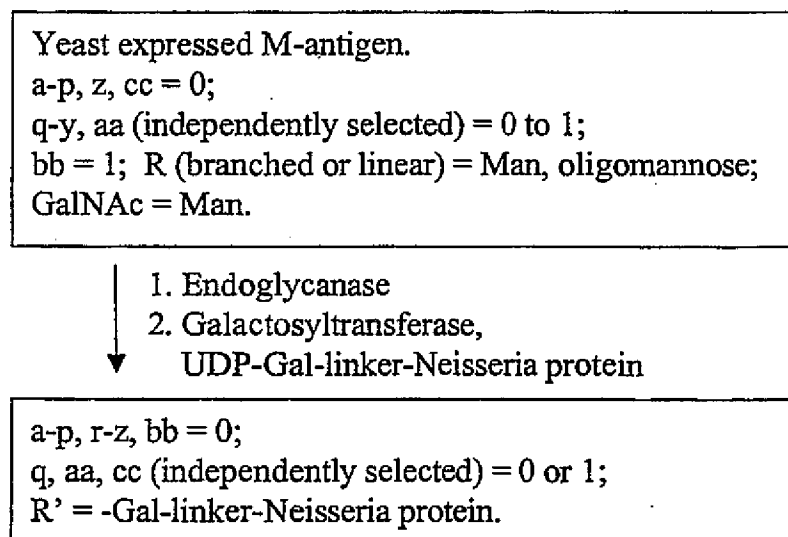


FIG. 46J

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Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1; bb = 1;

R (branched or linear) = Man, oligomannose;

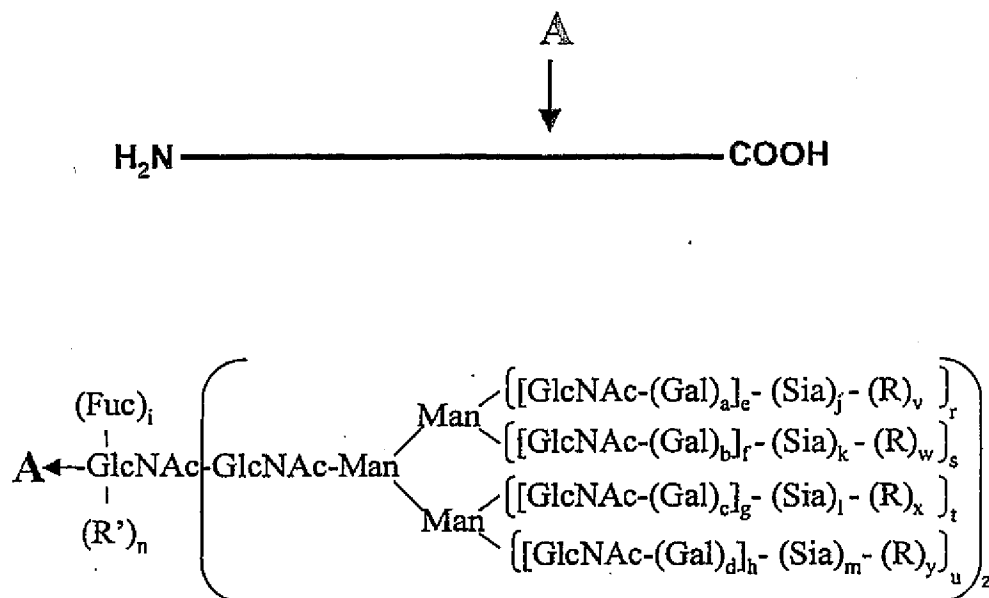
GalNAc = Man.

- 
1. mannosidases
 2. GNT 1 & 2, UDP-GlcNAc
 3. UDP-Gal, Galactosyltransferase,
 4. CMP-SA, sialyltransferase

a, c, e, g, j, l, q, r, t, aa (independently selected) = 0 or 1;
b, d, f, h, k, m-p, s, u-z, cc = 0; bb = 1.

FIG. 46K

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 47A

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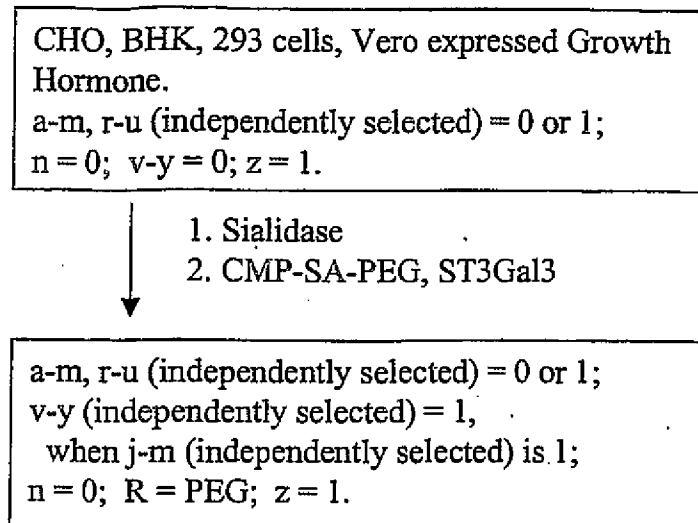


FIG. 47B

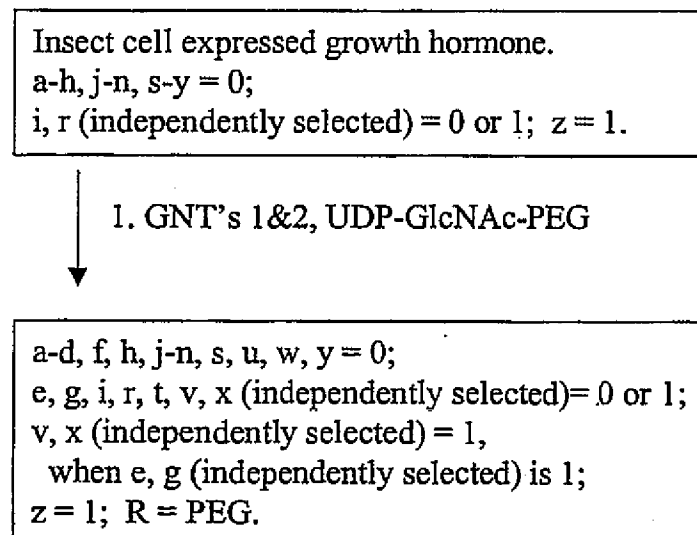


FIG. 47C

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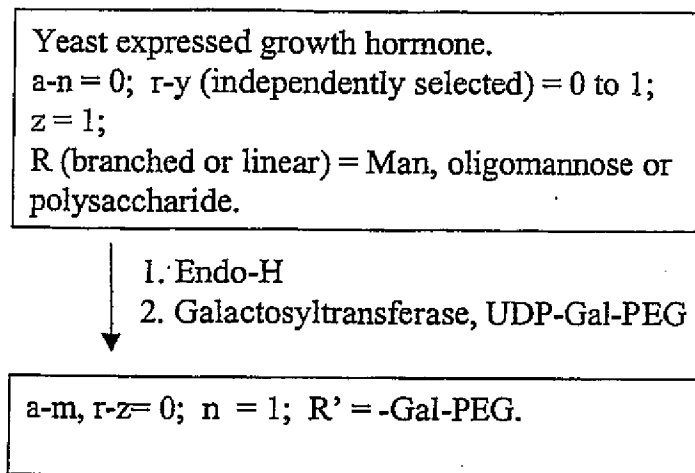
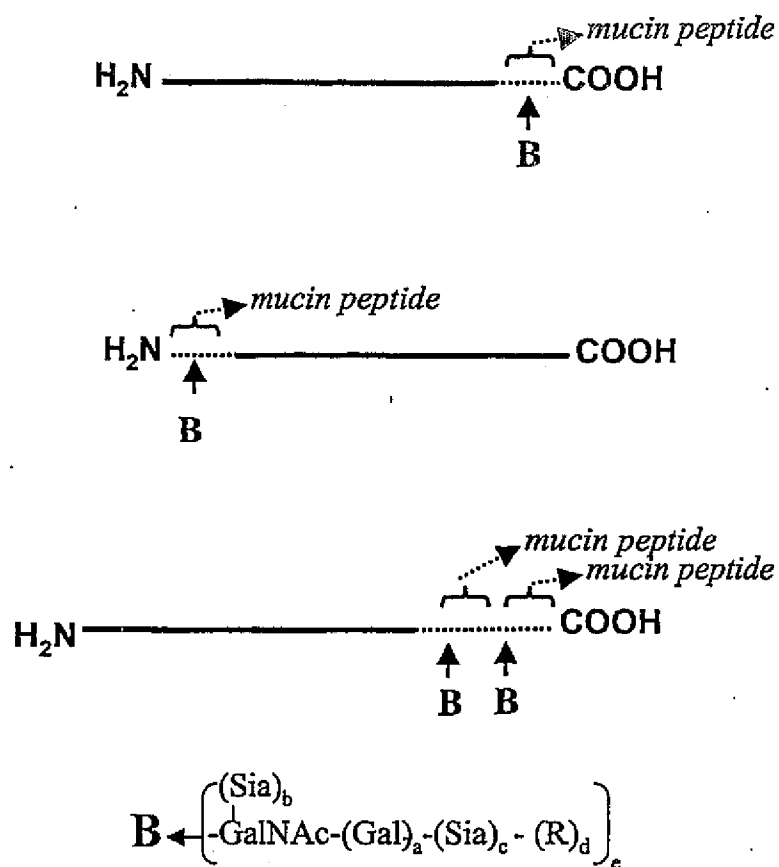


FIG. 47D

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a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 47E

219/497

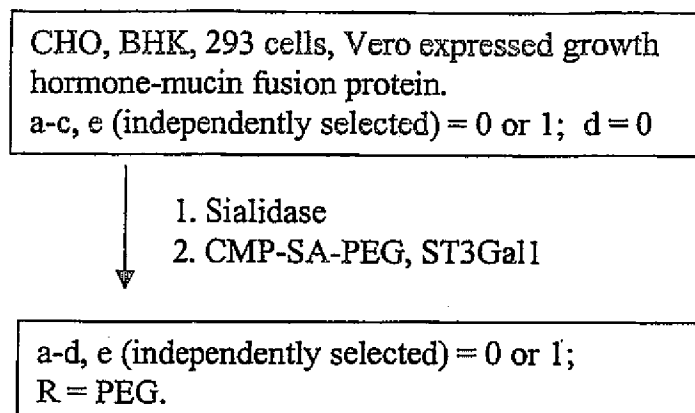


FIG. 47F

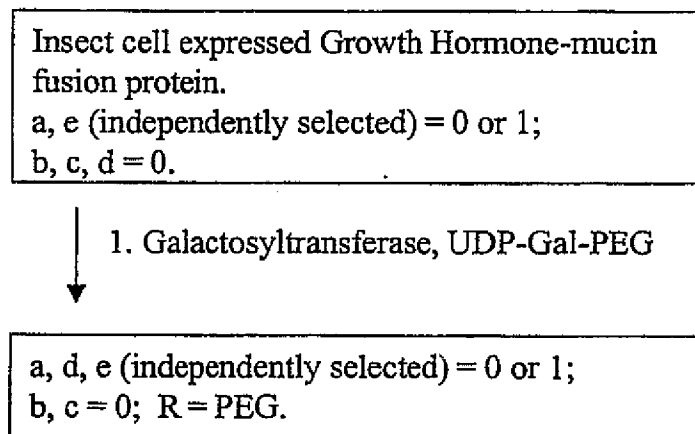


FIG. 47G

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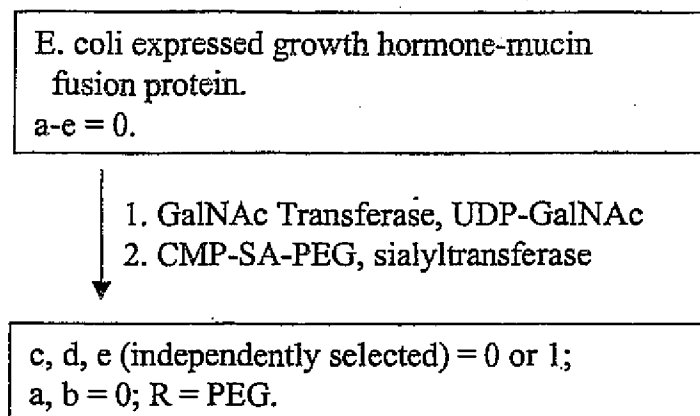


FIG. 47H

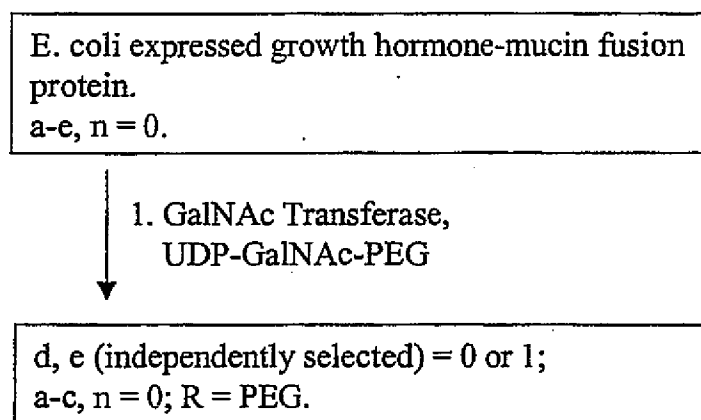


FIG. 47I

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E. coli expressed growth hormone-mucin fusion protein.

a-e, n = 0.

- ↓
1. GalNAc Transferase,
UDP-GalNAc-linker-SA-CMP
 2. ST3Gal3, asialo-transferrin
 - ↓ 3. CMP-SA, ST3Gal3

d, e (independently selected) = 0 or 1;
a-c, n = 0; R = linker-transferrin.

FIG. 47J

E. coli expressed growth hormone
(N)—no mucin peptide.

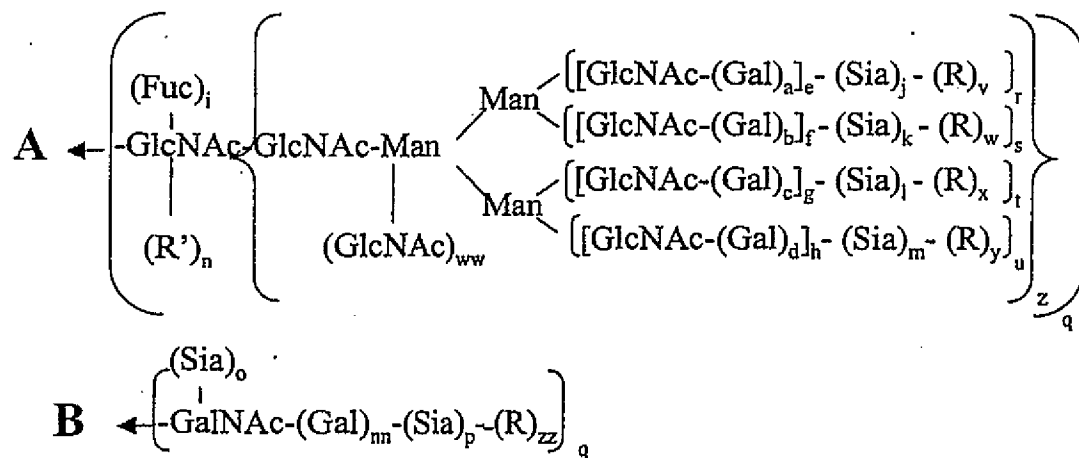
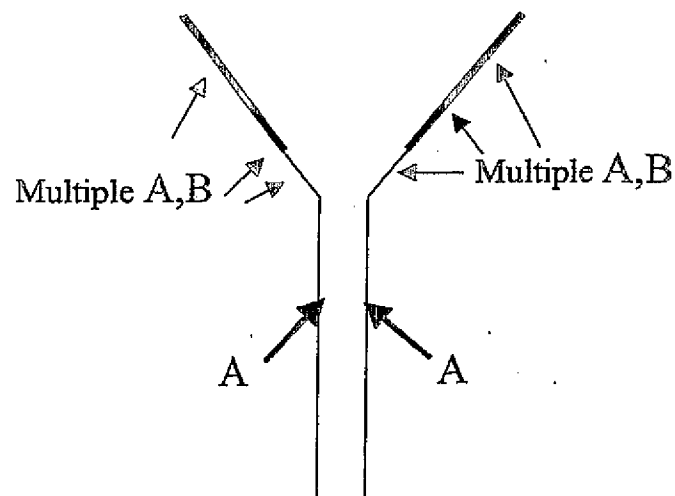
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
 2. ST3Gal3, asialo-transferrin
 - ↓ 3. CMP-SA, ST3Gal3

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 47K

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a-d, i-m, q-u, w, z, nm, ww, zz. (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

n, v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 48A

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CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA, ST3Gal1
2. galactosyltransferase, UPD-Gal
3. CMP-SA-PEG, ST3Gal3

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 48B

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. sialidase
2. CMP-SA-PEG, ST3Gal1

a-i, p-u, z, aa (independently selected) = 0 or 1;
n = 1; o, j-m, v-y = 0; R = PEG.

FIG. 48C

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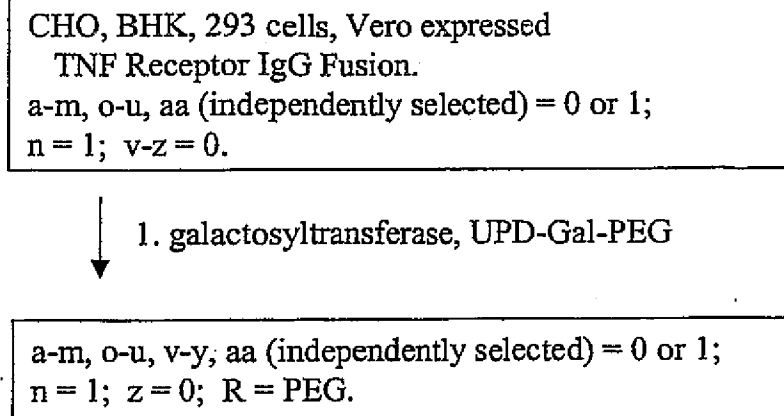


FIG. 48D

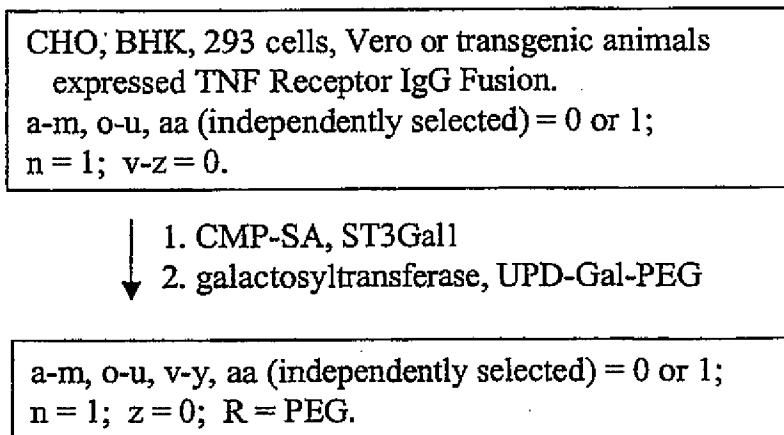


FIG. 48E

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CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

↓
1. CMP-SA-levulinate, ST3Gal1
2. H₄N₂-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 48F

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.

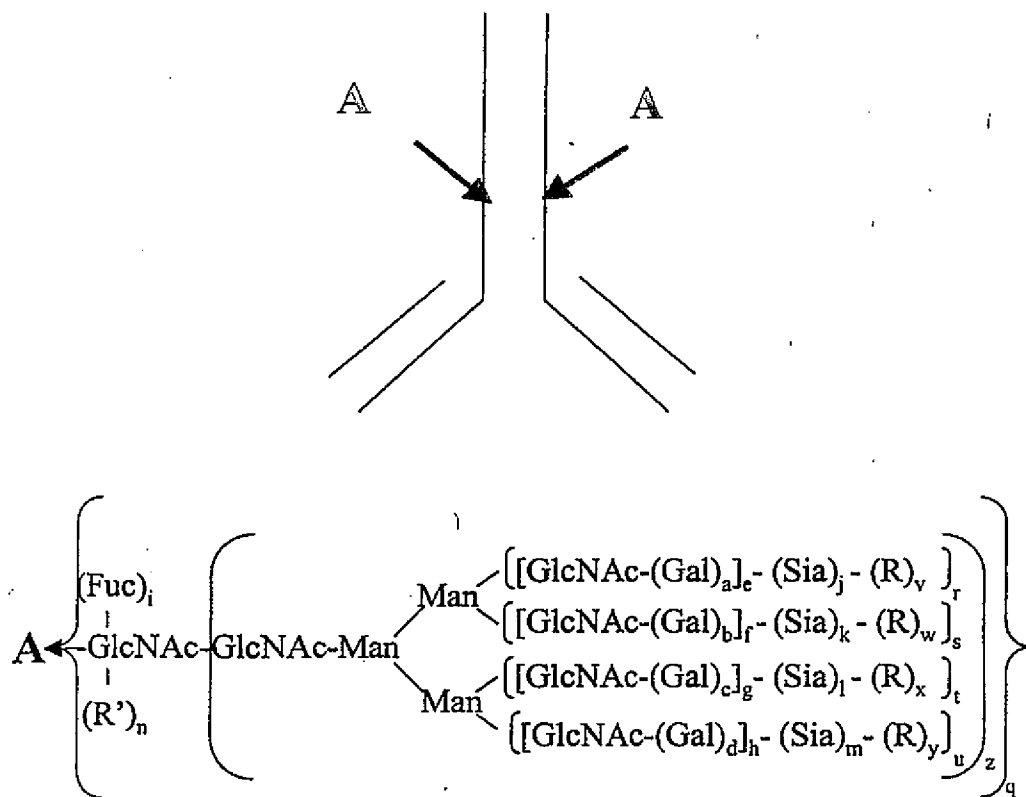
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

↓
1. CMP-SA-PEG, α 2,8-ST

a-i, o, q-u, v-z, aa (independently selected) = 0 or 1;
n = 1; j-m, p (independently selected) = 0 to 2;
v-z (independently selected) = 1,
when j-m, p (independently selected) is 2;
R = PEG.

FIG. 48G

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a-d, i, l, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

 $j-k$ (independently selected) = 0 or 1.

$M = 0$ to 20.

$$n, v-y = 0; \quad z = 0 \text{ or } 1;$$

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 49A

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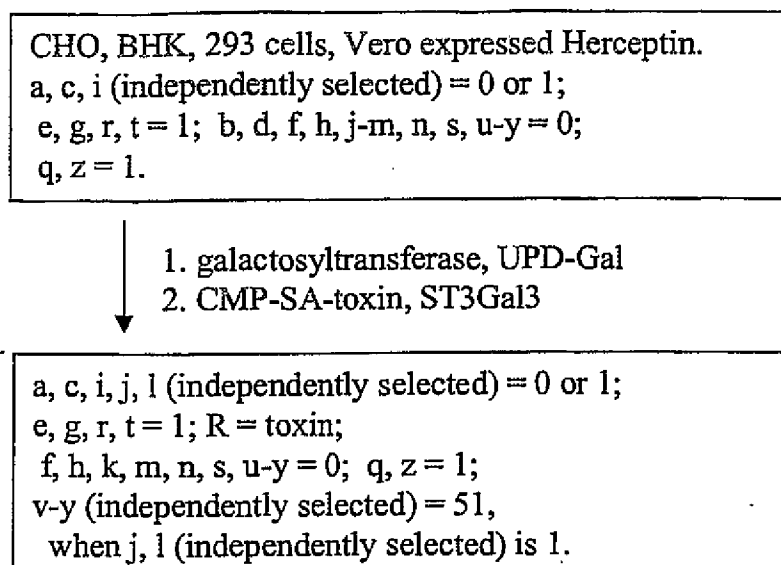


FIG. 49B

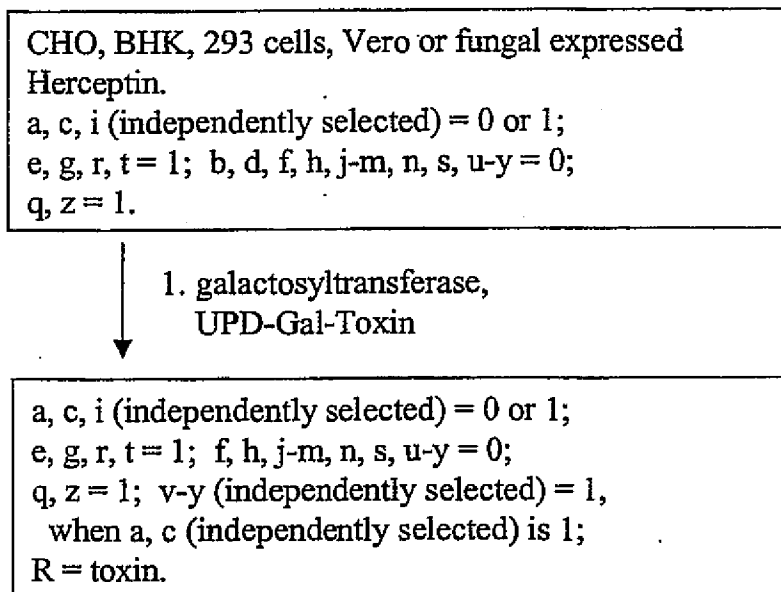


FIG. 49C

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Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H

2. Galactosyltransferase, UDP-Gal

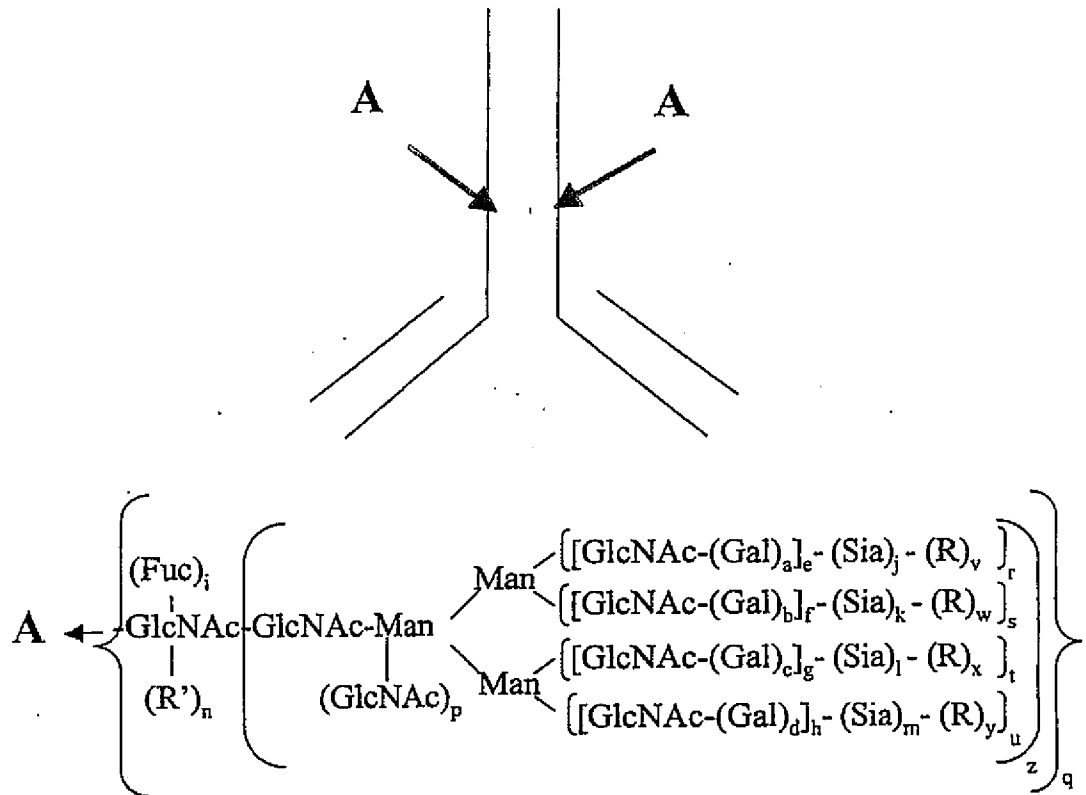
↓ 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 49D

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a-d, i, p-u, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

$$j\text{-m (independently selected)} = 0 \text{ or } 1.$$
$$n, v-y=0; z=0 \text{ or } 1;$$

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 50A

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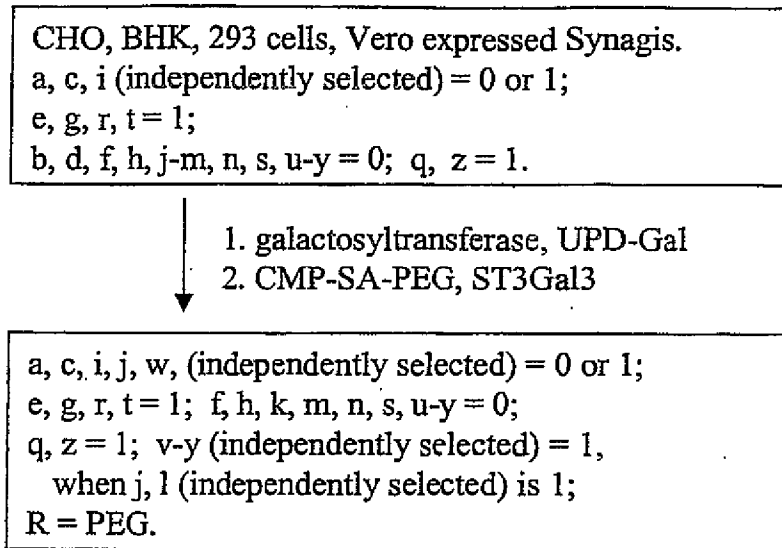


FIG. 50B

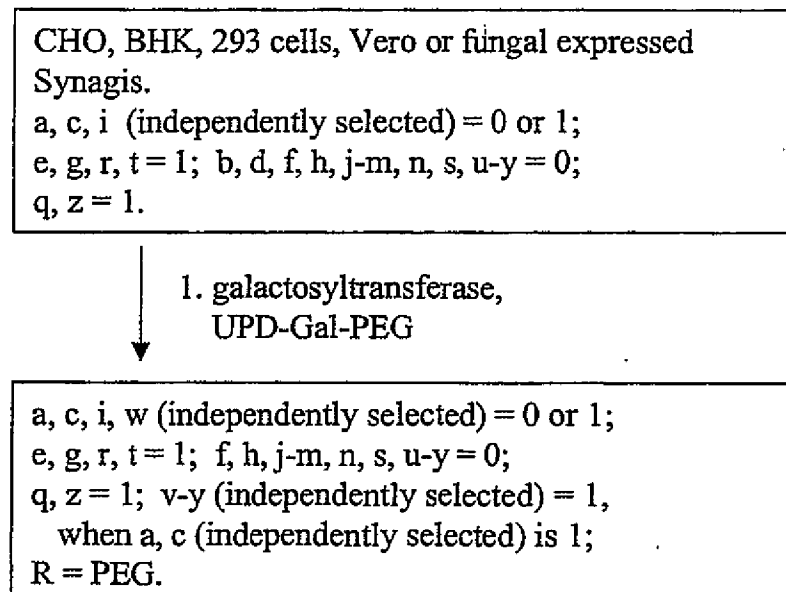


FIG. 50C

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Fungi expressed Synagis.

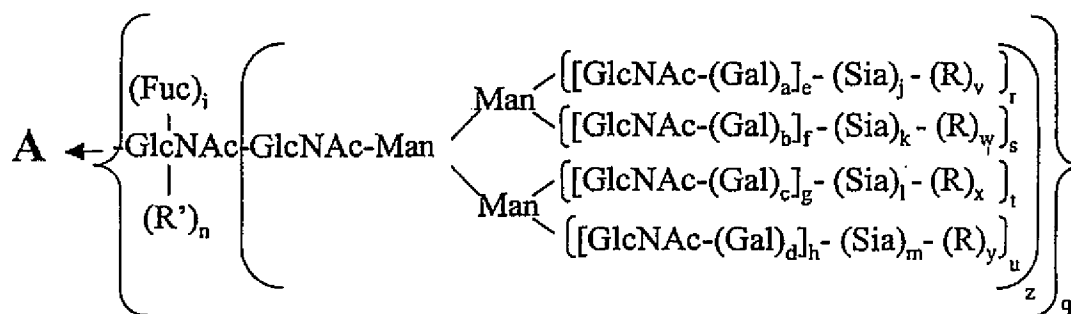
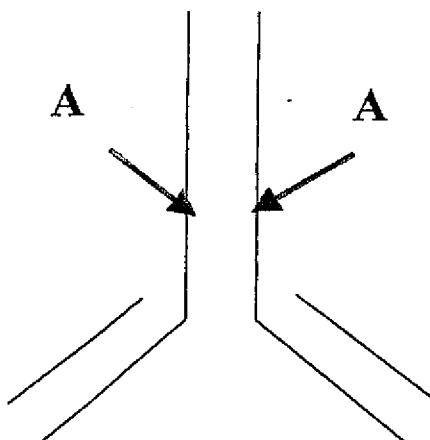
e, g, i, r, t (independently selected) = 0 or 1;
a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. Endo-H
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 50D

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a-d, i, q-u, w (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 51A

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CHO, BHK, 293 cells, Vero expressed Remicade.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when j, l (independently selected) is 1;
 R = PEG.

FIG. 51B

CHO, BHK, 293 cells, Vero or fungal expressed
 Remicade.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.



1. galactosyltransferase,
UPD-Gal-PEG

a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when a, c (independently selected) is 1;
 R = PEG.

FIG. 51C

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Fungi expressed Remicade.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

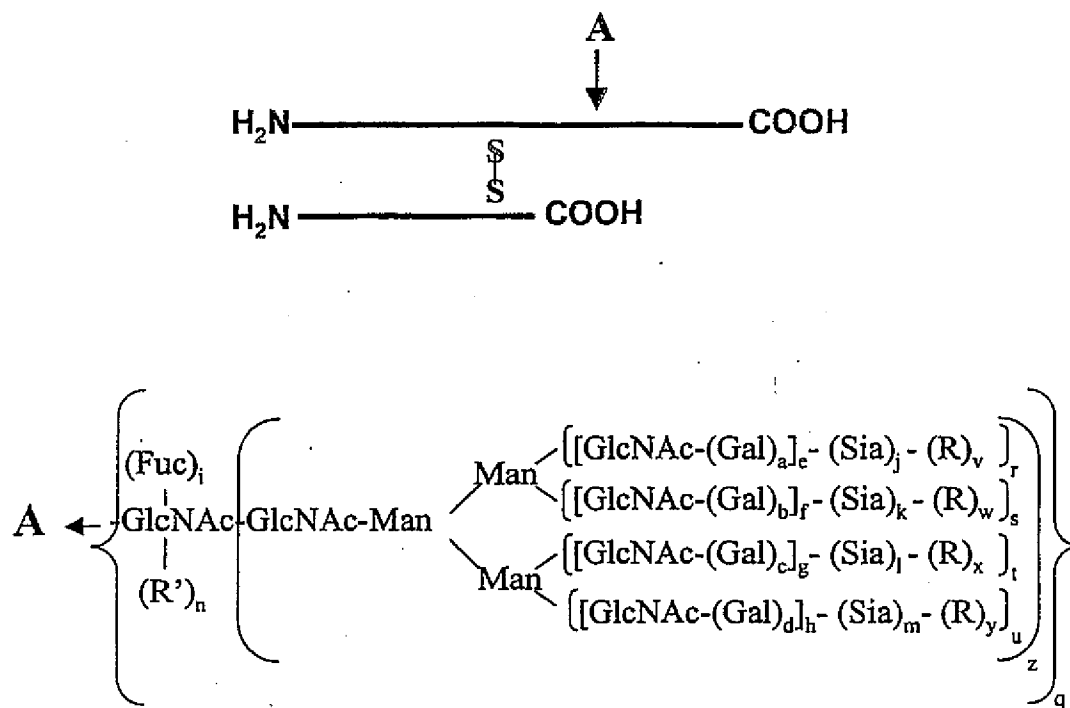
- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z= 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 52A

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CHO, BHK, 293 cells, Vero expressed Reopro.
 a-m, r-u (independently selected) = 0 or 1;
 n = 0; v-y = 0; z = 1.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;
 v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 n = 0; R = PEG; z = 1.

FIG. 52B

Insect cell expressed Reopro.
 a-h, j-n, s-y = 0; i, r (independently selected) = 0 or 1;
 z = 1.



1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;
 e, g, i, r, t, v, x (independently selected) = 0 or 1;
 v, x (independently selected) = 1,
 when e, g (independently selected) is 1;
 z = 1; R = PEG.

FIG. 52C

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Yeast expressed Reopro.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

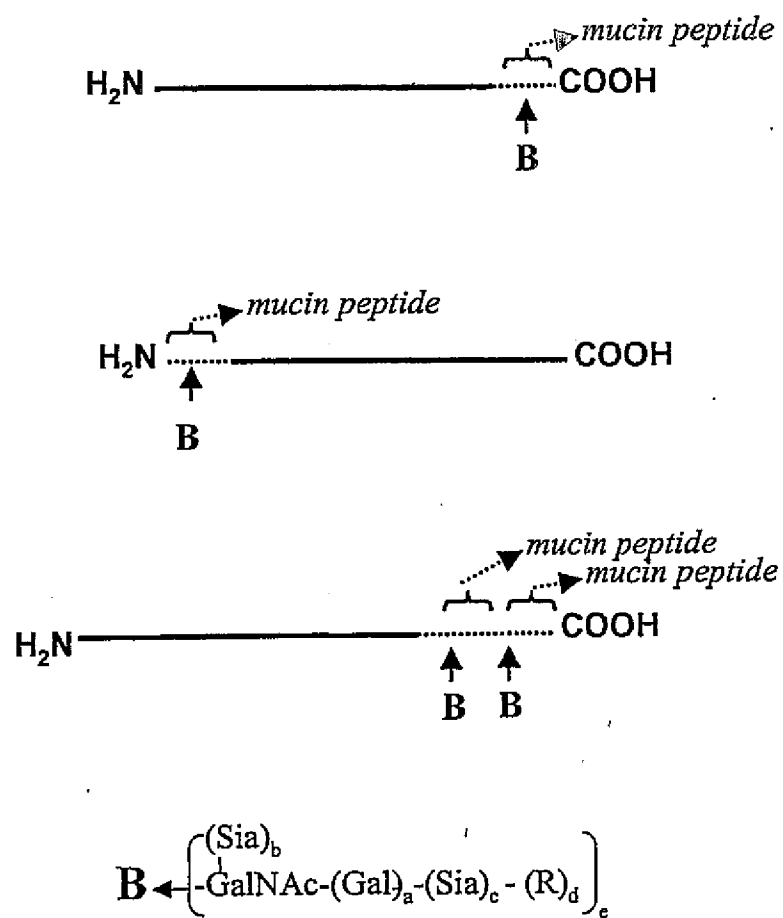
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z=0; n = 1; R' = -Gal-PEG.

FIG. 52D

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer

FIG. 52E

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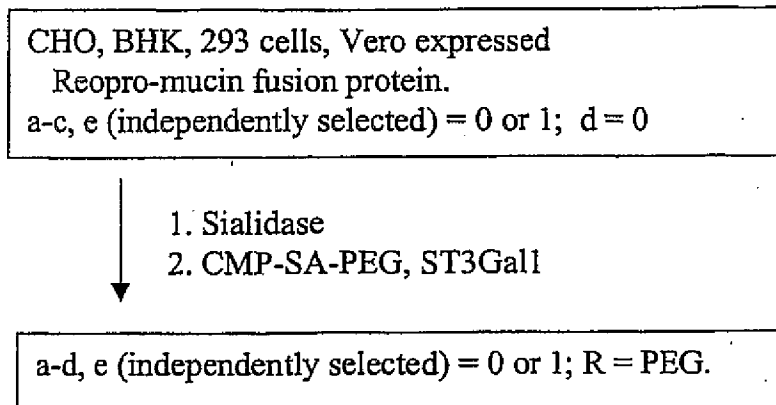


FIG. 52F

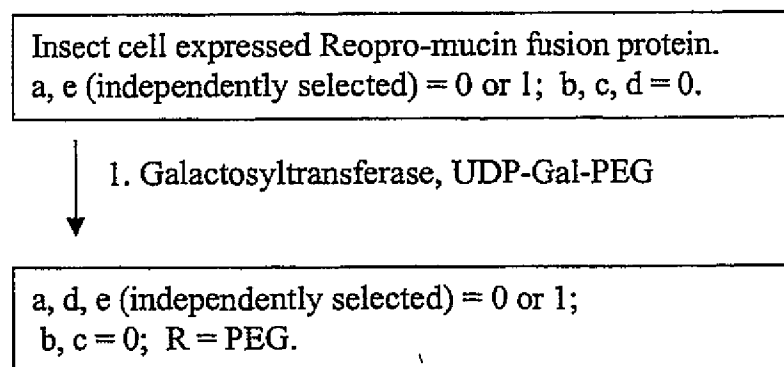


FIG. 52G

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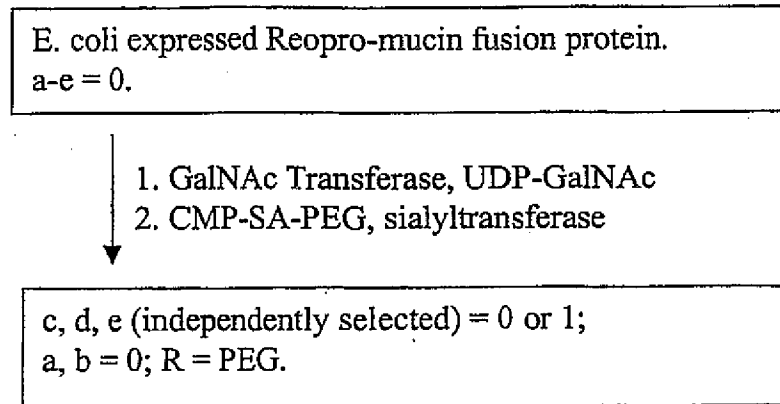
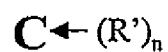
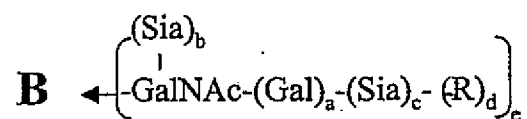
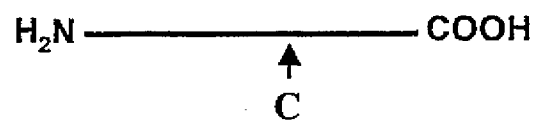
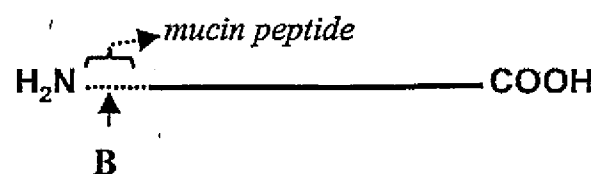
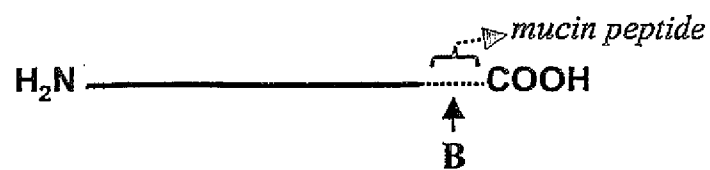


FIG. 52H

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a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 52I

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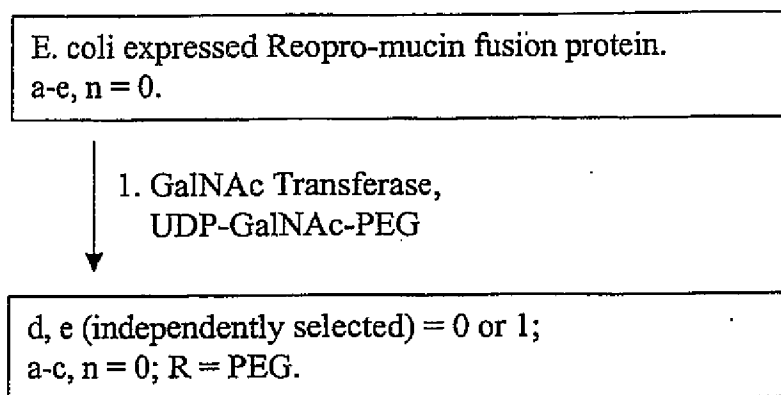


FIG. 52J

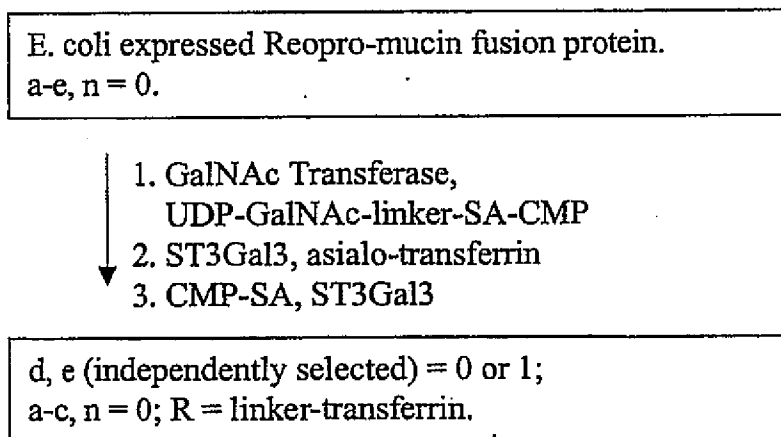


FIG. 52K

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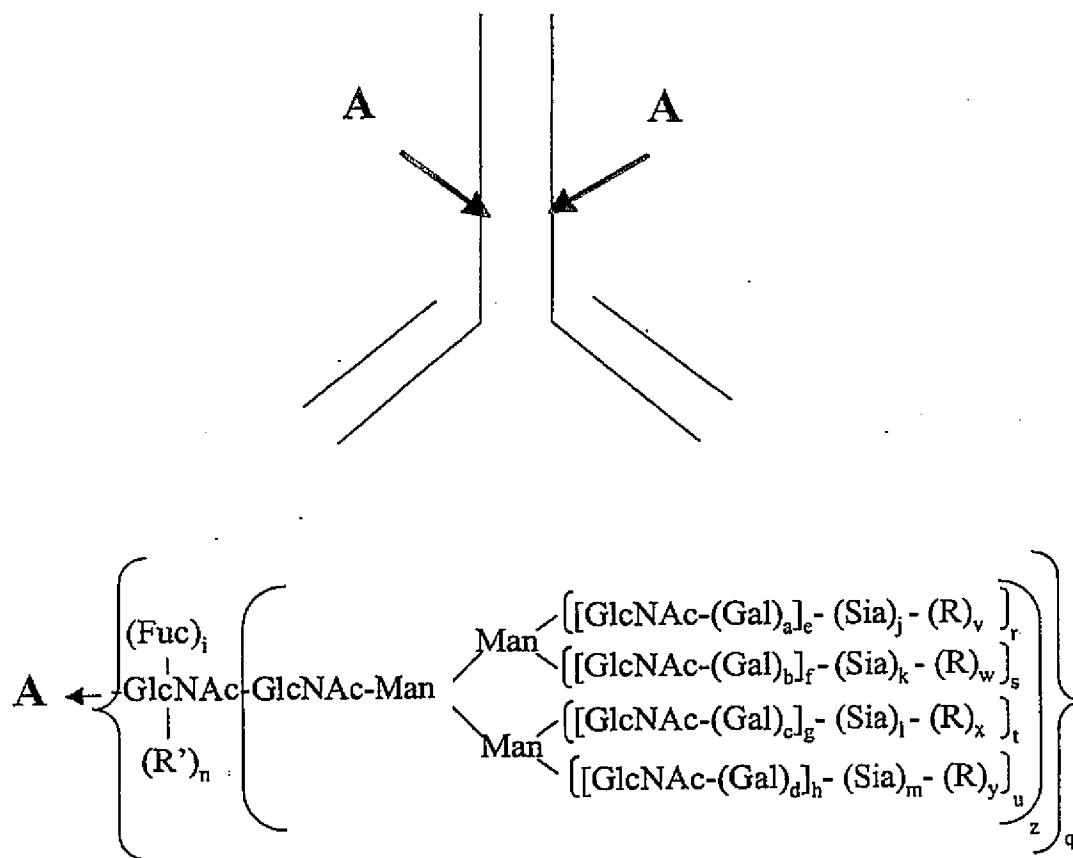
E. coli expressed Reopro(N)—no mucin peptide.
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
2. ST3Gal3, asialo-transferrin
3. CMP-SA, ST3Gal3

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 52L

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

z

FIG. 53A

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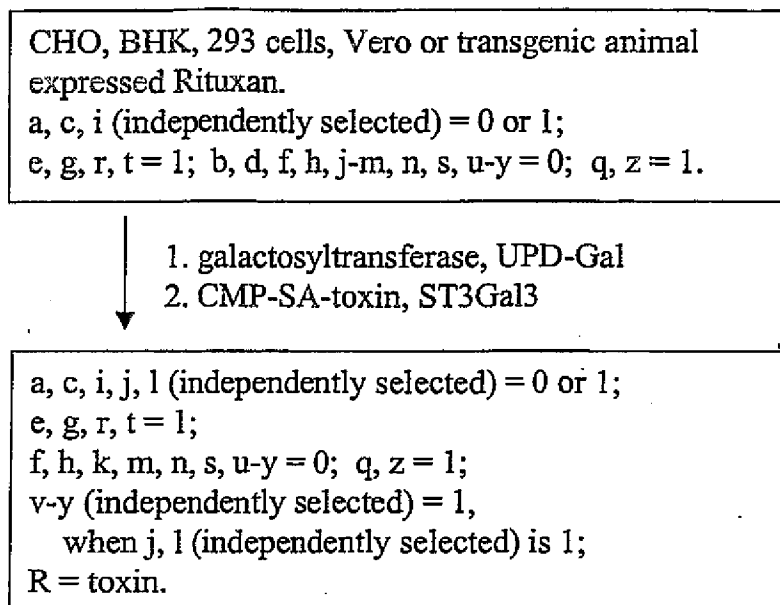


FIG. 53B

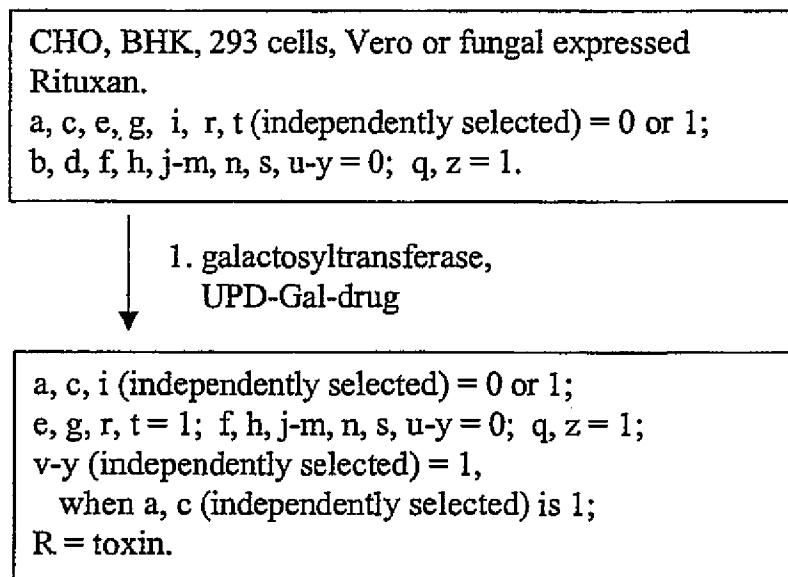


FIG. 53C

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Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H

2. Galactosyltransferase, UDP-Gal

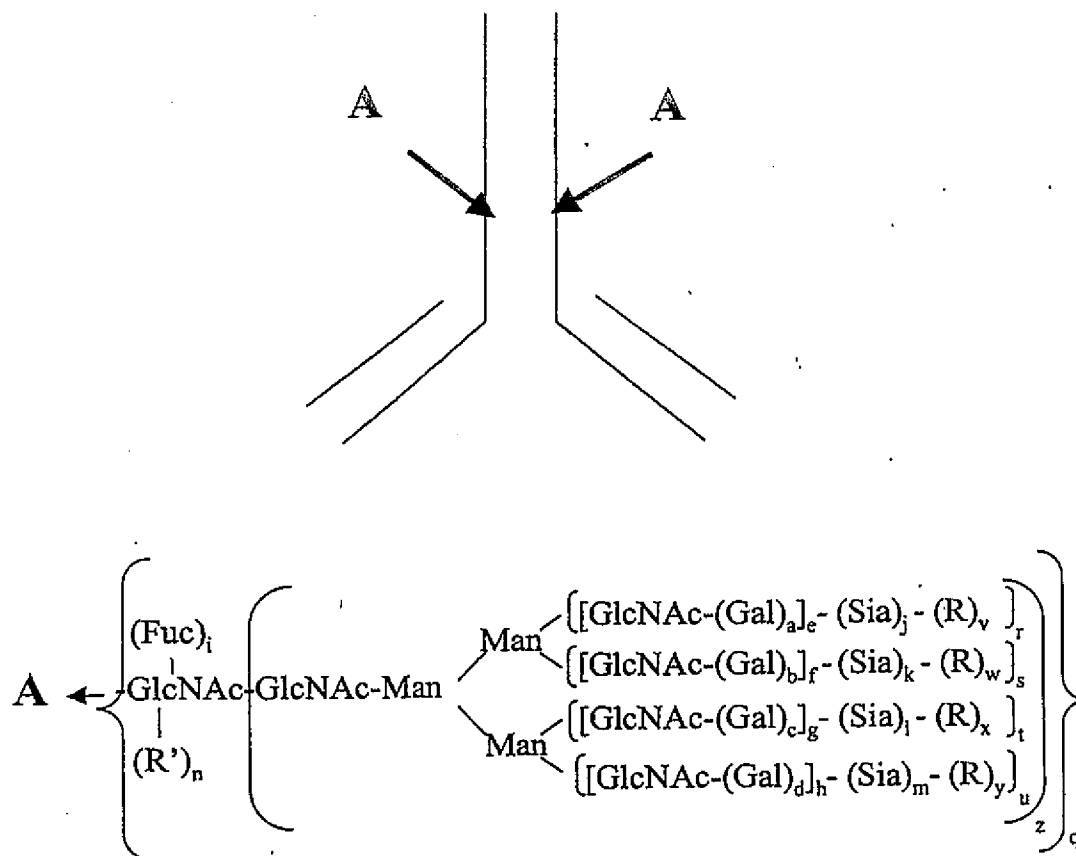
↓ 3. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 53D

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

 j -m (independently selected) = 0 or 1.
$$n, v-y=0; z=0 \text{ or } 1;$$

R = polymer, toxin, radioisotope-complex, drug, glycoconjugate, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 53E

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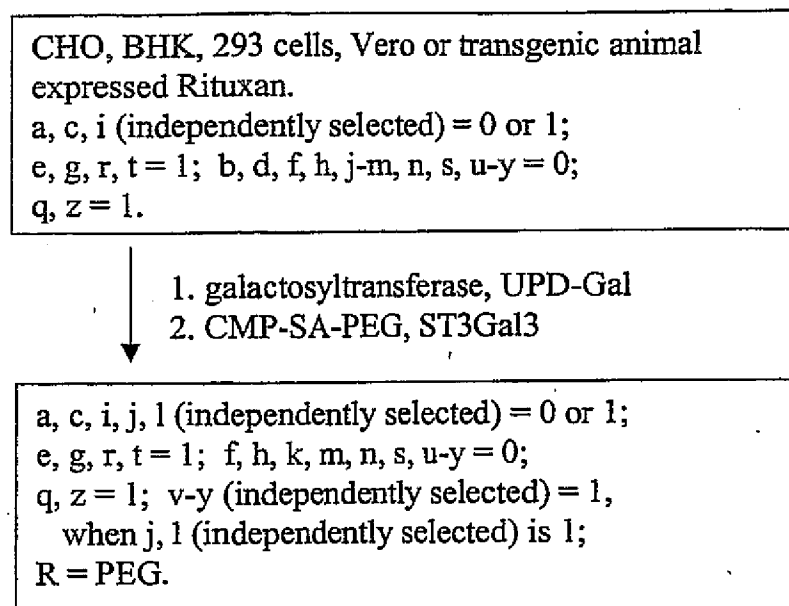


FIG. 53F

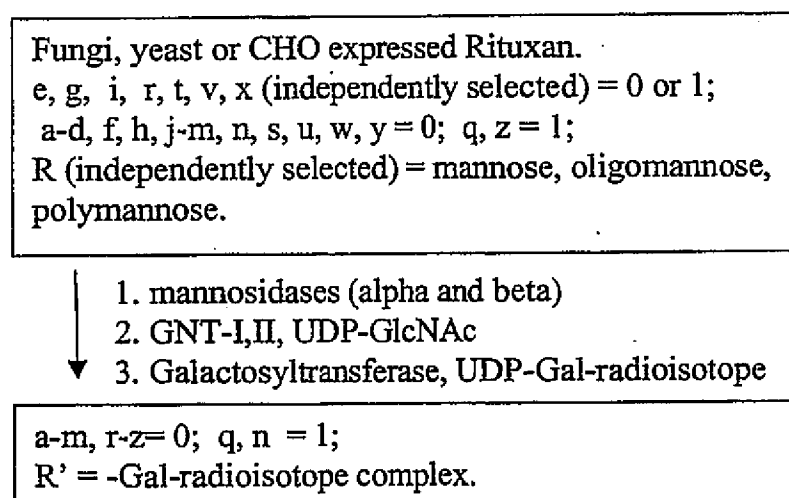
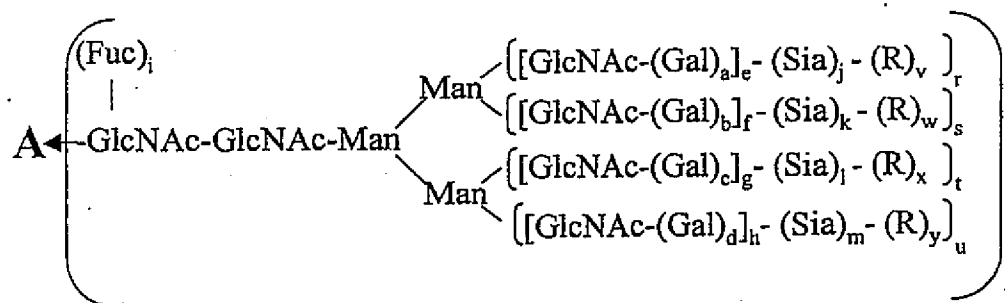
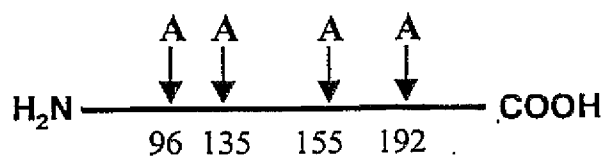


FIG. 53G

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a-d, i, q-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = mannose, polymer.

FIG. 54A

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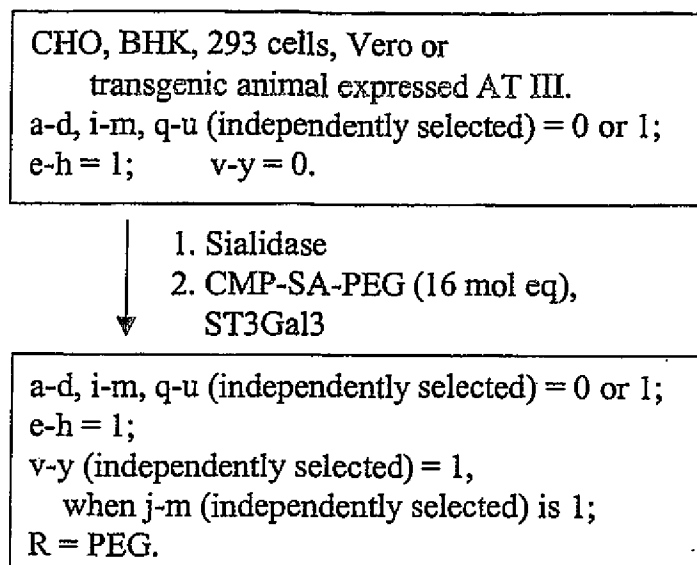


FIG. 54B

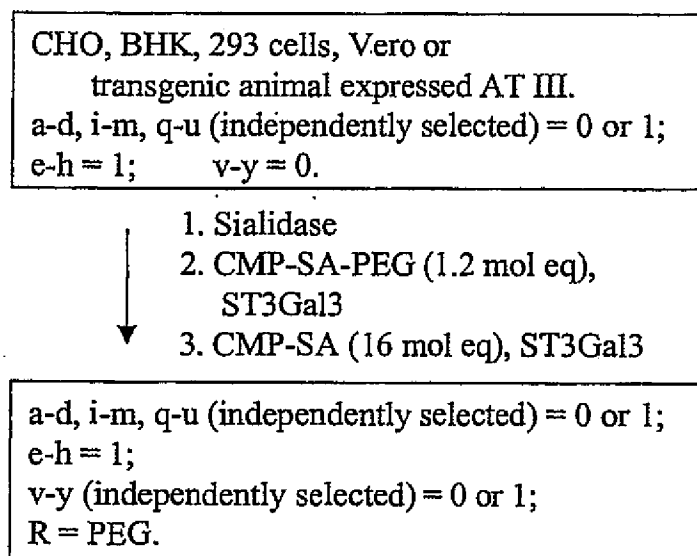


FIG. 54C

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NSO expressed AT III.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3
- ↓

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1;

v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 54D

CHO, BHK, 293 cells, Vero or

transgenic animal expressed AT III.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3
- ↓

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1;

v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 54E

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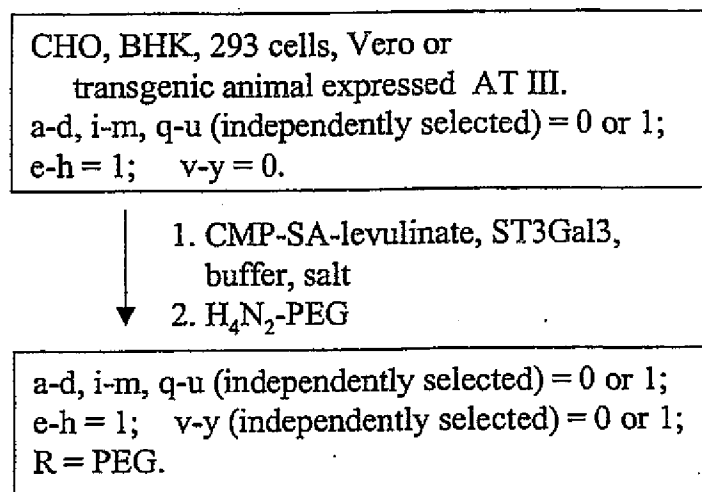


FIG. 54F

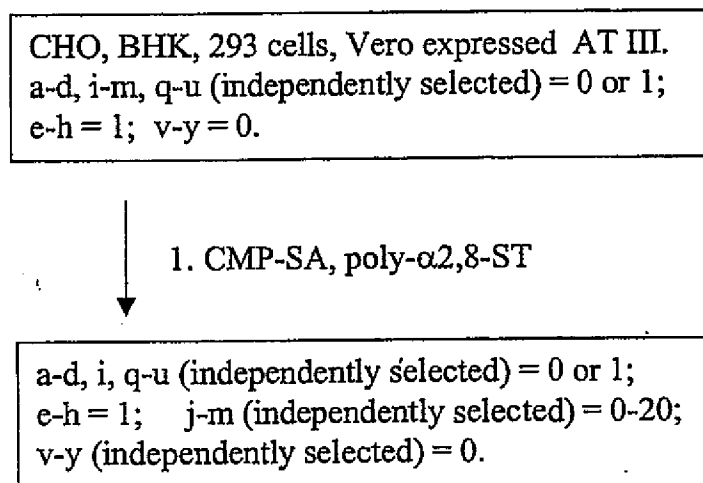
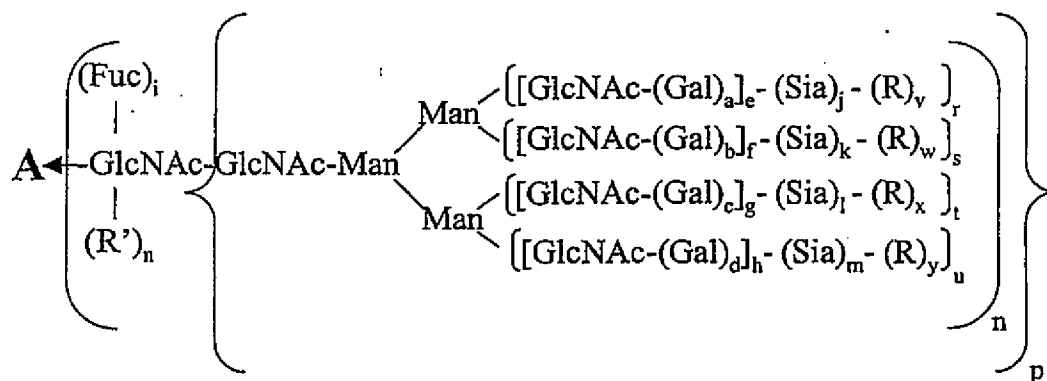
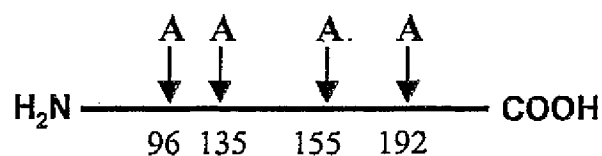


FIG. 54G

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a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100.

R = polymer, linker, mannose.

$R' = H, \text{ sugar, glycoconjugate.}$

FIG. 54H

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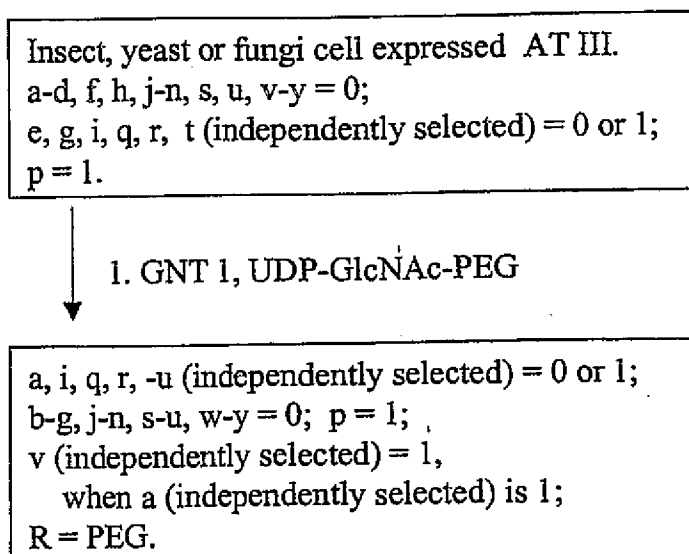


FIG. 54I

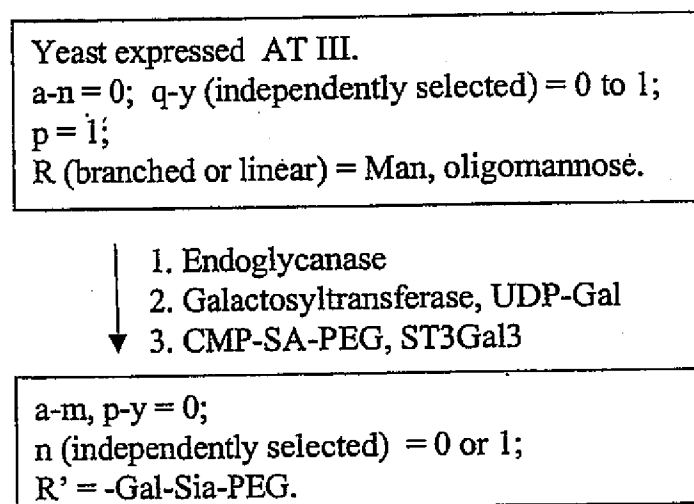


FIG. 54J

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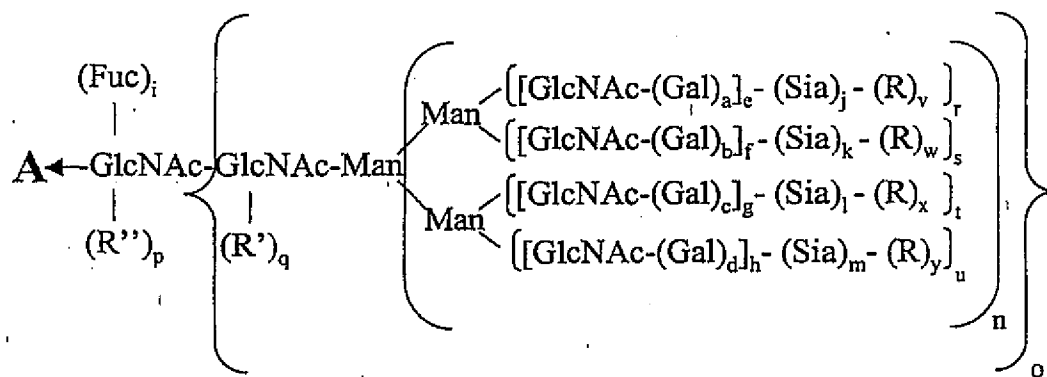
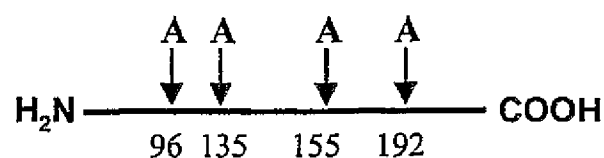
CHO, BHK, 293 cells, Vero expressed AT III.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, transferrin
treated with endoglycanase

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 54K

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer.

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 54L

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Yeast expressed AT III.

a-h, i-m, p, q = 0;

R (independently selected) = mannose,
oligomannose, polymannose;

r-u, v-y (independently selected) = 0 or 1;

n, o = 1.

- ↓ 1. endoglycanase
↓ 2. Galactosyltransferase, UDP-Gal-PEG

a-h, i-o, q, r-u, v-y = 0; p = 1.

R'' = Gal-PEG.

FIG. 54M

Plant expressed AT III.

a-d, f-h, j-m, p, s-u, v-y = 0;

e, i, q, r (independently selected) = 0 or 1;

n, o = 1; R' = xylose.

- ↓ 1. xylosidase
↓ 3. Galactosyl transferase, UDP-Gal-PEG

b-d, f-h, j-m, p, q, s-u, w-y = 0;

a, e, i, r (independently selected) = 0 or 1;

n, o = 1; R = PEG.

FIG. 54N

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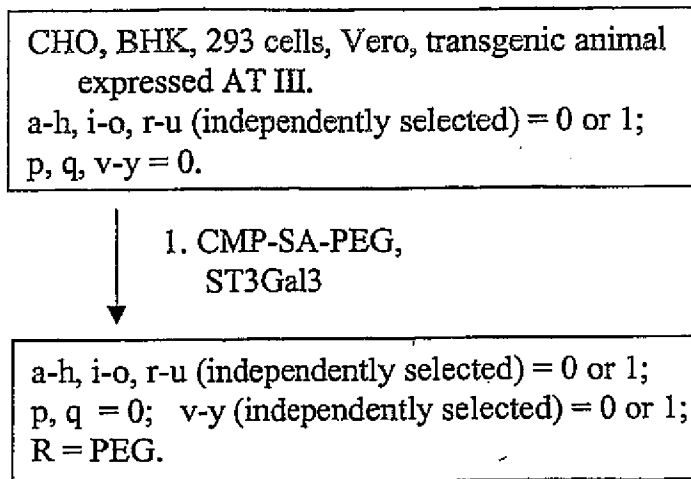
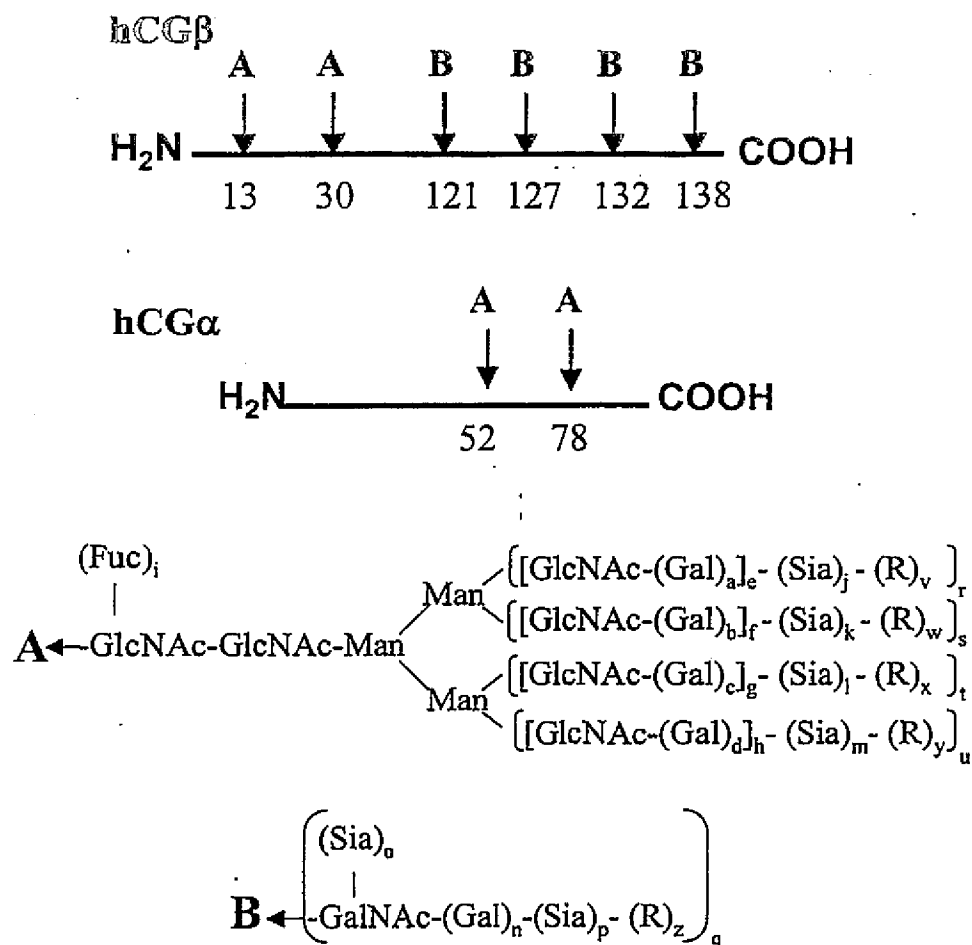


FIG. 54O

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; R = polymer

FIG. 55A

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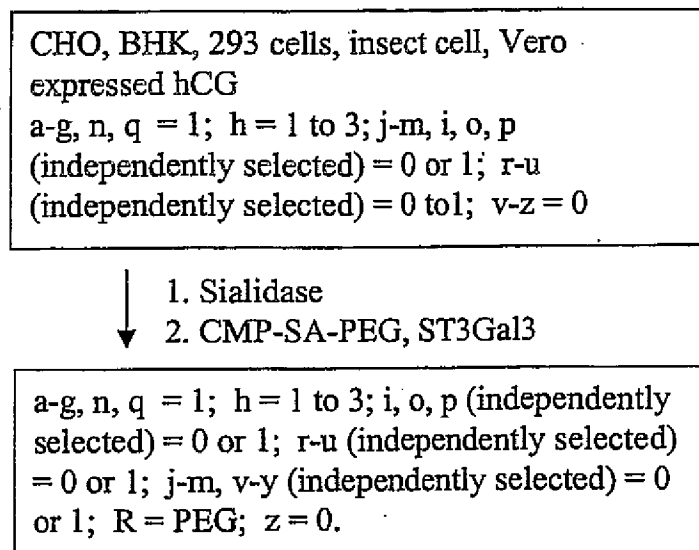


FIG. 55B

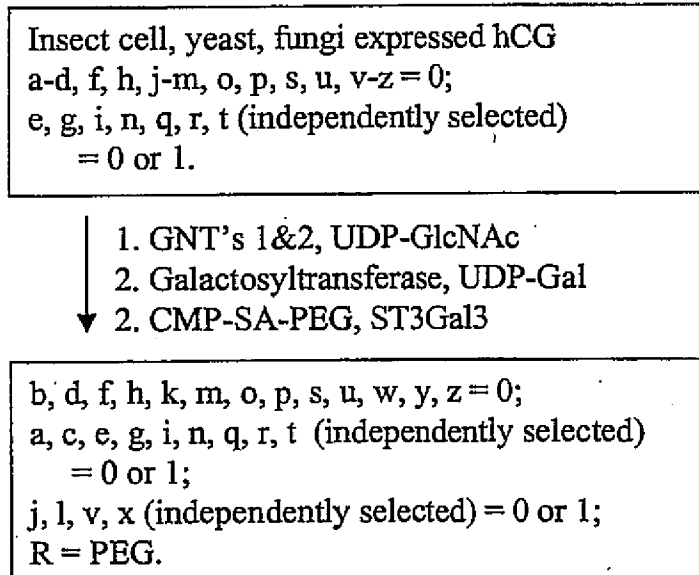


FIG. 55C

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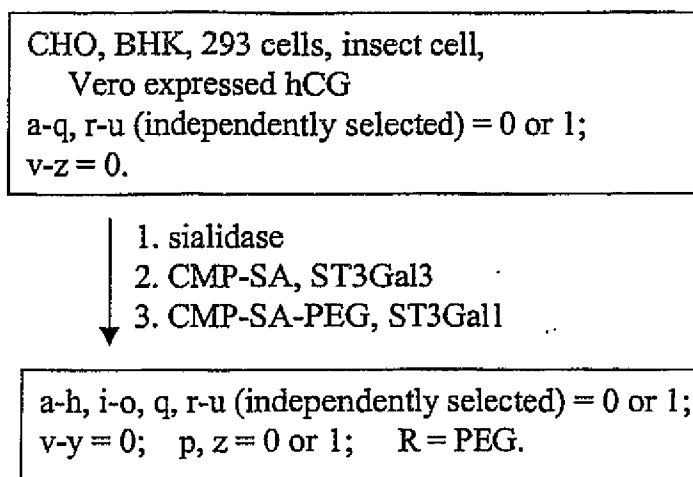


FIG. 55D

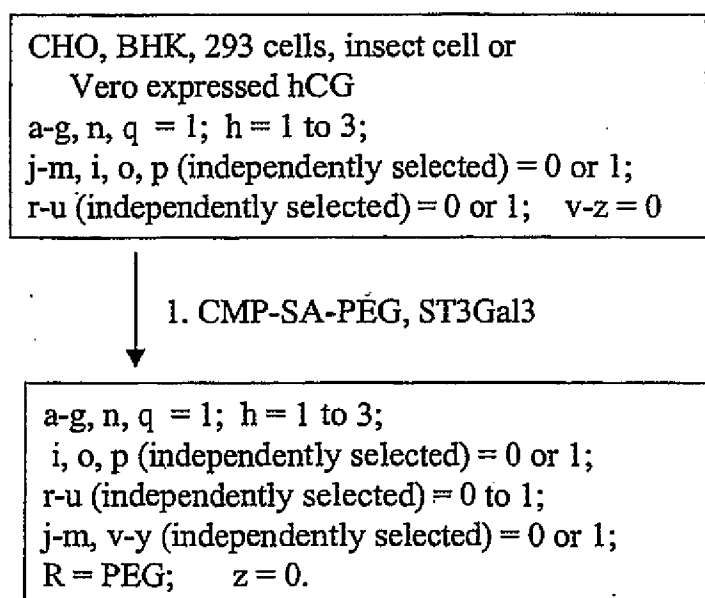


FIG. 55E

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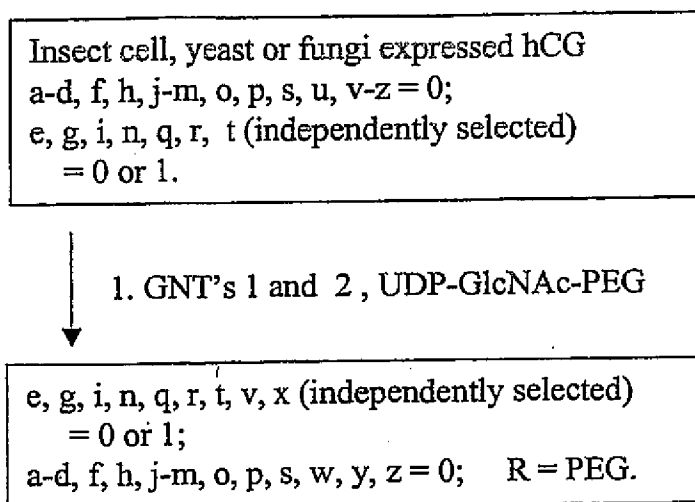


FIG. 55F

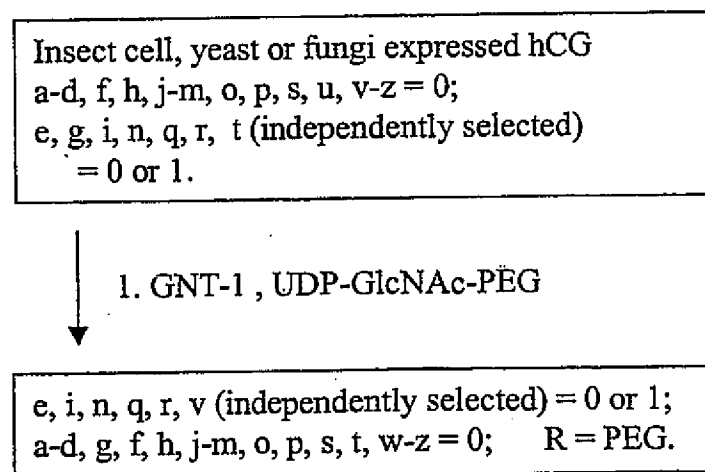


FIG. 55G

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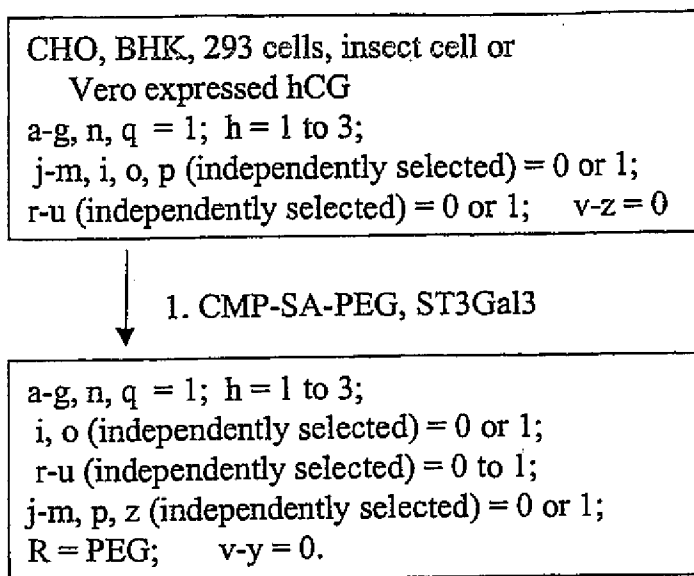


FIG. 55H

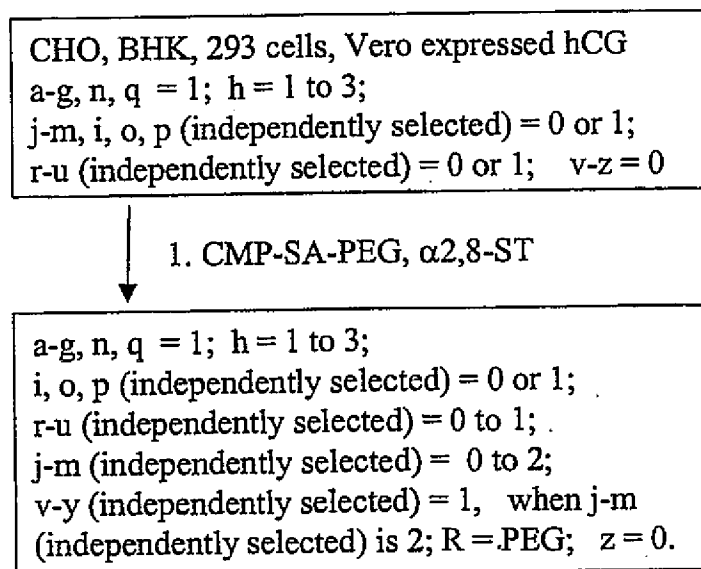


FIG. 55I

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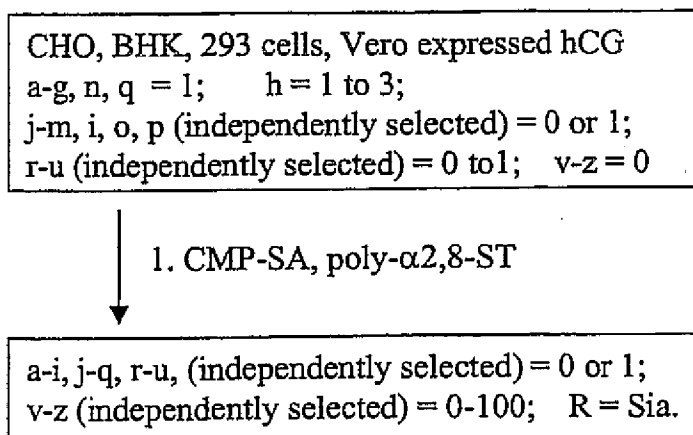


FIG. 55J

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CHO, BHK, 293 cells, insect cells, Vero expressed
and secreted alpha-galactosidase
a-h, i-m, q-u (independently selected) = 0 or 1;
z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Endo-H
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;
n, v-y = 0; z = 1; and when z = 0 and q = 1,
then n (independently selected) = 0 or 1;
R' = Gal-PEG-transferrin.

FIG. 56B

CHO, BHK, 293 cells, Insect cells,
Vero expressed and secreted alpha-galactosidase
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1; n, v-y
= 0; and when a-n = 0, then r-u (independently selected) = 0
or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
2. CMP-SA-linker-Mannose-6-phosphate
ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1;
n = 0; z = 1; R = mannose-6-phosphate; and when a-n
= 0, then r-u (independently selected) = 0 or 1;
v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

FIG. 56C

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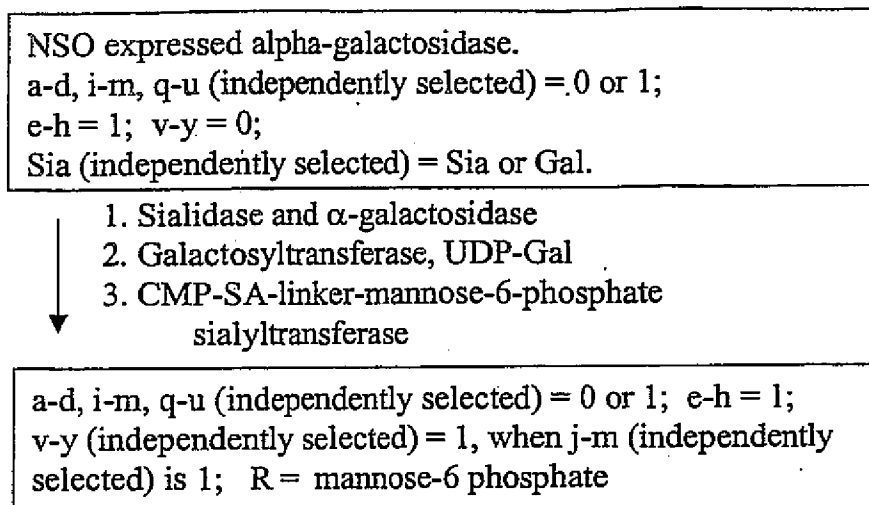


FIG. 56D

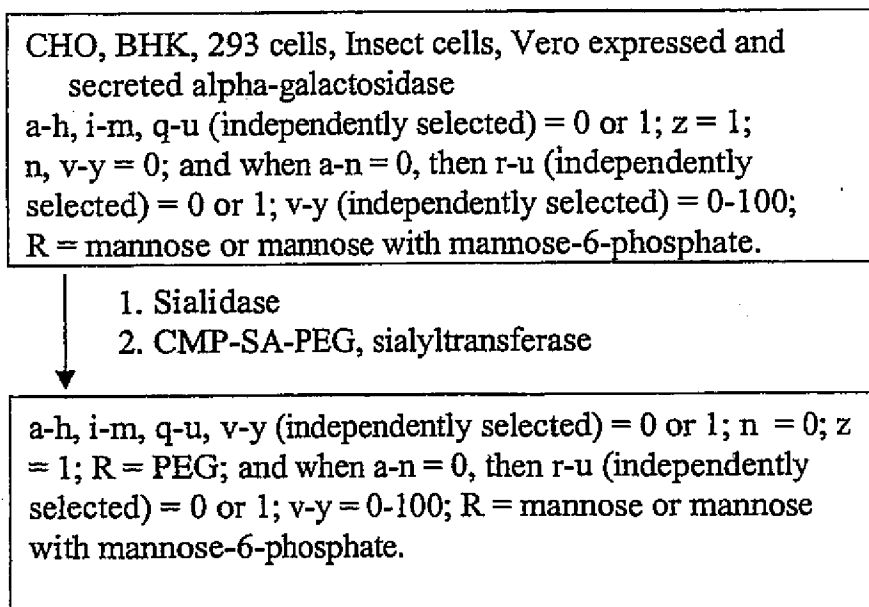


FIG. 56E

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CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-galactosidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate;
v-y (independently selected) = 0 or 1;
R = mannose-linker-ApoE.

FIG. 56F

CHO, BHK, 293 cells, Insect cells, Vero, yeast,
fungi expressed alpha-galactosidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H
2. galactosyltransferase,
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;
R' = galactose-linker-alpha2-macroglobulin.

FIG. 56G

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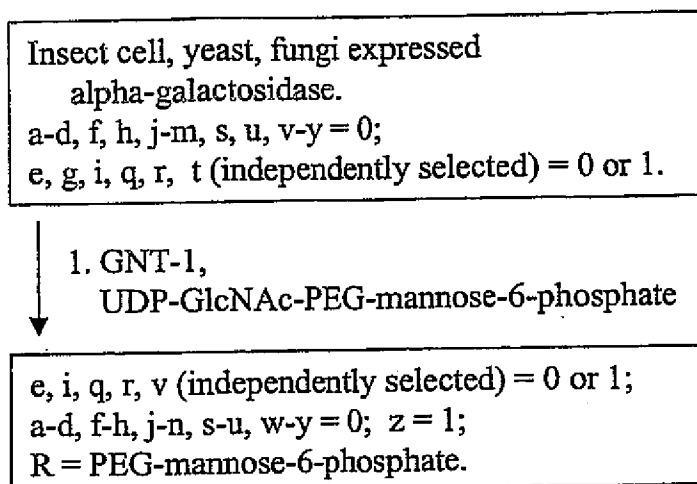


FIG. 56H

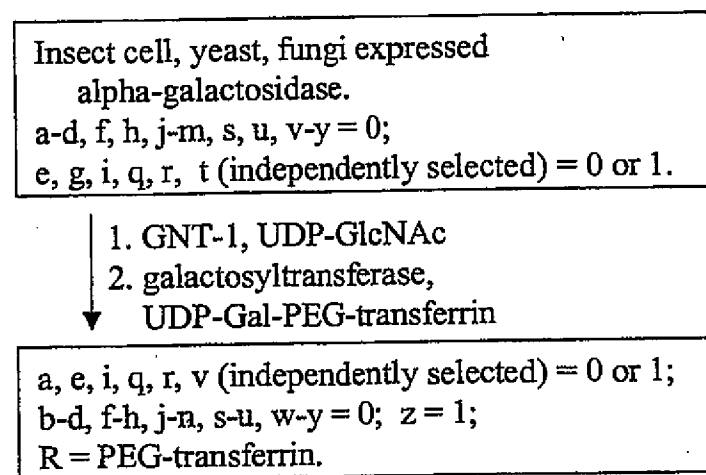


FIG. 56I

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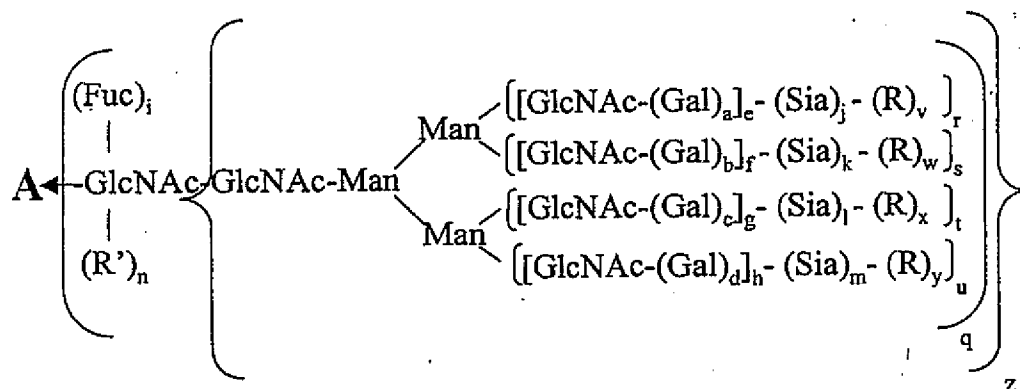
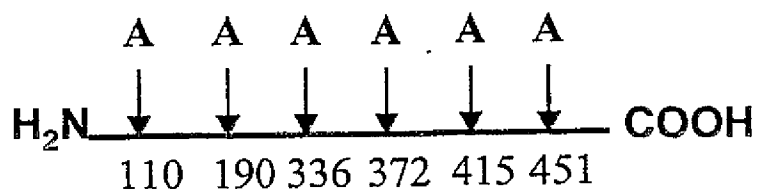
Insect cell, yeast, fungi expressed
alpha-galactosidase.
a-d, f, h, j-m, s, u, v-y = 0;
e, g, i, q, r, t (independently selected) = 0 or 1.

- ↓
1. GNT-1 and 2, UDP-GlcNAc
2. galactosyltransferase, UDP-Gal
3. sialyltransferase,
CMP-SA-PEG-melanotransferrin

a, c, e, g, i, j, l, q, r, t, v, x (independently
selected) = 0 or 1;
b, d, f, h, k, m, n, s, u, w, y = 0;
z = 1; R = PEG-melanotransferrin.

FIG. 56J

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a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 57A

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CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Endo-H
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;
n, v-y = 0; z = 1; and when z = 0 and q = 1, then n
(independently selected) = 0 or 1; R' = Gal-PEG-transferrin.

FIG. 57B

CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
2. CMP-SA-linker-Mannose-6-phosphate ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;
z = 1; R = mannose-6-phosphate; and when a-n = 0,
then r-u (independently selected) = 0 or 1;
v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

FIG. 57C

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NSO expressed alpha-iduronidase.

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;
v-y = 0; Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-linker-mannose-6-phosphate sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = mannose-6 phosphate

FIG. 57D

CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
 2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;
z = 1; R = PEG; and when a-n = 0, then r-u
(independently selected) = 0 or 1; v-y = 0-100;
R = mannose or mannose with mannose-6-phosphate.

FIG. 57E

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CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-iduronidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1; j-m (independently
selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate;
v-y (independently selected) = 0 or 1;
R = mannose-linker-ApoE.

FIG. 57F

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-iduronidase.
a-i, v-y = 0; q (independently selected) = 0 or 1;
z = 1; r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H
2. galactosyltransferase,
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;
R' = galactose-linker-alpha2-macroglobulin.

FIG. 57G

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Insect cell, yeast, fungi expressed
alpha-iduronidase.
a-d, f, h, j-m, s, u, v-y = 0;
e, g, i, q, r, t (independently selected) = 0 or 1.

↓
1. GNT-1,
UDP-GlcNAc-PEG-mannose-6-phosphate

e, i, q, r, v (independently selected) = 0 or 1;
a-d, f-h, j-n, s-u, w-y = 0; z = 1;
R = PEG-mannose-6-phosphate.

FIG. 57H

Insect cell, yeast, fungi expressed
alpha-iduronidase.
a-d, f, h, j-m, s, u, v-y = 0;
e, g, i, q, r, t (independently selected) = 0 or 1.

↓
1. GNT-1, UDP-GlcNAc
2. galactosyltransferase,
UDP-Gal-PEG-transferrin

a, e, i, q, r, v (independently selected) = 0 or 1;
b-d, f-h, j-n, s-u, w-y = 0; z = 1;
R = PEG-transferrin.

FIG. 57I

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Insect cell, yeast, fungi expressed
alpha-iduronidase.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.

- ↓
1. GNT-1 and 2, UDP-GlcNAc
2. galactosyltransferase, UDP-Gal
3. sialyltransferase,
CMP-SA-PEG-melanotransferrin

a, c, e, g, i, j, l, q, r, t, v, x

(independently selected) = 0 or 1;

b, d, f, h, k, m, n, s, u, w, y = 0; z = 1;

R = PEG-melanotransferrin.

FIG. 57J

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FIG. 58A

ACCCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAT
GCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAG
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGT
GCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGCTG
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATA
GCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGATCT
CCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCG
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCC
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCT
TTCCAGCGCCGGGCAGGAGGGGTCCTGGTTGCCTCCCATCTGCAGAG
CTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTG
A

FIG. 58B

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His
Leu Ala Gln Pro

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FIG. 59A

GCGCCTCTTATGTACCCACAAAAATCTATTTTCAAAAAAGTTGCTCTA
AGAATATAGTTATCAAGTTAAGTAAAATGTCAATAGCCTTTTAATTTA
ATTTTTAATTGTTTTATCATTCTTTGCAATAATAAAACATTAACTTTAT
ACTTTTTAATTTAATGTATAGAATAGAGATATACATAGGATATGTAAA
TAGATACACAGTGTATATGTGATTAAAATATAATGGGAGATTCAATC
AGAAAAAAGTTTCTAAAAAGGCTCTGGGGTAAAAGAGGAAGGAAAC
AATAATGAAAAAAATGTGGTGAGAAAAACAGCTGAAAACCCATGTA
AAGAGTGTATAAAGAAAGCAAAAAGAGAAGTAGAAAGTAACACAGG
GGCATTGGAATAATGTAAACGAGTATGTTCCCTATTTAAGGCTAGGC
ACAAAGCAAGGTCTTCAGAGAACCTGGAGCCTAAGGTTTAGGCTCAC
CCATTTCAACCAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCCTGGGCTAGCAGG
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAATCTCTCTTTTCTCC
TGCTTGAAGGACAGACATGACTTTGGATTTCCCCAGGAGGAGTTTGG
CAACCAGTTCCAAAAGGCTGAAACCATCCCTGTCCTCCATGAGATGA
TCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTT
GGGATGAGACCCTCCTAGACAAATTCTACACTGAACTCTACCAGCAG
CTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAGA
GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT
TCCAAAGAATCACTCTCTATCTGAAAGAGAAGAAATACAGCCCTTGT
GCCTGGGAGGTTGTCAGAGCAGAAATCATGAGATCTTTTTCTTTGTCA
ACAACTTGCAAGAAAGTTTAAGAAGTAAGGAATGAAAAGTGGTTCA
ACATGGAAATGATTTTCATTGATTCTGATGCCAGCTCACCTTTTTATG
ATCTGCCATTTCAAAGACTCATGTTTCTGCTATGACCATGACACGATT
TAAATCTTTTCAAATGTTTTTAGGAGTATTAATCAACATTGTATTAG
CTCTTAAGGCACTAGTCCCTTACAGAGGACCATGCTGACTGATCCATT
ATCTATTTAAATATTTTTAAAATATTATTTATTTAACTATTTATAAAAC
AACTATTTTTTGTTCATATTATGTCATGTGCACCTTTGCACAGTGGTTA
ATGTAATAAAATGTGTTCTTTGTATTTGGTAAATTTATTTTGTGTGTT
CATTGAACTTTTGCTATGGAACCTTTGTACTTGTTTATTCTTTAAAATG
AAATTCCAAGCCTAATTGTGCAACCTGATTACAGAATAACTGGTACA
CTTCATTTGTCCATCAATATTATTTCAAGATATAAGTAAAAATAAAC
TTTCTGTAAACCAAGTTGTATGTTGTACTCAAGATAACAGGGTGAACC
TAACAAATACAATTCTGCTCTCTTGTGTATTTGATTTTTGTATGAAAA
AACTAAAAATGGTAATCATACTTAATTATCAGTTATGGTAAATGGT
ATGAAGAGAAGAAGGAACG

FIG. 59B

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Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser
Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr
Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala
Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr
Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu
Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe
Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val
Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu
Arg Ser Lys Glu

FIG. 59C

ATGGCCCTCCTGTTCCCTCTACTGGCAGCCCTAGTGATGACCAGCTAT
AGCCCTGTTGGATCTCTGGGCTGTGATCTGCCTCAGAACCATGGCCTA
CTTAGCAGGAACACCTTGGTGCTTCTGCACCAAATGAGGAGAATCTCC
CCTTTCTTGTGTCTCAAGGACAGAAGAGACTTCAGGTTCCCCCAGGAG
ATGGTAAAAGGGAGCCAGTTGCAGAAGGCCCATGTCATGTCTGTCTCT
CCATGAGATGCTGCAGCAGATCTTCAGCCTCTTCCACACAGAGCGCTC
CTCTGCTGCCTGGAACATGACCCTCCTAGACCAACTCCACACTGGACT
TCATCAGCAACTGCAACACCTGGAGACCTGCTTGCTGCAGGTAGTGG
GAGAAGGAGAATCTGCTGGGGCAATTAGCAGCCCTGCACTGACCTTG
AGGAGGTA CTTCAGGGAATCCGTGTCTACCTGAAAGAGAAGAAATA
CAGCGACTGTGCCTGGGAAGTTGTCAGAATGGAAATCATGAAATCCT
TGTTCTTATCAACAAACATGCAAGAAAGACTGAGAAGTAAAGATAGA
GACCTGGGCTCATCTTGA

FIG. 59D

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr Ser Pro Val
Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg Asn Thr
Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu Cys Leu Lys Asp
Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys Gly Ser Gln Leu Gln Lys
Ala His Val Met Ser Val Leu His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His
Thr Glu Arg Ser Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr
Gly Leu

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FIG. 60A

ATGACCAACAAGTGTCTCCTCCAAATTGCTCTCCTGTTGTGCTTCTCC
ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCTACAAAGA
AGCAGCAATTTTCAGTGTGAGAAGCTCCTGTGGCAATTGAATGGGAG
GCTTGAATATTGCCTCAAGGACAGGATGAACTTTGACATCCCTGAGG
AGATTAAGCAGCTGCAGCAGTTCCAGAAGGAGGACGCCGCATTGACC
ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA
TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA
TGTCTATCATCAGATAAACCATCTGAAGACAGTCCTGGAAGAAAAAC
TGGAGAAAGAAGATTTTACCAGGGGAAACTCATGAGCAGTCTGCAC
CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA
GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAAATCCTAAGGA
ACTTTTACTTCATTAACAGACTTACAGGTTACCTCCGAAACTGAAGAT
CTCCTAGCCTGTCCCTCTGGGACTGGACAATTGCTTCAAGCATTCTTC
AACCAGCAGATGCTGTTTAAGTGACTGATGGCTAATGTACTGCAAAT
GAAAGGACACTAGAAGATTTTGAAATTTTATTAAATTATGAGTTATT
TTTATTTAT TTAAATTTTATTTTGGAAAATAAATTATTTTGGTGC

FIG. 60B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala
Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp
Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu
Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp
Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile
Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val
Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

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FIG. 61A

ATGGTCTCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCCACGGCGT
CCTGCACCCGGCGCCGGCGCGCCAACGCGTTCCTGGAGGAGCTGCGGC
CGGGCTCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA
GGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC
TGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA
GAATGGGGGCTCCTGCAAGGACCAGTCCAGTCCATATCTGCTTCT
GCCTCCCTGCCTTCGAGGGGCCGGAAGTGTGAGACGCACAAGGATGAC
CAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAGCAGTACTGCAG
TGACCACACGGGCACCAAGCGCTCCTGTCTGGTGCCACGAGGGGTACT
CTCTGCTGGCAGACGGGGTGTCTTGCACACCCACAGTTGAATATCCA
TGTGGAAAAATACCTATTCTAGAAAAAAGAAATGCCAGCAAACCCCA
AGGCCGAATTGTGGGGGGCAAGGTGTGCCCCAAAGGGGAGTGTCCA
TGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGGAC
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA
AATCAAGAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGAC
CTCAGCGAGCACGACGGGGATGAGCAGAGCCGGCGGGTGGCGCAGG
TCATCATCCCCAGCACGTACGTCCCGGGCACCACCAACCACGACATC
GCGCTGCTCCGCCTGCACCAGCCCGTGGTCTCACTGACCATGTGGTG
CCCCTCTGCTGCCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC
GTGCGCTTCTCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGG
CGCCACGGCCCTGGAGCTCATGGTGCTCAACGTGCCCCGGCTGATGA
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAAT
ATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCCCACATGCCACCCACTACCGGG
GCACGTGGTACCTGACGGGCATCGTCAGCTGGGGCCAGGGGCTGCGCA
ACCGTGGGGCCACTTTGGGGTGTACACCAGGGTCTCCCAGTACATCGA
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCCAGGAGTCCTCC
TGCGAGCCCCATTCCC

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FIG. 61B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys
Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val Leu His Arg Arg Arg
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

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FIG. 62A

ATGCAGCGCGTGAACATGATCATGGCAGAATCACCAAGCCTCATCAC
CATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTTTCTT
GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAA
TTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAAT
GTATGGAAGAAAAGTGTAGTTTTTGAAGAACCACGAGAAGTTTTTGAA
AACACTGAAAAGACAACCTGAATTTTGGAAGCAGTATGTTGATGGAGA
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG
ACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGA
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT
GAGGGATATCGACTTGCAGAAAACCAGAAGTCCTGTGAACCAGCAGT
GCCATTTCCATGTGGAAGAGTTTCTGTTTCACAACTTCTAAGCTCAC
CCGTGCTGAGGCTGTTTTTCCTGATGTGGACTATGTAAATCCTACTGA
AGCTGAAACCATTTTGGATAACATCACTCAAGGCACCCAATCATTTA
ATGACTTCACTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAA
TTCCCTTGGCAGGTTGTTTTGAATGGTAAAGTTGATGCATTCTGTGGA
GGCTCTATCGTTAATGAAAAATGGATTGTAAGTGTGCTGCCCAGTGTGT
GAAACTGGTGTAAAATTACAGTTGTTCGAGGTGAACATAATATTGA
GGAGACAGAACATACAGAGCAAAAGCGAAATGTGATTTCGAGCAATT
ATTCCTCACCACAACACTACAATGCAGCTATTAATAAGTACAACCATGA
CATTGCCCTTCTGGAAGTGGACGAACCCTTAGTGCTAAACAGCTACG
TTACACCTATTTGCATTGCTGACAAGGAATACACGAACATCTTCCTCA
AATTTGGATCTGGCTATGTAAGTGGCTGGGCAAGAGTCTTCACAAA
GGGAGATCAGCTTTAGTTCTTCAGTACCTTAGAGTTCCACTTGTTGAC
CGAGCCACATGTCTTCGATCTACAAAGTTCACCATCTATAACAACAT
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTCATGTCAAGGAG
ATAGTGGGGGACCCCATGTTACTGAAGTGGGAAGGGACAGTTTCTTA
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAAATA
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAGGAAA
AAACAAAGCTCACTTAATGAAAGATGGATTTCCAAGGTTAATTCATT
GGAATTGAAAATTAACAG

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FIG. 62B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu
Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala
Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe
Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu
Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr
Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys
Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn
Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys
Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu
Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser
Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr
Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser
Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe
Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val
Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr
Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn
Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn
His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr
Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln
Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe
Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser
Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu
Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr
Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr

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FIG. 63A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCCA
GAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCC
AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCC
ACTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAG
AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG
GGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTG
TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT
GCTGATTTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT
GTGAGATAAACTCTCCTTTTCCTTACCATAACCACTTTGACACGCTTC
AAGGATATACTGCAGCTTTACTGCCTTCCTCCTTATCCTACAGTACAA
TCAGCAGTCTAGTTCTTTTCATTTGGAATGAATACAGCATTAAAGCTTG
TTCCACTGCAAATAAAGCCTTTTAAATCATC

FIG. 63B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
Lys Ser

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FIG. 63C

ATGAAGACACTCCAGTTTTTCTTCCTTTTCTGTTGCTGGAAAGCAATC
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA
AGAAGAATGTCGTTTCTGCATAAGCATCAACACCACTTGGTGTGCTG
GCTACTGCTACACCAGGGATCTGGTGTATAAGGACCCAGCCAGGCCC
AAAATCCAGAAAACATGTACCTTCAAGGAACTGGTATATGAAACAGT
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCCTTGTATACATACCC
AGTGGCCACCCAGTGTCACTGTGGCAAGTGTGACAGCGACAGCACTG
ATTGTACTGTGCGAGGCCTGGGGCCCAGCTACTGCTCCTTTGGTGAAA
TGAAAGAATAA

FIG. 63D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

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FIG. 64A

CCCGGAGCCGGACCGGGGCCACCGCGCCCGCTCTGCTCCGACACCGC
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCT
GCACCGCCGAGCTTCCCGGGATGAGGGCCCCCGGTGTGGTCAACCGG
CGCGCCCCAGGTCGCTGAGGGACCCCGGCCAGGCGCGGAGATGGGG
GTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCTGCTGTCG
CTCCCTCTGGGCCTCCCAGTCCTGGGCGCCCCACCACGCCTCATCTGT
GACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT
ATCACTGTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGAT
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTG
CTGTCGGAAGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCC
CAGCCGTGGGAGCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG
CCTTCGCAGCCTCACCCTCTGCTTCGGGCTCTGCGAGCCCAGAAGG
AAGCCATCTCCCCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACA
ATCACTGCTGACACTTTCCGCAAACTCTTCCGAGTCTACTCCAATTTC
CTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC
TCACCAACATTGCTTGTGCCACACCCTCCCCCGCCACTCCTGAACCCC
GTCGAGGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA
GTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGC
AACTCTGAGATCTAAGGATGTCACAGGGGCCAACTTGAGGGCCCAGAG
CAGGAAGCATTGAGAGAGCAGCTTTAAACTCAGGGACAGAGCCATG
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC
AGGACACGCTTTGGAGGCGATTTACCTGTTTTTCGCACCTACCATCAGG
GACAGGATGACCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAG
GTCTCACGGGCATGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA
CCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGCTGGCCTCTGG
CTCTCATGGGGTCCAAGTTTTGTGTATTCTTCAACCTCATTGACAAGA
ACTGAAACCACCAAAAAAAAAAAAAA

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FIG. 64B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu Leu Ser
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

FIG. 65

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp

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FIG. 66A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT
CTCTGCACCCGCCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGC
ATGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGA
GACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAT
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGT
ACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTG
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGA
ACCTGAAGGACTTTCTGCTTGTTCATCCCCTTTGACTGCTGGGAGCCAG
TCCAGGAGTGA

FIG. 66B

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu

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FIG. 67A

ATGAAATATACAAGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTTG
GGTTCTCTTGGCTGTTACTGCCAGGACCCATATGTAAAAGAAGCAGA
AAACCTTAAGAAATATTTTAATGCAGGTCATTCAGATGTAGCGGATA
ATGGAACCTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGT
GACAGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAACCT
TTTTAAAACTTTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA
CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG
AAACGAGATGACTTCGAAAAGCTGACTAATTATTCGGTAACTGACTT
GAATGTCCAACGCAAAGCAATACATGAACTCATCCAAGTGATGGCTG
AACTGTCCGCGCAGCAGCTAAAACAGGGAAGCGAAAAAGGAGTCAGAT
GCTGTTTCGAGGTCGAAGAGCATCCCAGTAA

FIG. 67B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu
Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr
Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser
Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val
Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys
Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln
Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys
Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln

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FIG. 68A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA
TCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATC
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAA
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC
CCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGA
ATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTC
CAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT
GACCACCGGCAATGGCCTGTTCTCAGCGAGGGCCTGAAGCTAGTGG
ATAAGTTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTC
ACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACG
ATTACGTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAG
GAGCTTGACAGAGACACAGTTTTTGTCTCTGGTGAATTACATCTTCTTT
AAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAG
AGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATG
AAGCGTTTAGGCATGTTTAAACATCCAGCACTGTAAGAAGCTGTCCAG
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT
TCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACC
CACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTGC
CAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAA
GAGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGG
CTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAGCTCTCCAAG
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGC
TGCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATCCCCCCCCGA
GGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATAC
CAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAAT
AACTGCCTCTCGCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCC
CTGGATGACATTAAAGAAGGGTTGAGCTGG

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FIG. 68B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val
Phe Ala Leu Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys
Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val
Val Asn Pro Thr Gln Lys

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FIG. 69A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTTT
GTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGTGGTCT
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTTCAAGTCCTTCCA
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTTCGTGGGCATCAGGT
GCCCCCCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGT
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCCGACCTTTCCT
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGGCGACG
GATGGAGCTGAGTATGGGGCCCATCCAGGCTAATCACACGGGCACAG
GCCTGCTACTGACCCTGCAGCCAGAACAGAAAGTTCCAGAAAGTGAAG
GGATTTGGAGGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC
CTGTCACCCCCTGCCCAAATTTGCTACTTAAATCGTACTTCTCTGAA
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTTCCA
GTTGCACAACTTCAGCCTCCCAGAGGAAGATACCAAGCTCAAGATAC
CCCTGATTCACCGAGCCCTGCAGTTGGCCCAGCGTCCCGTTTCACTCC
TTGCCAGCCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG
GTGAATGGGAAGGGGTCACTCAAGGGACAGCCCGGAGACATCTACC
ACCAGACCTGGGCCAGATACTTTGTGAAGTTCCTGGATGCCTATGCTG
AGCACAAGTTACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCT
GCTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGGGCTTCACCCCT
GAACATCAGCGAGACTTCATTGCCCCGTGACCTAGGTCTACCCCTCGCC
AACAGTACTCACCACAATGTCCGCCTACTCATGCTGGATGACCAACGC
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTTCT
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCCA
ACACCATGCTCTTTGCCTCAGAGGCCTGTGTGGGCTCCAAGTTCTGGG
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGC
CACAGCATCATCACGAACCTCCTGTACCATGTGGTTCGGCTGGACCGAC
TGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAA
CTTTGTGACAGTCCCATCATTGTAGACATCACCAAGGACACGTTTTA
CAAACAGCCCATGTTCTACCACCTTGGCCACTTCAGCAAGTTCATTCC
TGAGGGCTCCCAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC
TGGACGCAGTGGCACTGATGCATCCCGATGGCTCTGCTGTTGTGGTCG
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG
CTGTGGGCTTCCTGGAGACAATCTCACCTGGCTACTCCATTACACCT
ACCTGTGGCATCGCCAGTGATGGAGCAGATACTCAAGGAGGCACTGG
GCTCAGCCTGGGCATTAAAGGGACAGAGTCAGCTCACACGCTGTCTG
TGACTAAAGAGGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGT

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FIG. 69A-2

AAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTCCCCTCTAGGTGGT
GCCCAGGGCTGGAGGCCCTAGAAAAAGATCAGTAAGCCCCAGTGTC
CCCCCAGCCCCCATGCTTATGTGAACATGCGCTGTGTGCTTGCTT
TGGAAGCT

FIG. 69B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser
Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser
Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys
Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr
Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly
Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu
Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser
Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser
Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser
Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu
Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile
Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu
His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp
Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg
Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val
Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro
Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser
Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu
Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr
Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu
Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn
Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu
Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

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FIG. 70A

ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG
AGCAGTCTTCGTTTCGCCCAGCCAGGAAATCCATGCCCGATTTCAGAA
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAACGCA
GATGATATAACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA
GCAACCGGGTGGAATATTGCTGGTGCAACAGTGGCAGGGCACAGTGC
CACTCAGTGCCCTGTCAAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG
GGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTCTGTGCCAGTG
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATAACCAGGGCCA
CGTGCTACGAGGACCAGGGCATCAGCTACAGGGGCACGTGGAGCAC
AGCGGAGAGTGGCGCCGAGTGCACCAACTGGAACAGCAGCGCGTTG
GCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG
GCCTGGGGAACCACAACTACTGCAGAAACCCAGATCGAGACTCAA
GCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCT
GCAGCACCCCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGG
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGTGC
CTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTTTACAC
AGCACAGAACCCAGTGCCAGGCACTGGGCCTGGGCAAACATAATT
ACTGCCGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTC
CACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG
GAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCT
TTGCCAAGCACAGGAGGTCGCCGGGAGAGCGGTTCTGTGCGGGGGC
ATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCCTGCTTCCAG
GAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATA
CCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA
TACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACAT
TGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCAGGAGA
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTG
CCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGC
CTTGTCTCCTTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTCAGACT
GTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAG
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCC
CAGGCAAACCTTGACGACGCCTGCCAGGGCGATTTCGGGAGGCCCCCT
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT
GGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAG
GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGACC
AGGAACACCCGACTCCTCAAAAGCAAATGAGATCC

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FIG. 70B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys
Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg
Asp Asn Met Arg Pro

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FIG. 71A

ATCACTCTCTTTAATCACTACTCACATTAACCTCAACTCCTGCCACAA
TGTACAGGATGCAACTCCTGTCTTGCAATTGCACTAATTCTTGCACTTG
TCACAAACAGTGACCTACTTCAAGTTCGACAAAGAAAACAAAGAAA
ACACAGCTACAACCTGGAGCATTACTGCTGGATTACAGATGATTTTG
AATGGAATTAATAATTACAAGAATCCCAAACCTCACCAGGATGCTCAC
ATTTAAGTTTTACATGCCCAAGAAGGCCACAGAACTGAAACAGCTTC
AGTGTCTAGAAGAAGAACTCAAACCTCTGGAGGAAGTGCTGAATTTA
GCTCAAAGCAAAAACCTTTCACCTTAAGACCCAGGGACTTAATCAGCAA
TATCAACGTAATAGTTCTGGAACATAAGGGATCTGAAACAACATTCA
TGTGTGAATATGCAGATGAGACAGCAACCATTGTAGAATTTCTGAAC
AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAACTTGATAA
TTAAGTGCTTCCCCTTAAACATATCAGGCCTTCTATTTATTTATTTA
AATATTTAAATTTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG
TAACTATTATTCTTAATCTTAAACTATAAATATGGATCTTTTATGAT
TCTTTTTGTAAGCCCTAGGGGCTCTAAAATGGTTTACCTTATTTATCC
CAAAAATATTTATTATTATGTTGAATGTTAAATATAGTATCTATGTAG
ATTGGTTAGTAAACTATTTAATAAATTTGATAAATATAAAAAAAAAA
AAACAAAAAAAAAAAA

FIG. 71B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr
Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys
Gln Ser Ile Ile Ser Thr Leu Thr

FIG. 72A-1

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ATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTGCGATTCT
GCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAACGTGCA
TGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG
ATTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGT
GTACAAAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTCAACAT
CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCC
AGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCT
TCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCT
TCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAG
AAGATGATAAAGTCTTCCCTGGTGAAGCCATACATATGTCTGGCAG
GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTAC
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGG
CCTCATTGGAGCCCTACTAGTATGTAGAGAAGGGAGTCTGGCCAAGG
AAAAGACACAGACCTTGCACAAATTTATACTACTTTTTGCTGTATTTG
ATGAAGGGAAAAGTTGGCACTCAGAAACAAAGAACTCCTTGATGCA
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCTAAAATGCACACAG
TCAATGGTTATGTAAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAA
GTGCACTCAATATTCCTCGAAGGTCACACATTTCTTGTGAGGAACCAT
CGCCAGGCGTCCTTGGAATCTCGCCAATAACTTTCTTACTGCTCAA
ACACTCTTGATGGACCTTGGACAGTTTCTACTGTTTTGTCATATCTCT
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT
CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCGGAAG
ACTATGATGATGATCTTACTGATTCTGAAATGGATGTGGTCAGGTTTG
ATGATGACAACTCTCCTTCCTTTATCCAAATTCGCTCAGTTGCCAAGA
AGCATCCTAAAACTTGGGTACATTACATTGCTGCTGAAGAGGAGGAC
TGGGACTATGCTCCCTTAGTCCTCGCCCCCGATGACAGAAGTTATAAA
AGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAA
AAAAGTCCGATTTATGGCATAACAGATGAAACCTTTAAGACTCGTG
AAGCTATTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG
AAGTTGGAGACACACTGTTGATTATATTTAAGAATCAAGCAAGCAGA
CCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTAT
TCAAGGAGATTACCAAAGGTGTAAACATTTGAAGGATTTTCCAAT
TCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGACTGTAGAAG
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC
TCCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACCAGATA
ATGTCAGACAAGAGGAATGTCATCCTGTTTTCTGTATTTGATGAGAAC
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTTCTCCCAATCCA
GCTGGAGTGCAGCTTGAGGATCCAGAGTTCCAAGCCTCCAACATCAT
GCACAGCATCAATGGCTATGTTTTTGATAGTTTGCAGTTGTCAGTTTG
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTGGAGCACAGA
CTGACTTCCTTTCTGTCTTCTTCTCTGGATATACCTTCAAACACAAAAT

FIG. 72A-2

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GGTCTATGAAGACACACTCACCCATTCCCATTTCTCAGGAGAACTGT
CTTCATGTCGATGGAAAACCCAGGTCTATGGATTCTGGGGTGCCACA
ACTCAGACTTTTCGGAACAGAGGCATGACCGCCTTACTGAAGGTTTCT
AGTTGTGACAAGAACAACACTGGTGATTATTACGAGGACAGTTATGAAGA
TATTTTCAGCATACTTGCTGAGTAAAAACAATGCCATTGAACCAAGAA
GCTTCTCCCAGAATTCAAGACACCGTAGCACTAGGCCAAAAGCAATTT
AATGCCACCACAATTCCAGAAAATGACATAGAGAAGACTGACCCTTG
GTTTGACACACAGAACACCTATGCCTAAAATACAAAATGTCTCCTCTA
GTGATTTGTTGATGCTCTTGCGACAGAGTCCTACTCCACATGGGCTAT
CCTTATCTGATCTCCAAGAAGCCAAATATGAGACTTTTTCTGATGATC
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA
CACTTCAGGCCACAGCTCCATCACAGTGGGGACATGGTATTTACCCC
TGAGTCAGGCCTCCAATTAAGATTAAATGAGAACTGGGGACAACCTG
CAGCAACAGAGTTGAAGAACTTGATTTCAAAGTTTCTAGTACATCA
AATAATCTGATTTCAACAATTCCATCAGACAATTTGGCAGCAGGTACT
GATAATACAAGTTCCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT
AGTCAATTAGATAACCACTCTATTTGGCAAAAAGTCATCTCCCCTTACT
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAATAATGATTCAA
GTTGTTAGAATCAGGTTTAATGAATAGCCAAGAAAGTTCATGGGGAA
AAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGGAAAAGA
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAGTT
AGCATCTCTTTGTTAAAGACAAAACAACTTCCAATAATTCAGCAACT
AATAGAAAGACTCACATTGATGGCCCATCATTATTAATTGAGAATAG
TCCATCAGTCTGGCAAAATATATTAGAAAGTGACACTGAGTTTAAAA
AAGTGACACCTTTGATTCATGACAGAATGCTTATGGACAAAATGCT
ACAGCTTTGAGGCTAAATCATATGTCAAATAAACTACTTCATCAA
AAACATGGAAATGGTCCAACAGAAAAAAGAGGGGCCCATTCACCA
GATGCACAAAATCCAGATATGTGCTTCTTTAAGATGCTATTCTTGCCA
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAACTCTCTGAA
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCCTTAGGACCAG
AAAAATCTGTGGAAGGTCAGAAATTTCTTGTCTGAGAAAAACAAAGTG
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA
TGGTTTTTCCAAGCAGCAGAAACCTATTTCTTACTAACTTGGATAATT
TACATGAAAATAATACACACAATCAAGAAAAAAAATTTCAGGAAGA
AATAGAAAAGAAGGAAACATTAATCCAAGAGAATGTAGTTTTGCCTC
AGATACATACAGTGACTGGCACTAAGAATTTTCATGAAGAACCTTTTC
TACTGAGCACTAGGCCAAAATGTAGAAGGTTTCATATGACGGGGCATA
TGCTCCAGTACTTCAAGATTTTAGGTCATTAAATGATTCAACAAATAG
AACAAAGAAACACACAGCTCATTCTCAAAAAAAGGGGAGGAAGAA
AACTTGGAAGGCTTGGGAAATCAAACCAGCAAATTGTAGAGAAATAT
GCATGCACCACAAGGAATATCTCTAATAACAAGCCAGCAGAAATTTG
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCCTA

FIG. 72A-3

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GAAGAAACAGAACTTGAAAAAAGGATAATTGTGGATGACACCTCAAC
CCAGTGGTCCAAAAACATGAAACATTTGACCCCGAGCACCCCTCACAC
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAAATAGA
TCTCCATTACCCATTGCAAAGGTATCATCATTTCCATCTATTAGACCTA
TATATCTGACCAGGGTCCTATTCCAAGACAACCTCTTCTCATCTTCCAG
CAGCATCTTATAGAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT
TTCTTACAAGGAGCCAAAAAATAACCTTTCTTTAGCCATTCTAACC
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG
TGCCACAAATTCAGTCACATACAAGAAAGTTGAGAACACTGTTCTCCC
GAAACCAGACTTGCCCAAAACATCTGGCAAAGTTGAATTGCTTCCAA
AAGTTCACATTTATCAGAAGGACCTATTCCCTACGGAACTAGCAATG
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA
CAGAGGGAGCGATTAAGTGGAATGAAGCAAACAGACCTGGAAAAGT
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAAGACTCCCTCCAA
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC
AAAAGAAGAGTGGAAATCCCAAGAGAAGTCACCAGAAAAAACAGCT
TTTAAGAAAAAGGATACCATTTTGTCCCTGAACGCTTGTGAAAGCAAT
CATGCAATAGCAGCAATAAATGAGGGACAAAATAAGCCCGAAATAG
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA
AACCACACAGTCTTGAAACGCCATCAACGGGAAATAACTCGTACTAC
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCATATCAGT
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAATC
AGAGCCCCCGCAGCTTTCAAAGAAAACACGACACTATTTTATTGCTG
CAGTGGAGAGGGCTCTGGGATTATGGGATGAGTAGCTCCCCACATGTT
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGTTCAAGAAAGT
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT
GGAGAACTAAATGAACATTTGGGACTCCTGGGGCCATATATAAGAGC
AGAAGTTGAAGATAATATCATGGTAACTTTCAGAAATCAGGCCTCTC
GTCCCTATTCTTCTATTCTAGCCTTATTTCTTATGAGGAAGATCAGAG
GCAAGGAGCAGAACCTAGAAAAAACTTTGTCAAGCCTAATGAAACCA
AACTTACTTTTGGAAAGTGCAACATCATATGGCACCCACTAAAGAT
GAGTTTGAAGTGCAGAGCCTGGGCTTATTTCTCTGATGTTGACCTGGAA
AAAGATGTGCACTCAGGCCTGATTGGACCCCTTCTGGTCTGCCACACT
AACACACTGAACCCTGCTCATGGGAGACAAGTGACAGTACAGGAATT
TGCTCTGTTTTTACCATCTTTGATGAGACCAAAGCTGGTACTTCACT
GAAAATATGGAAAGAACTGCAGGGCTCCCTGCAATATCCAGATGGA
AGATCCCCTTTTAAAGAGAATTATCGCTTCCATGCAATCAATGGCTA
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGA
TTCGATGGTATCTGCTCAGCATGGGCAGCAATGAAAACATCCATTCT
ATTCATTTAGTGGACATGTGTTCACTGTACGAAAAAAGAGGAGTA
TAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGAGACAGTGA

FIG. 72A-4

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AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGGGAATGCCTTATTGG
CGAGCATCTACATGCTGGGATGAGCACACTTTTTCTGGTGTACAGCAA
TAAGTGTGAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATTT
TCAGATTACAGCTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG
CCAGACTTCATTATTCCGGATCAATCAATGCCTGGAGCACCAAGGAG
CCCTTTTCTTGGATCAAGGTGGATCTGTTGGCACCAATGATTATTAC
GGCATCAAGACCCAGGGTGGCCGTCAGAAGTTCTCCAGCCTCTACAT
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA
CTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATG
TGGATTTCATCTGGGATAAAACACAATATTTTAAACCCTCCAATTATTG
CTCGATACATCCGTTTGCACCCAACCTCATTATAGCATTTCGAGCACTC
TTCGCATGGAGTTGATGGGCTGTGATTTAAATAGTTGCAGCATGCCAT
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA
TCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAGCTCGA
CTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA
CAGGAGTAACTACTCAGGGAGTAAATCTCTGCTTACCAGCATGTAT
GTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC
TCTCTTTTTTCAGAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGA
CTCCTTCACACCTGTGGTGAACCTCTAGACCCACCGTACTGACTCG
CTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGCCCTGAG
GATGGAGGTTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC
CACTGCAGCACCTGCCACTGCCGTACCTCTCCCTCCTCAGCTCCAGG
GCAGTGTCCCTCCCTGGCTTGCCTTCTACCTTTGTGCTAAATCCTAGC
AGACACTGCCTTGAAGCCTCCTGAATTAATCATCAGTCCTGCATT
TCTTTGGTGGGGGGCCAGGAGGGTGCATCCAATTTAACTTAACTCTTA
CCTATTTTCTGCAGCTGCTCCCAGATTACTCCTTCCTTCCAATATAACT
AGGCAAAAAGAAGTGAGGAGAAACCTGCATGAAAGCATTCTTCCCTG
AAAAGTTAGGCCTCTCAGAGTCACCACTTCTCTGTTGTAGAAAAACT
ATGTGATGAACTTTGAAAAAGATATTTATGATGTTAACATTTACAGGT
TAAGCCTCATACGTTTAAAATAAACTCTCAGTTGTTTATTATCCTGA
TCAAGCATGGAACAAAGCATGTTTCAGGATCAGATCAATACAATCTT
GGAGTCAAAGGCAAATCATTGGACAATCTGCAAAATGGAGAGAA
TACAATACTACTACAGTAAAGTCTGTTTCTGCTTCCTTACACATAGA
TATAATTATGTTATTTAGTCATTATGAGGGGCACATTCTTATCTCAA
AACTAGCATTCTTAACTGAGAATTATAGATGGGGTTCAAGAATCCC
TAAGTCCCCTGAAATTATATAAGGCATTCTGTATAAATGCAAATGTGC
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATTCT
GACCAATAAAAAATAAGTCAGGAGGATGCAATTGTTGAAAGCTTTG
AAATAAAATAACAATGTCTTCTTGAAATTTGTGATGGCCAAGAAAGA
AAATGATGA

FIG. 72B-1

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser
Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe
Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile
Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro
Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr
Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly
Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys
Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser
Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg
Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu
Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln
Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp
Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu
Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn
Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val
Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr
Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro
Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser
Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile
Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser
Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn
Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln
Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys
His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val
Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe

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FIG. 72B-2

Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr
Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn
Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln
Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp
Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu
Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu
Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val
Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr
Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu
Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu
Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly
Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn
Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly
Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly
Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu
Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp
Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser
Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser
Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala
Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg
Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro
Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu
Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly
Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp
Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile
Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr
Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln
Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg
Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys
Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val
Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe
Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu
Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn
Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu
Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile
Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile
Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro

FIG. 72B-3

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Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu
 Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr
 Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr
 Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser
 Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro
 Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu
 Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys
 Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu
 Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu
 Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile
 Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly
 Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg
 Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg
 Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu
 Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg
 Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp
 Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val
 Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro
 Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg
 Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro
 Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu
 Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
 Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr
 Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu
 Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln
 Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu
 Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr
 Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro
 Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly
 Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys
 Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr
 Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu
 His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr
 Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln
 Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala
 Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile
 Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser
 Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly
 Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile

FIG. 72B-4

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Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr
His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn
Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr
Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu
His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu
Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln
Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser
Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe
Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu
Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg
Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr

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FIG. 73A

TCCACCTGTCCCCGCAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC
GAGCCGCCGTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG
GCGCGCCTGCTTCTCTGCGTCCTGGTCGTGAGCGACTCCAAAGGCAGC
AATGAACTTCATCAAGTTCCATCGAACTGTGACTGTCTAAATGGAGGA
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCACTGGTGCAACTGC
CCAAAGAAATTTCGGAGGGGCAGCACTGTGAAATAGATAAGTCAAAAAC
CTGCTATGAGGGGAATGGTCACTTTTACCGAGGAAAGGCCAGCACTG
ACACCATGGGCGCGCCCTGCCTGCCCTGGAACCTTGCCACTGTCCTTC
AGCAAACGTACCATGCCCCACAGATCTGATGCTCTTCAGCTGGGCCTGG
GGAAACATAATTACTGCAGGAACCCAGACAACCGGAGGCGACCCCTGG
TGCTATGTGCAGGTGGGCCTAAAGCCGCTTGTCCAAGAGTGCATGGT
GCATGACTGCGCAGATGGAAAAAAGCCCTCCTCTCCTCCAGAAGAAT
TAAAATTTCAGTGTGGCCAAAAGACTCTGAGGCCCCCGCTTTAAGATTA
TTGGGGGAGAATTCACCACCATCGAGAACCAGCCCTGGTTTGCGGCC
ATCTACAGGAGGCACCGGGGGGGCTCTGTACCTACGTGTGTGGAGG
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT
TGATTACCCAAAGAAGGAGGACTACATCGTCTACCTGGGTGCTCAA
GGCTTAACTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGAAAAC
CTCATCCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGA
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA
AGCTGATTTCCACCGGGAGTGTCAGCAGCCCCACTACTACGGCTCTG
AAGTCACCACCAAAAATGCTGTGTGCTGCTGACCCACAGTGGAAAACA
GATTCCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC
CCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTAC
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA
GGGTCCCCAGGGAGGAAACGGGCACCAACCCGCTTTCTTGCTGGTTGTC
ATTTTTCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA
AGAT

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FIG. 73B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu

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FIG. 74A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA
TAGACTACTTTTTTTTCTTTAAGCAGCAAAAGGAGAAAATTGTCATCA
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC
ACCATCATCTCAGGATGAGGGGCATGAAGCTGCTGGGGGCGCTGCTG
GCACTGGCGGCCCTACTGCAGGGGGGCCGTGTCCCTGAAGATCGCAGC
CTTCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCT
CGTCAGCTACATTGTGCAGATCCTGAGCCGCTATGACATCGCCCTGGT
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGCTGG
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTTCGTGTA
CAGGCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT
GTCAGGTTCTTCTCCCGGTTACAGAGGTCAGGGAGTTTGCCATTGTT
CCCCTGCATGCGGCCCCGGGGGACGCAGTAGCCGAGATCGACGCTCT
CTATGACGTCTACCTGGATGTCCAAGAGAAATGGGGCTTGGAGGACG
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT
CCCAGTGGTCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGGC
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT
ATGACAGGATCGTGGTTGCAGGGATGCTGCTCCGAGGCGCCGTTGTTT
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG
CTGAAGTGAGCAGCCCCTCCCCACACCAGTTGAACTGCAG

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FIG. 74B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu Leu Gln
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val
Glu Val Met Leu Lys

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FIG. 75A

GCTGCATCAGAAGAGGCCATCAAGCACATCACTGTCCTTCTGCCATGG
CCCTGTGGATGCGCCTCCTGCCCCTGCTGGCGCTGCTGGCCCTCTGGG
GACCTGACCCAGCCGCAGCCTTTGTGAACCAACACCTGTGCGGCTCAC
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT
ACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGTGGGGCA
GGTGGAGCTGGGCGGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACG
CAGCCCGCAGGCAGCCCCCACCCGCCGCTCCTGCACCGAGAGAGA
TGGAATAAAGCCCTTGAACCAGC

FIG. 75B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly
Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

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FIG. 76A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT
TTCTGTTCCCAATCCTCTGGGATTCTTTCCCGATCACCAGTTGGACCCT
GCGTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC
GGGCCAGGGTTCACCCCAACACACGGCGGTCTTTTGGGGTGGAGCCC
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCCTG
TTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAAGTCCACAACA
TTCCACCAAGCTCTGCTAGATCCCAGAGTGAGGGGGCCTATATTTTCT
GCTGGTGGCTCCAGTTCCGGAACAGTAAACCCTGTTCCGACTACTGTC
TCACCCATATCGTCAATCTTCTCGAGGACTGGGGACCCTGCACCGAAC
ATGGAGAGCACAACATCAGGATTCTAGGACCCCTGCTCGTGTACACA
GGCGGGGTTTTTCTTGTTGACAAGAATCCTCACAATACCACAGAGTCT
AGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGGAGCACCCACGTG
TCCTGGCCAAAATTTCGCAGTCCCCAACCTCCAATCACTCACCAACCTC
TTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTTT
ATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTTGGTTC
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCTCTACTTCCAGGAA
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCTGCT
CAAGGAACCTCTATGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC
GGAAACTGCACCTTGTAATCCCATCCCATCATCCTGGGCTTTCGCAAGA
TTCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA
GTGCCATTTGTTCAAGTGGTTCGCAGGGCTTTCCCCCACTGTTTGGCTTT
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT
TGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATAC
ATTTGA

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FIG. 76B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
Trp Val Tyr Ile

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FIG. 77A

CGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA
CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGC
CCTGGCTTCAAGAGGGGAGTGCCTTCCCAACCATTCCTTATCCAGGC
CTTTTGACAACGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCT
TTGACACCTACCAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG
AAGTATTCATTCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG
TCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAA
CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGA
GCCCCGTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG
CGCCTCTGACAGCAACGTCTATGACCTCCTAAAGGACCTAGAGGAAG
GCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGGACT
GGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACA
CAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAG
GAAGGACATGGCAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCG
CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG
TGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGT
GCCCAACAGCCTTGTCTAATAAAATTAAGTTGCATC

FIG. 77B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp
Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln
Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr
Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala
Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile
Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

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FIG. 78A

ATGTATTCCAATGTGATAGGAACTGTAACCTCTGGAAAAAGGAAGGT
TTATCTTTTGTCTTGCTGCTCATTGGCTTCTGGGACTGCGTGACCTGT
CACGGGAGCCCTGTGGACATCTGCACAGCCAAGCCGCGGGACATTCC
CATGAATCCCATGTGCATTTACCGCTCCCCGGAGAAGAAGGCAACTG
AGGATGAGGGCTCAGAACAGAAGATCCCGGAGGCCACCAACCGGCG
TGTCTGGGAACTGTCCAAGGCCAATTCCCGCTTTGCTACCACTTTCTA
TCAGCACCTGGCAGATTCCAAGAATGACAATGATAACATTTTCCTGTC
ACCCCTGAGTATCTCCACGGCTTTTGCTATGACCAAGCTGGGTGCCTG
TAATGACACCCTCCAGCAACTGATGGAGGTATTTAAGTTTGACACCAT
ATCTGAGAAAACATCTGATCAGATCCACTTCTTCTTTGCCAAACTGAA
CTGCCGACTCTATCGAAAAGCCAACAAATCCTCCAAGTTAGTATCAGC
CAATCGCCTTTTTTGAGACAAATCCCTTACCTTCAATGAGACCTACCA
GGACATCAGTGAGTTGGTATATGGAGCCAAGCTCCAGCCCCCTGGACT
TCAAGGAAAATGCAGAGCAATCCAGAGCGGCCATCAACAAATGGGTG
TCCAATAAGACCGAAGGCCGAATCACCGATGTCATTCCCTCGGAAGC
CATCAATGAGCTCACTGTTCTGGTGCTGGTTAACACCATTTACTTCAA
GGGCCTGTGGAAGTCAAAGTTCAGCCCTGAGAACACAAGGAAGGAAC
TGTTCTACAAGGCTGATGGAGAGTCGTGTTTCAGCATCTATGATGTACC
AGGAAGGCAAGTTCCGTTATCGGCGCGTGGCTGAAGGCACCCAGGTG
CTTGAGTTGCCCTTCAAAGGTGATGACATCACCATGGTCCTCATCTTG
CCCAAGCCTGAGAAGAGCCTGGCCAAGGTGGAGAAGGAACCTACCCC
AGAGGTGCTGCAGGAGTGGCTGGATGAATTGGAGGAGATGATGCTGG
TGGTCCACATGCCCCGCTTCCGCATTGAGGACGGCTTCAGTTTGAAGG
AGCAGCTGCAAGACATGGGCCTTGTCGATCTGTTCAGCCCTGAAAAG
TCCAAACTCCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTC
TCAGATGCATTCCATAAGGCATTTCTTGAGGTAAATGAAGAAGGCAG
TGAAGCAGCTGCAAGTACCGCTGTTGTGATTGCTGGCCGTTTCGCTAAA
CCCCAACAGGGTGACTTTCAAGGCCAACAGGCCTTTCCTGGTTTTTAT
AAGAGAAGTTCCTCTGAACACTATTATCTTCATGGGCAGAGTAGCCA
ACCCTTGTGTTAAGTAA

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FIG. 78B

Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val Tyr Leu Leu
Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys His Gly Ser Pro Val Asp
Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn Pro Met Cys Ile Tyr Arg Ser
Pro Glu Lys Lys Ala Thr Glu Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr
Asn Arg Arg Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr
Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr Leu Gln Gln
Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Ile His
Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser
Lys Leu Val Ser Ala Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu
Thr Tyr Gln Asp Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe
Lys Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu Thr Val Leu
Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Ser Pro Glu
Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser
Met Met Tyr Gln Glu Gly Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln
Val Leu Glu Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys
Pro Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg Phe Arg
Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met Gly Leu Val Asp
Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile Val Ala Glu Gly Arg Asp Asp
Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser
Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg
Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys

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FIG. 79A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCAG
AATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCA
ATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCCA
CTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAGA
GTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCCACAGTAATGGG
GGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTT
ATTATCACAAATCTTAA

FIG. 79B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
Lys Ser

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FIG. 79C

ATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC
GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCAT
CAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCA
CCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCG
TGCTGCAGGGGGTCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACC
GCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCCGCGCGGCG
TGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCAC
TCTGCCGCCGCAGCACTGACTGCGGGGGTCCCAAGGACCACCCC
TTGACCTGTGATGACCCCGCTTCCAGGACTCCTCTTCTCAAAGGCC
CCTCCCCCAGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGAC
ACCCCGATCCTCC CACAATAA

FIG. 79D

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr
Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala
Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly
Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val
Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg
Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys
Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp
Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser
Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln

FIG. 80A

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ATGCGTCCCCTGCGCCCCCGCGCCGCGCTGCTGGCGCTCCTGGCCTCG
CTCCTGGCCGCGCCCCCGGTGGCCCCGGCCGAGGCCCCGCACCTGGT
GCAGGTGGACGCGGCCCGCGCGCTGTGGCCCCTGCGGCGCTTCTGGA
GGAGCACAGGCTTCTGCCCCCGCTGCCACACAGCCAGGCTGACCAG
TACGTCTCAGCTGGGACCAGCAGCTCAACCTCGCCTATGTGGGCGCC
GTCCCTCACCGCGGCATCAAGCAGGTCCGGACCCACTGGCTGCTGGA
GCTTGTACCAACCAGGGGGTCCACTGGACGGGGCCTGAGCTACAAC
TCACCCACCTGGACGGGTACTTGGACCTTCTCAGGGAGAACCAGCTCC
TCCAGGGTTTGAGCTGATGGGCAGCGCCTCGGGCCACTTCACTGACT
TTGAGGACAAGCAGCAGGTGTTTGAGTGGAAGGACTTGGTCTCCAGC
CTGGCCAGGAGATACATCGGTAGGTACGGACTGGCGCATGTTTCCAA
GTGGAACCTTCGAGACGTGGAATGAGCCAGACACCACGACTTTGACA
ACGTCTCCATGACCATGCAAGGCTTCTGAACACTACGATGCCTGCT
CGGAGGGTCTGCGCGCCGCCAGCCCCGCCCTGCGGCTGGGAGGCCCC
GGCGACTCCTTCCACACCCACCGCGATCCCCGCTGAGCTGGGGCCTC
CTGCGCCACTGCCACGACGGTACCAACTTCTTCACTGGGGAGGCGGG
CGTGCGGCTGGACTACATCTCCCTCCACAGGAAGGGTGCGCGCAGCT
CCATCTCCATCCTGGAGCAGGAGAAGGTCGTCGCGCAGCAGATCCGG
CAGCTCTTCCCCAAGTTCGCGGACACCCCCATTTACAACGACGAGGCG
GACCCGCTGGTGGGCTGGTCCCTGCCACAGCCGTGGAGGGCGGACGT
GACCTACGCGGCCATGGTGGTGAAGGTCATCGCGCAGCATCAGAACC
TGCTACTGGCCAACACCACCTCCGCCTTCCCCTACGCGCTCCTGAGCA
ACGACAATGCCTTCCTGAGCTACCACCCGCACCCCTTCGCGCAGCGCA
CGCTACCCGCGCGCTTCCAGGTCAACAACACCCGCCCGCCGCACGTG
CAGCTGTTGCGCAAGCCGGTGCTCACGGCCATGGGGCTGCTGGCGCT
GCTGGATGAGGAGCAGCTCTGGGCCGAAGTGTCGCAGGCCGGGACCG
TCCTGGACAGCAACCACACGGTGGGCGTCCTGGCCAGCGCCCACCGC
CCCCAGGGCCCCGGCCGACGCCTGGCGCGCCGCGGTGCTGATCTACGC
GAGCGACGACACCCGCGCCCAACCCAAACCGCAGCGTCGCGGTGACCC
TGCGGCTGCGCGGGGTGCCCCCGGCCCGGGCCTGGTCTACGTCACG
CGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCGAGTGGCGGCG
CCTGGGCCGGCCCGTCTTCCCCACGGCAGAGCAGTTCCGGCGCATGC
GCGCGGCTGAGGACCCGGTGGCCGCGGCGCCCCGCCCTTACCCGCC
GGCGGCCGCTGACCCTGCGCCCCGCGCTGCGGCTGCCGTCGCTTTTG
CTGGTGACGTGTGTGCGCGCCCCGAGAAGCCGCCCGGGCAGGTCAC
GCGGCTCCGCGCCCTGCCCCTGACCCAAGGGCAGCTGGTTCTGGTCTG
GTCGGATGAACACGTGGGCTCCAAGTGCCTGTGGACATACGAGATCC
AGTTCTCTCAGGACGGTAAGGCGTACACCCCGGTACGACAGGAAGCCA
TCGACCTTCAACCTCTTTGTGTTTACGCCAGACACAGGTGCTGTCTCT
GGCTCCTACCGAGTTCGAGCCCTGGACTACTGGGCCCCGACCAGGCCC
CTTCTCGGACCCTGTGCCGTACCTGGAGGTCCCTGTGCCAAGAGGGCC
CCCATCCCCGGGCAATCCATGA

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FIG. 80B

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu
Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val Gln Val Asp Ala Ala
Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu
Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala
Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu
Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His
Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu
Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val
Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly
Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His His Asp
Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys
Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His Asp
Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His
Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln
Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala
Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala
Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr
Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro
His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg
Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala
Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu
Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala
Asp Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro
Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu
Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp
Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg
Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu
Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala
Arg Pro Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln
Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr
Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro
Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr
Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro
Tyr Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro

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FIG. 81A

ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGCGCGCTTGCGCT
TCGCTTCCTGGCCCTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACT
GGACAATGGATTGGCAAGGACGCCTACCATGGGCTGGCTGCACTGGG
AGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCAGATTCCTGC
ATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGA
AGGCTGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTG
GATGGCTCCCCAAAGAGATTCAGAAGGCAGACTTCAGGCAGACCCTC
AGCGCTTTCCTCATGGGATTCGCCAGCTAGCTAATTATGTTACAGCA
AAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAAACCTGC
GCAGGCTTCCCTGGGAGTTTTGGATACTACGACATTGATGCCCAGACC
TTTGCTGACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGT
GACAGTTTGGAAAATTTGGCAGATGGTTATAAGCACATGTCCTTGGCC
CTGAATAGGACTGGCAGAAGCATTGTGTACTCCTGTGAGTGGCCTCTT
TATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGACAGTAC
TGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAGT
ATAAAGAGTATCTTGGAAGTGGACATCTTTTAACCAGGAGAGAATTGTT
GATGTTGCTGGACCAGGGGGTTGGAATGACCCAGATATGTTAGTGAT
TGGCAACTTTGGCCTCAGCTGGAATCAGCAAGTAACTCAGATGGCCCT
CTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTCCGACA
CATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGC
CATCAATCAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGG
GAGACAACCTTTGAAGTGTGGGAACGACCTCTCTCAGGCTTAGCCTGG
GCTGTAGCTATGATAAACCAGGCAGGAGATTGGTGGACCTCGCTCTTAT
ACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCTGCC
TGCTTCATCACACAGCTCCTCCCTGTGAAAAGGAAGCTAGGGTTCTAT
GAATGGACTTCAAGGTAAAGAAGTCACATAAATCCCACAGGCACTGT
TTTGCTTCAGCTAGAAAATACAATGCAGATGTCATTAAAAGACTTACT
TTAA

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FIG. 81B

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe
Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly Leu Ala
Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met Cys Asn Leu Asp
Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys Leu Phe Met Glu Met Ala Glu
Leu Met Val Ser Glu Gly Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp
Cys Trp Met Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln
Arg Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys
Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe Pro Gly Ser Phe
Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp Trp Gly Val Asp Leu Leu Lys
Phe Asp Gly Cys Tyr Cys Asp Ser Leu Glu Asn Leu Ala Asp Gly Tyr Lys His
Met Ser Leu Ala Leu Asn Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro
Leu Tyr Met Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser Ile Leu
Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala Gly Pro Gly Gly Trp
Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe Gly Leu Ser Trp Asn Gln Gln
Val Thr Gln Met Ala Leu Trp Ala Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp
Leu Arg His Ile Ser Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala
Ile Asn Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met Ile Asn
Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val Ala Ser Leu Gly Lys
Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr Gln Leu Leu Pro Val Lys Arg Lys
Leu Gly Phe Tyr Glu Trp Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr
Val Leu Leu Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu

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FIG. 82A

ATGGCGCCCGTCGCCGTCTGGGCGCGCTGGCCGTCGGACTGGAGCT
CTGGGCTGCGGCGCACGCCTTGCCCGCCCAGGTGGCATTACACCTA
CGCCCCGGAGCCCGGGAGCATGCCGGCTCAGAGAATACTATGACC
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCA
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG
GACAGCACATACACCCAGCTCTGGAAGTGGGTTCGAGTGTGCTGAG
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAACTCAAGCCTGCAC
TCGGGAACAGAACC GCATCTGCACCTGCAGGCCCGGCTGGTACTGCG
CGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAG
TGCCGCCCCGGGCTTCGGCGTGGCCAGACCAGGAAGTGAACATCAGA
CGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTTCTCCAACACGACTTC
ATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACTGGTGGCCAT
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA
CCCGGAGTATGGCCCCAGGGGCAGTACACTTACCCAGCCAGTGTCC
ACACGATCCCAACACACGCAGCCAACTCCAGAAGCCAGCACTGCTCC
AAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCAGCTGAAGG
GAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAAGTGTGTCATCATGAC
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC
CTCACTTGCCCTGCCGATAAGGCCCGGGGTACACAGGGCCCCGAGCAG
CAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGA
GAGCTCGGCCAGTGCCTTGGACAGAAGGGCGCCCACTCGGAACCAGC
CACAGGCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCCGGGC
CAGCACCGGGAGCTCAGATTCTTCCCCTGGTGGCCATGGGACCCAGG
TCAATGTACCTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT
CACAGTGCTCCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC
AGCCCCTCGGAGTCCCCGAAGGACGAGCAGGTCCCCTTCTCCAAGGA
GGAATGTGCCTTTCGGTACAGCTGGAGACGCCAGAGACCCTGCTGG
GGAGCACCGAAGAGAAGCCCCTGCCCTTGGAGTGCCTGATGCTGGG
ATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGTCGTAGCCAAGG
TGGGCTGAGCCCTGGCAGGATGACCCTGCGAAGGGGCCCTGGTCCTT
CCAGGC

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FIG. 82B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly
Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro
Asp Ala Gly Met Lys Pro Ser

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FIG. 83A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

FIG. 83B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
Gly Thr Leu Val Thr Val Ser Ser

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FIG. 84A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ser

FIG. 84B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 85A

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGA
GAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGTTCGTTGGCTCAAGC
ATCCACTGGTATCAGCAAAGAACAATGGTTCTCCAAGGCTTCTCATA
AAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCCAGGTTTAGTGGC
AGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT
GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTC
ACGTTTCGGCTCGGGGACAAATTTGGAAGTAAAAGAAGTGAAGCTTGA
GGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCT
CCTGTGTTGCCTCTGGATTCAATTTTCAGTAACCACTGGATGAACTGGG
TCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGA
TCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG
AGGTTACCATCTCAAGAGATGATTCCAAAAGTGCTGTCTACCTGCAA
ATGACCGACTTAAGAAGTGAAGACACTGGCGTTTATTACTGTTCCAGG
AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTC
ACAGTCTCC

FIG. 85B

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Glu Arg Val
Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His Trp Tyr Gln Gln
Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Met Ser Gly
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
Thr Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro
Phe Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu Glu Ser
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly
Phe Ile Phe Ser Asn His Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
Glu Trp Val Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr
Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg
Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

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FIG. 86A

ATGGAGACAGACACACTCCTGTTATGGGTGCTGCTGCTCTGGGTTCCA
GGTTCCACTGGTGACGTCAGGCGAGGGCCCCGGAGCCTGCGGGGCAG
GGACGCGCCAGCCCCACGCCCTGCGTCCCGGCCGAGTGCTTCGACC
TGCTGGTCCGCCACTGCGTGGCCTGCGGGCTCCTGCGCACGCCGCGGC
CGAAACCGGCCGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAG
CCGCAGGAGTCGGTGGGCGCGGGGGCCGGCGAGGCGGCGGTTCGACA
AAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGA
CCGTCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGA
AGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA
CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGG
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGT
CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG
CCTCCCGTGTTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
CCCTGTCTCCCGGGAAATGA

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FIG. 86B

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala
Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys Val Ala
Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro
Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

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FIG. 87

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Asp Gly Ile Val Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

FIG. 88

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr Ser Val Arg
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys
Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe
Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly Thr
Leu Val Thr Val Ser Ala

FIG. 89

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys

FIG. 90

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
Thr Leu Val Thr Val Ser Ser

FIG. 91

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Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala Pro
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
 Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 Ser Phe Asn Arg Gly Glu Cys

FIG. 92

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
 Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
 Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
 Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
 Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
 Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

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FIG. 93A

ATGGATTTTCAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCTTCA
GTCATAATGTCCAGAGGGCAAATTGTTCTCTCCCAGTCTCCAGCAATC
CTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCAGGGCCAG
CTCAAGTGTAAGTTACATCCACTGGTTCCAGCAGAAGCCAGGATCCTC
CCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCC
TGTTTCGCTTCAGTGGCAGTGGGTCTGGGACTTCTTACTCTCTCACAAT
CAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT
GGACTAGTAACCCACCCACGTTCGGAGGGGGGACCAAGCTGGAAATC
AAA

FIG. 93B

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser
Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu
Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln
Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser
Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn
Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 94A

ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTG
TCCTGTCCCAGGTACAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAAG
CCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACATTT
ACCAGTTACAATATGCACTGGGTAAAACAGACACCTGGTCGGGGCCT
GGAATGGATTGGAGCTATTTATCCCGGAAATGGTGATACTTCCTACAA
TCAGAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCA
GCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCG
GTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTC
AATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA

FIG. 94B

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val Leu Ser
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys
Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ala

FIG. 95A

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GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAATAAAA
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAACCTGGGCG
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA
CACACATTCCACAGAATTAATTCCTTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCC
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCT
TATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGC
GGTTTGACTCACGGGGATTTCGAAGTCTCCACCCCATTGACGTCAATG
GGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTGCGTA
ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGG
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG
GAGACGCCATCACAGATCTCTACCATGAGGGTCCCCGCTCAGCTCCT
GGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGATGGTACCAA
GGTGGAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
GCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCT
GCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG
ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAG
CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAG
TGTTGAATTCAGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCT
GTGACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTG
CCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCT
TGACCCTGGAAGGTGCCACTCCCCTGTCTTTCCCTAATAAAATGAGG
AAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTG
GGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG
GCATGCTGGGGATGCGGTGGGCTCTATGGAACCACTGGGGCTCGAC
AGCTATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGC
CCGCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCTACTT
GGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGT
TTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGA
TTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCAC

FIG. 95B

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CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTG
ACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAG
AGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGAACACAGACCC
GTCGACATGGGTGGAGCCTCATCTTGCTCTTCCTTGTGCGCTGTTGCTA
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT
CCTCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGC
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA
TGCCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTC
CTCTTCCCCCCTAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCT
GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGACTACAA
GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA
TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGATGAGCTGACCAGGAACCAGGTGAGCCTGACCTG
CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGA
GCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTG
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTGTG
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT
TCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCCTTCCTTGA
CCCTGGAAGGTGCCACTCCCAGTCTTCTCCTAATAAAATGAGGAAA
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGGTGGGG
TGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCA
TGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGACAGC
GCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCATA
ATGAGAAAAAAAGGAAAAATTAATTTTAACACCAATTCAGTAGTTGAT
TGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

FIG. 95C

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GCTGCGATTTTCGCGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTG
GTAGGATTTTATCCCCGCTGCCATCATGGTTCGACCATTGAACTGCAT
CGTCGCCGTGTCCCAAAATATGGGGATTGGCAAGAACGGAGACCTAC
CCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGACC
ACAACCTCTTCAGTGGAAGGTAAACAGAATCTGGTGATTATGGGTAG
GAAAACCTGGTTCTCCATTCTGAGACAATCGACCTTTAAAGGACA
GAATTAATATAGTTCTCAGTAGAGAACTCAAAGAACCACCACGAGGA
GCTCATTTTCTTGCCAAAAGTTTGGATGATGCCTTAAGACTTATTGAA
CAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAGG
CAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTTAGACT
CTTTGTGACAAGGATCATGCAGGAATTTGAAAGTGACACGTTTTTCCC
AGAAATTGATTTGGGGAAATATAAACTTCTCCCAGAATACCCAGGCG
TCCTCTCTGAGGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAA
GTCTACGAGAAGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGC
TCCCCTCCTAAAGTCATGCATTTTTATAAGACCATGGGACTTTTGCTG
GCTTTAGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGT
TTGCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCAC
TGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGG
AGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCT
ATGGAACCAGCTGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTT
ATTTGCATAATGAGAAAAAAAGGAAAATTAATTTTAACACCAATTCA
GTAGTTGATTGAGCAAATGCGTTGCCAAAAGGATGCTTTAGAGACA
GTGTTCTCTGCACAGATAAGGACAAACATTATTCAGAGGGAGTACCC
AGAGCTGAGACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGA
AATATGCTTGTCATCACGAAGCCTGATTCCGTAGAGCCACACCTTGG
TAAGGGCCAATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGG
CAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTC
TGACATAGTTGTGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAA
GATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC
GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGT
GTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGA
CCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTAT
CGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTGCTCGACGTTG
TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG
CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATC
ATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
CCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTA CTG
GATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATC
AGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATG
CCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCG

FIG. 95D

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AATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGC
CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG
TGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGT
GCTTTACGGTATCGCCGCTTCCCGATTTCGAGCGCATCGCCTTCTATC
GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGAC
CGACCAAGCGACGCCCAACCTGCCATCACGAGATTTTCGATTCCACCG
CCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCG
GCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCC
ACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATA
GCATCACAATAATTCACAAATAAAGCATTTTTTTTCACTGCATTCTAGTT
GTGGTTTGTCCAAACTCATCAATCTATCTTATCATGTCTGGATCGCGG
CCGCGATCCCGTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCC
TGTGTGAAATTGTTATCCGCTCACAATTCACACAACATACGAGCCGG
AGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCAC
ATTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTC
GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
TGCGTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTGCGCTC
GGTCGTTCCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA
TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA
GCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGC
TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATC
GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC
CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC
CTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG
GCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC
GTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGGTTTCAGCCCGAC
CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGA
CACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA
ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGA
AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA
CAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATT
ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC
GGGGTCTGACGCTCAGTGGAACGAAACTCACGTAAAGGGATTTTGG
TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAA
AATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTG
ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC
TATTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTAC
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGC
GAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCA
GCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTC
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTTCG

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FIG. 95E

CAGTTAATAGTTTGC GCAACGTTGTTGCCATTGCTACAGGCATCGTGG
TGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAAC
GATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTT
AGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTG
TTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGC
CATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT
TCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAA
TACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATC
ATTGGAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTG
TTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCA
GCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGG
CAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAA
TACTCATACTCTTCCTTTTCAATATTATTGAAGCATTTATCAGGGTTA
TTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACA
AATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT

FIG. 96A

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GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAATAAAA
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAACTGGGCG
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA
CACACATTCCACAGAATTAATTCCCCTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCC
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCT
TATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGATACC
GGTTTGACTCACGCGGATTTCCAAGTCTCCACCCCATGACGTCAATG
GGAGTTTGTGTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGG
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG
GAGACGCCATCACAGATCTCTCACTATGGATTTTCAGGTGCAGATTAT
CAGCTTCCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAAT
TGTTCTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAA
GGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAGTTACATCCACT
GGTTCCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTATGCCA
CATCCAACCTGGCTTCTGGAGTCCCTGTTCGCTTCAGTGGCAGTGGGT
CTGGGACTTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATG
CTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTCCG
GAGGGGGGACCAAGCTGGAAATCAAACGTACGGTGGCTGCACCATCT
GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTCC
TCTGTTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA
CAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG
TGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC
TGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTT
CAACAGGGGAGAGTGTTGAATTCAGATCCGTTAACGGTTACCAACTA
CCTAGACTGGATTTCGTGACAACATGCGGGCCGTGATATCTACGTATGAT
CAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTC
CCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTCC

FIG. 96B

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TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCT
ATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGG
AAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCA
GCTGGGGCTCGACAGCTATGCCAAGTACGCCCCCTATTGACGTCAATG
ACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGG
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCAT
GGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTTG
ACTCACGGGGATTTCOAAGTCTCCACCCCATTGACGTCAATGGGAGTT
TGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAAC
CCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTC
TATATAAGCAGAGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGA
ACACAGACCCGTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGT
CGCTGTTGCTACGCGTGTCTGTCCCAGGTACAACCTGCAGCAGCCTGG
GGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGG
CTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAACAGA
CACCTGGTCGGGGCCTGGAATGGATTGGAGCTATTTATCCCGGAAAT
GGTGATACTTCCTACAATCAGAAGTTCAAAGGCAAGGCCACATTGAC
TGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGA
CATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACG
GCGGTGACTGGTACTTCAATGTCTGGGGCGCAGGGACCACGGTCACC
GTCTCTGCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC
TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG
CCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG
GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACAC
ATGCCACACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT
CCTCTTCCCCC AAAACCAAGGACACCCTCATGATCTCCCGGACCCC
TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG
ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
CGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA
AGTGCAAGGTCTCCAACAAGCCCTCCCAGCCCCCATCGAGAAAACC
ATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT
GCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACGCTGACCT
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
AGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCT
GGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG
AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
GTAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTGT

FIG. 96C

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GACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCC
TTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTCCCCCGTGCCTTCCTTG
ACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAA
ATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGG
GTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGC
ATGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGACAG
CGCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCAT
AATGAGAAAAAAGGAAAATTAATTTTAAACACCAATTCAGTAGTTGA
TTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGGGCTGCGATTTTCG
CGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTATC
CCCGCTGCCATCATGGTTTCGACCATTGAACTGCATCGTCGCCGTGTCC
CAAAATATGGGGATTGGCAAGAACGGAGACCTACCCTGGCCTCCGCT
CAGGAACGAGTTCAAGTACTTCCAAAGAATGACCACAACCTCTTCAG
TGGAAGGTAAACAGAATCTGGTGATTATGGGTAGGAAAACCTGGTTC
TCCATTCTGAGAAGAATCGACCTTTAAAGGACAGAATTAATATAGTT
CTCAGTAGAGAACTCAAAGAACCACCACGAGGAGCTCATTTTCTTGC
CAAAAGTTTGGATGATGCCTTAAGACTTATTGAACAACCGGAATTGG
CAAGTAAAGTAGACATGGTTTGGATAGTCGGAGGCAGTTCTGTTTACC
AGGAAGCCATGAATCAACCAGGCCACCTTAGACTCTTTGTGACAAGG
ATCATGCAGGAATTTGAAAGTGACACGTTTTTCCAGAAATTGATTTG
GGGAAATATAAACTTCTCCCAGAATACCCAGGCGTCCTCTCTGA
GGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAAGTCTACGAGA
AGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGCTCCCCTCCTAA
AGCTATGCATTTTATAAGACCATGGGACTTTTGCTGGCTTTAGATCA
GCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTCCC
CCGTGCCTTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTA
ATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTAT
TCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCAGC
TGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTTATTTGCATAATG
AGAAAAAAGGAAAATTAATTTTAAACACCAATTCAGTAGTTGATTGA
GCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCTGCA
CAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAGACT
CCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTTGTC
ATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCCAAT
CTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCATATA
AGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAGTTG

FIG. 96D

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TGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAAGATGGATTGCA
CGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTG
GGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTC
AGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGC
CCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCA
CGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGG
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTG
TCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCA
ATGCGGCGGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCAC
CAAGCGAAACATCGCATCGAGCGAGCACGTA CT CGGATGGAAGCCGG
TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGC
CAGCCGA ACT GTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAG
GATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTG
GAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTG
GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA
AGAGCTTGCGGCGGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTAT
CGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGA
GTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGAC
GCCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCCTTCTATGA
AAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCT
CCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCCAACTTGTT
TATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTT
CACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAA
ACTCATCAATCTATCTTATCATGTCTGGATCGCGGCCGCGATCCCGTC
GAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
TATCCGCTCACAAATCCACACAACATACGAGCCGGAAGCATAAAGTG
TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT
GCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCA
TTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGC GTATTGGGC
GCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCCGGCT
GCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA
CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCA
GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC
ATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGT
CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCC
CCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC
CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
ATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAA
GCTGGGCTGTGTGCACGAACCCCCCGTT CAGCCCGACCGCTGCGCCTT
ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC

FIG. 96E

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GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG
TAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC
ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC
TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGC
TGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAA
AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC
TCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATC
AAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTAA
ATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG
CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCC
ATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG
CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC
ACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCG
AGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTA
ATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCGT
TTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTA
CATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTC
CGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTA
TGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCT
TTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA
TGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACC
GCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCT
TCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCG
ATGTAACCCACTCGTGCACCCAACCTGATCTTCAGCATCTTTTACTTTCA
CCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAA
AAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCT
TTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGG
ATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGC
GCACATTTCCCCGAAAAGTGCCACCT

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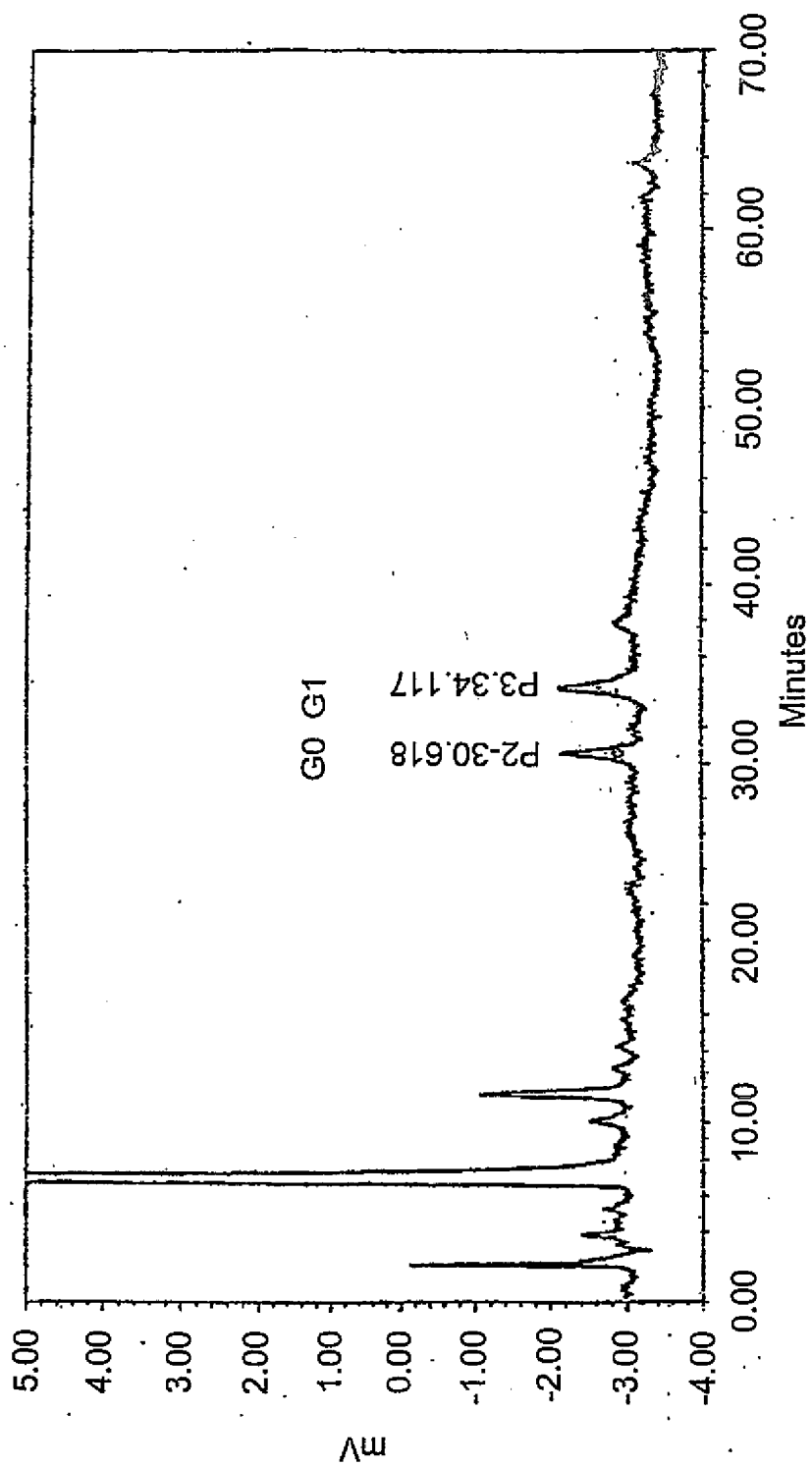


FIG. 97A

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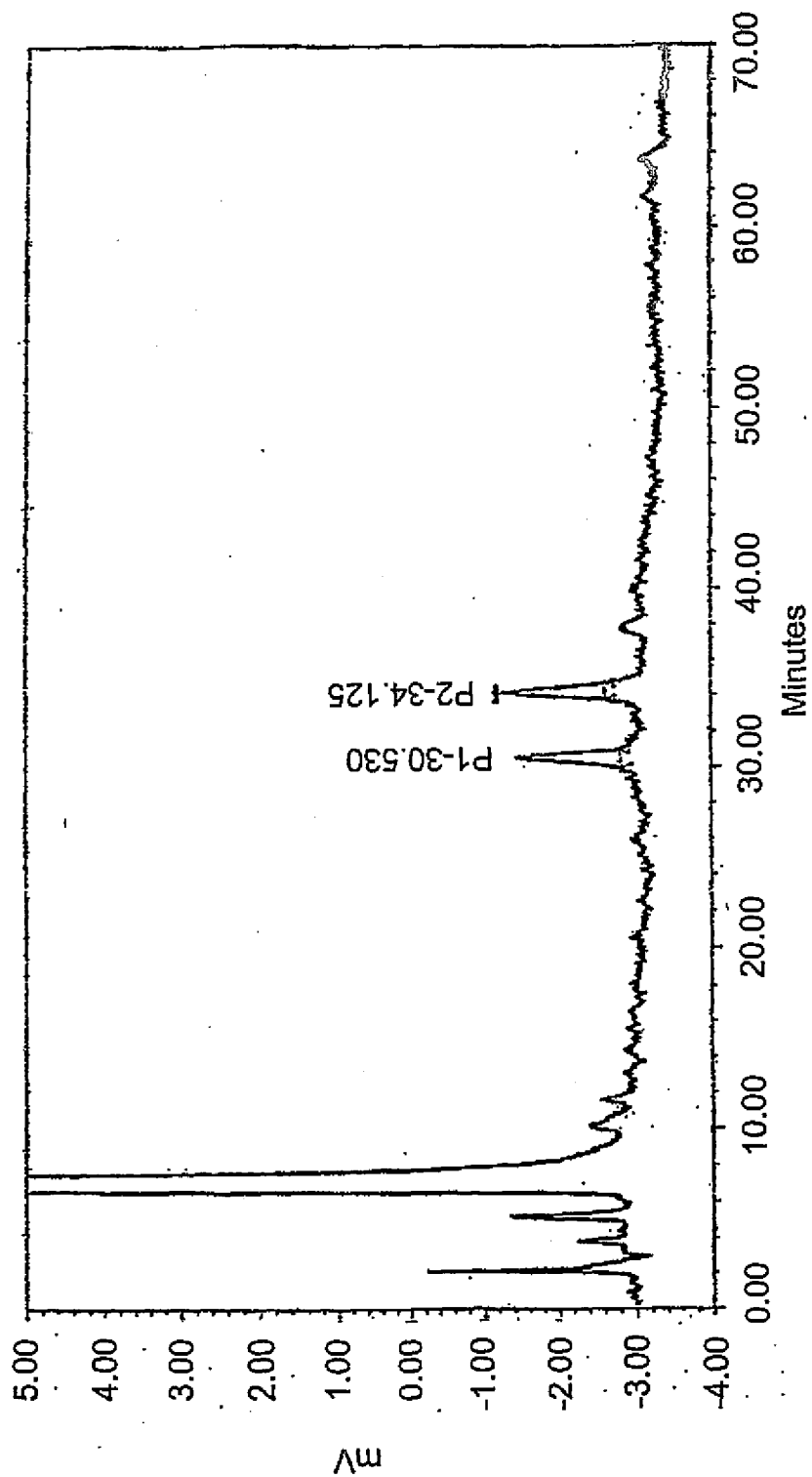


FIG. 97B

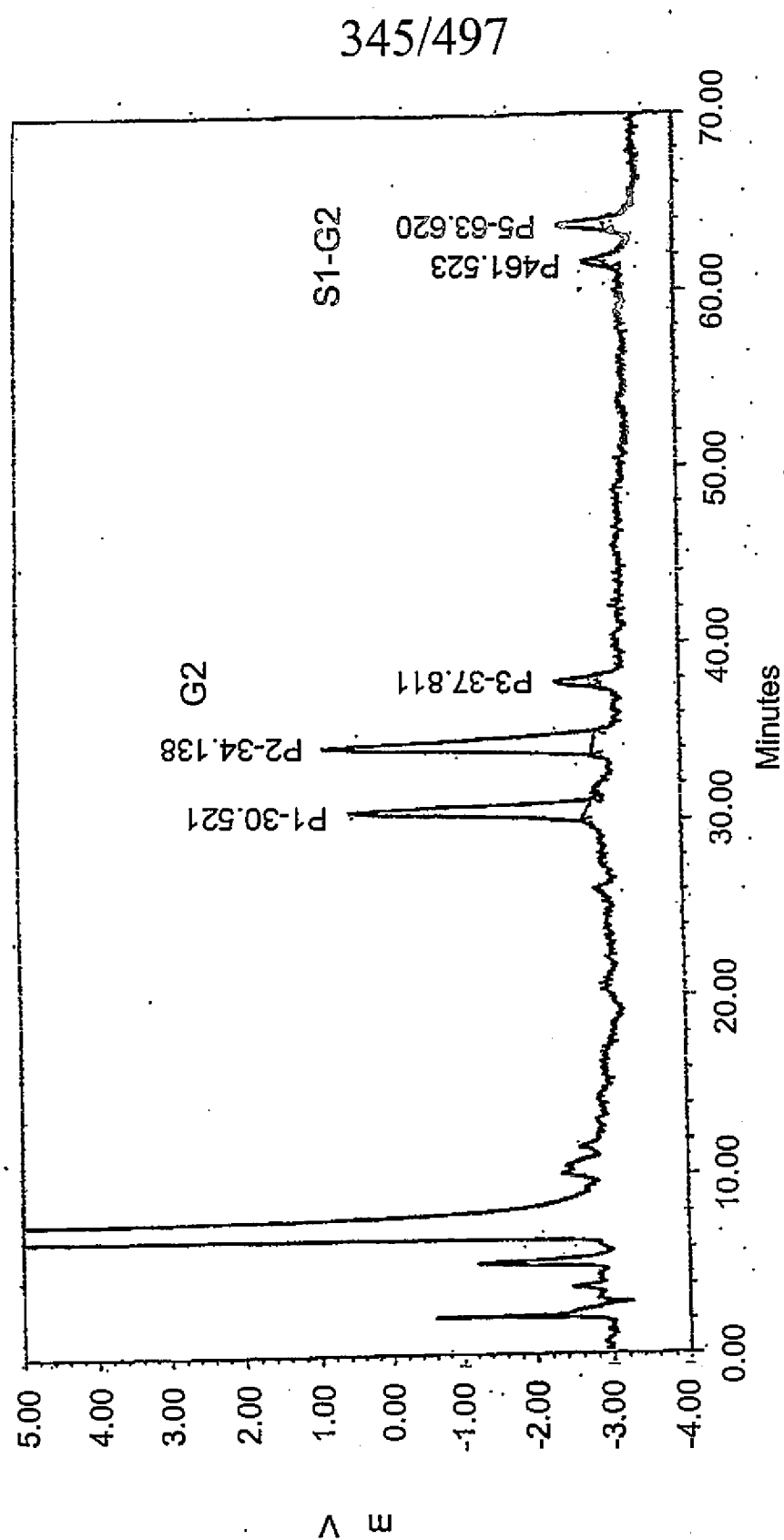


FIG. 97C

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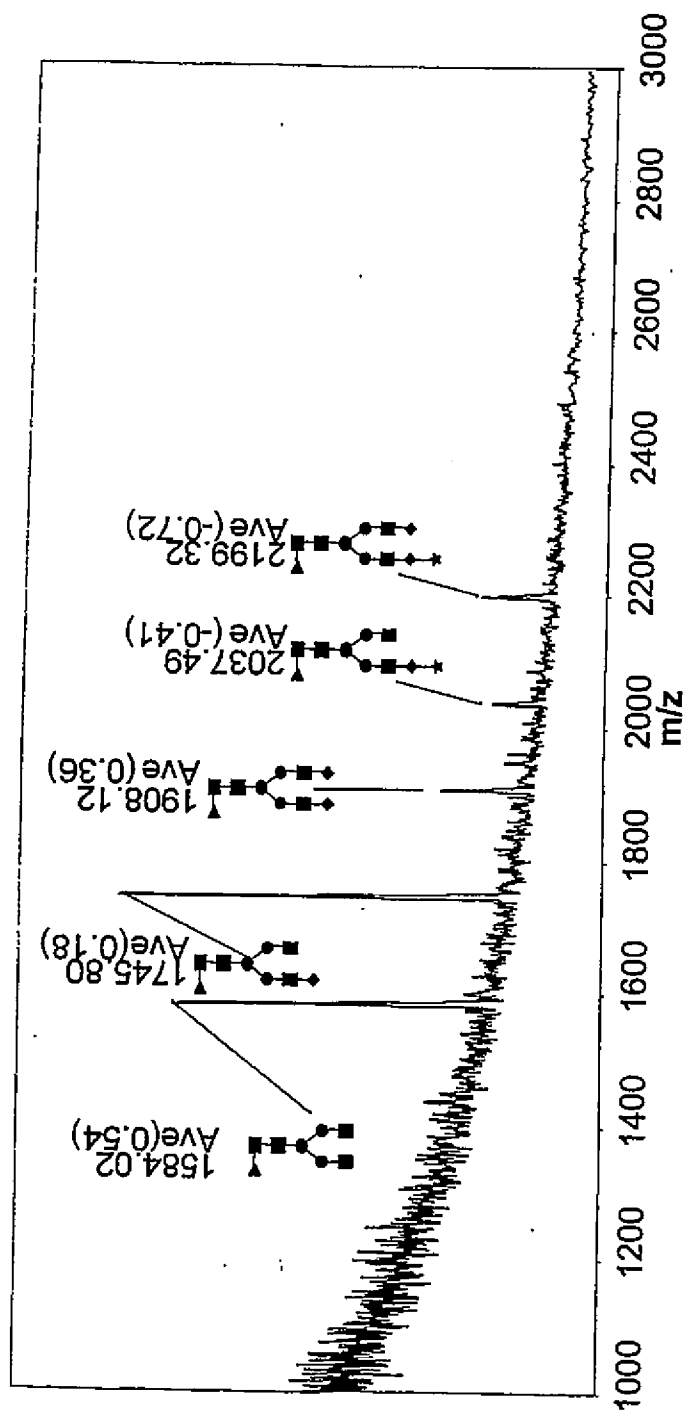


FIG. 98A

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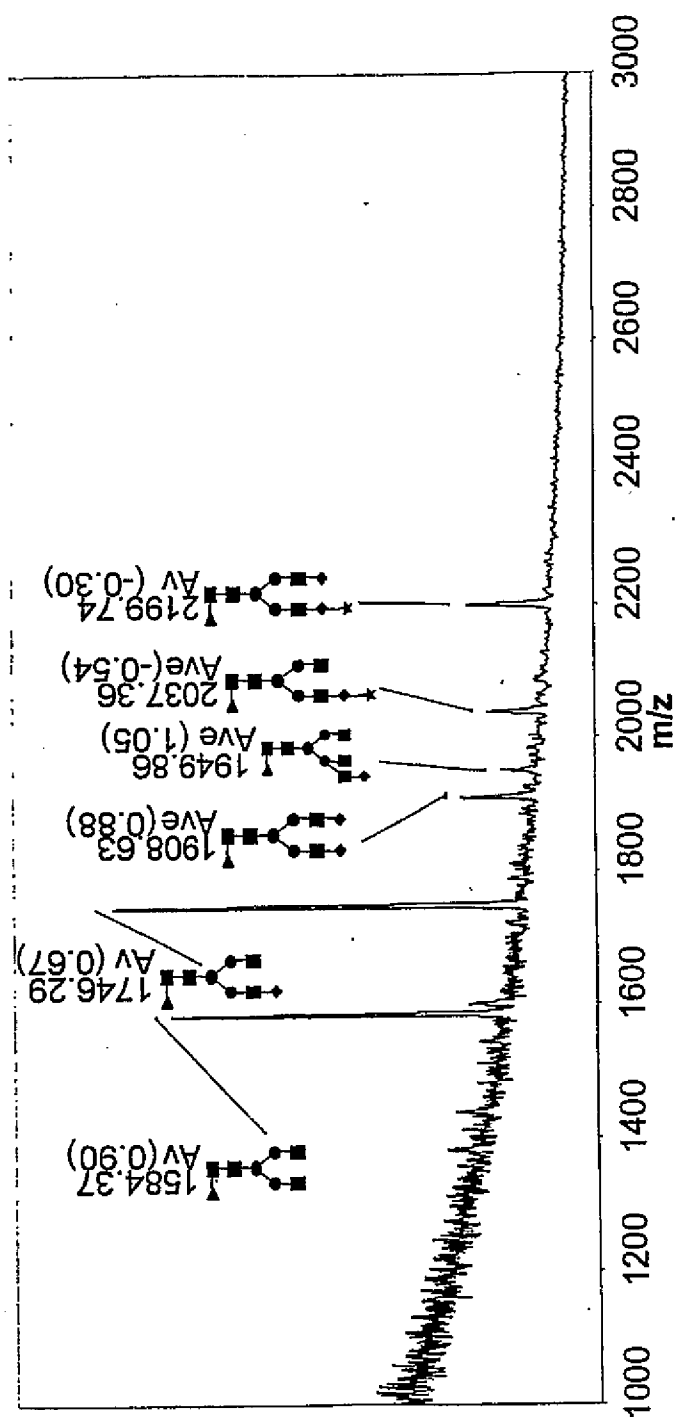


FIG. 98B

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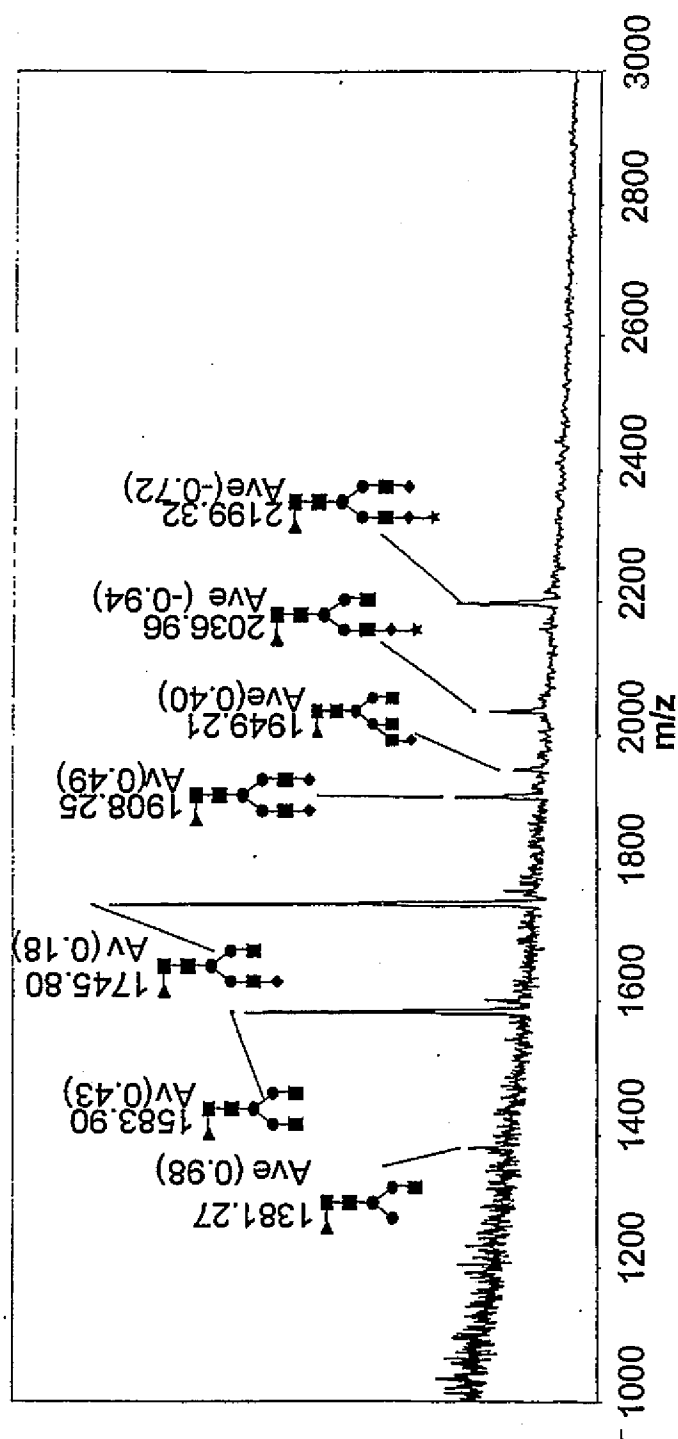


FIG. 98C

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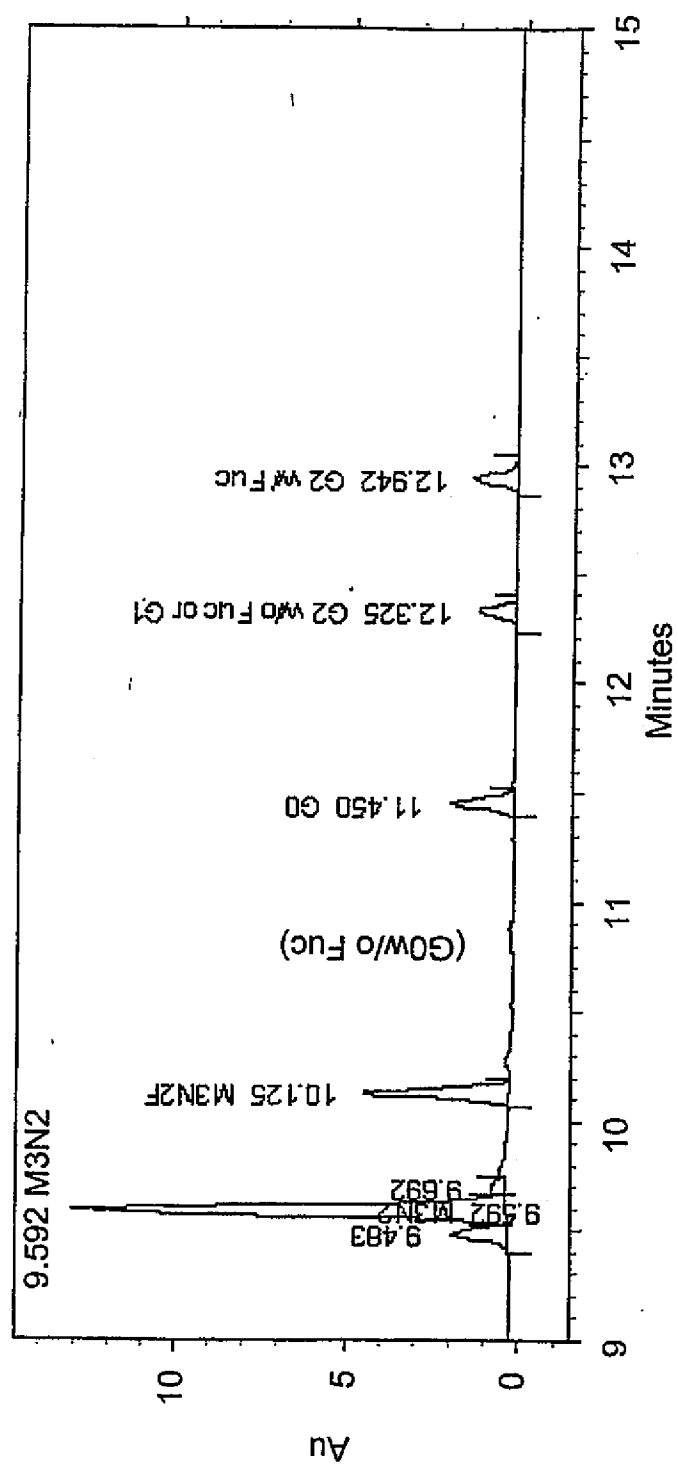


FIG. 99A

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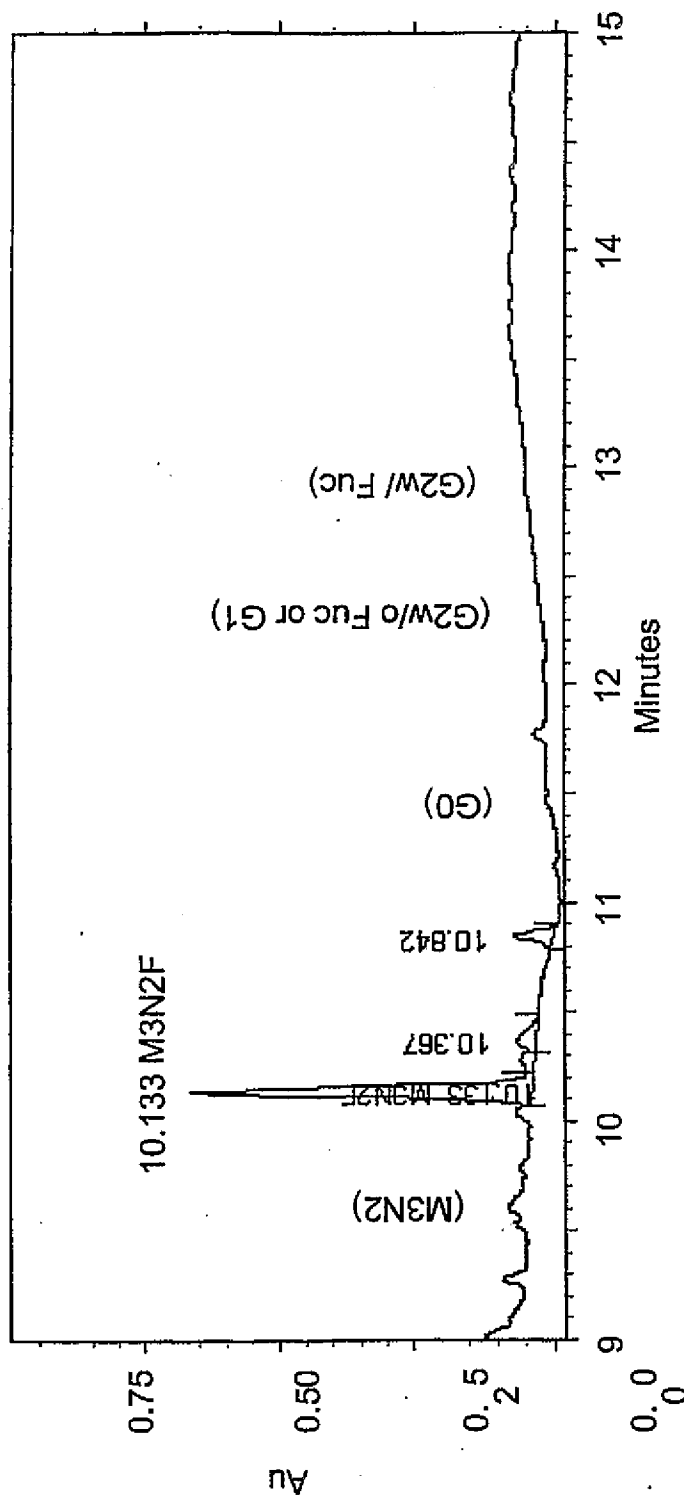


FIG. 99B

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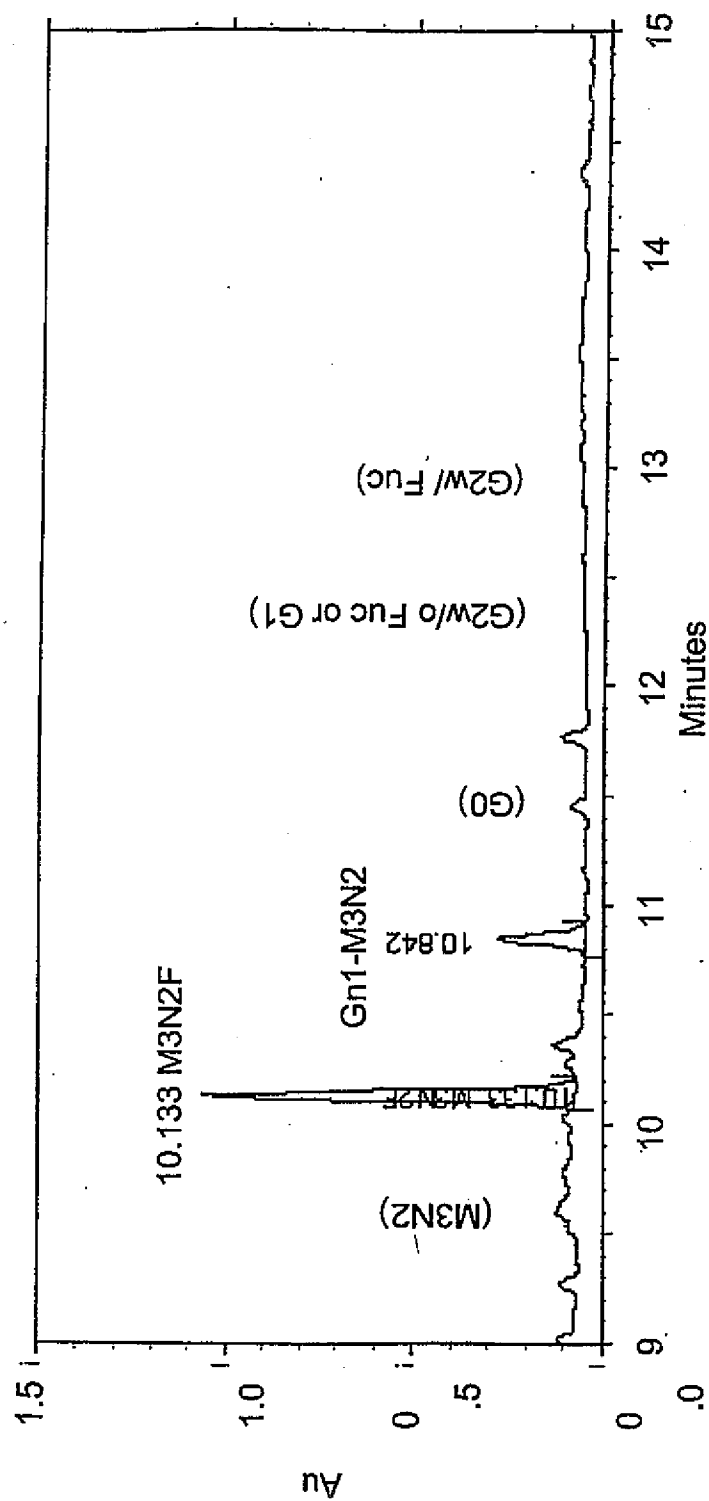


FIG. 99C

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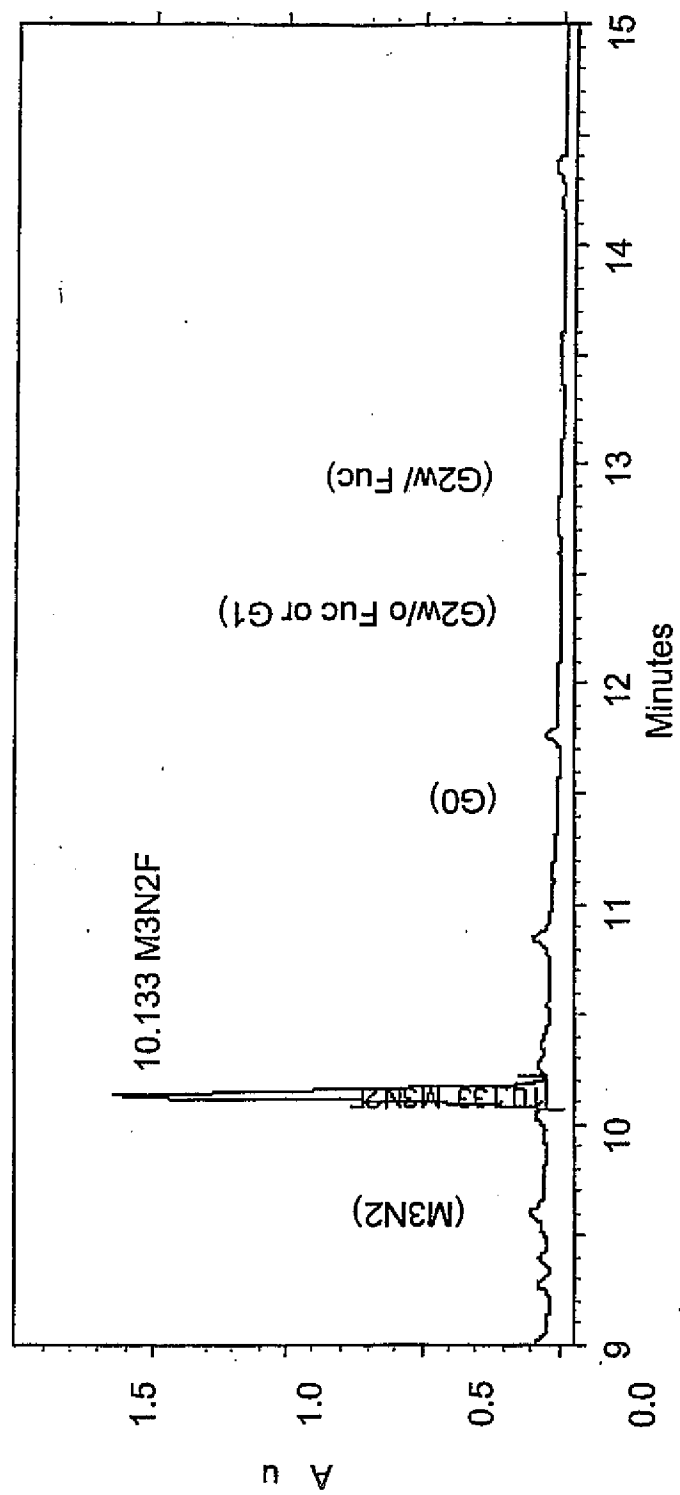


FIG. 99D

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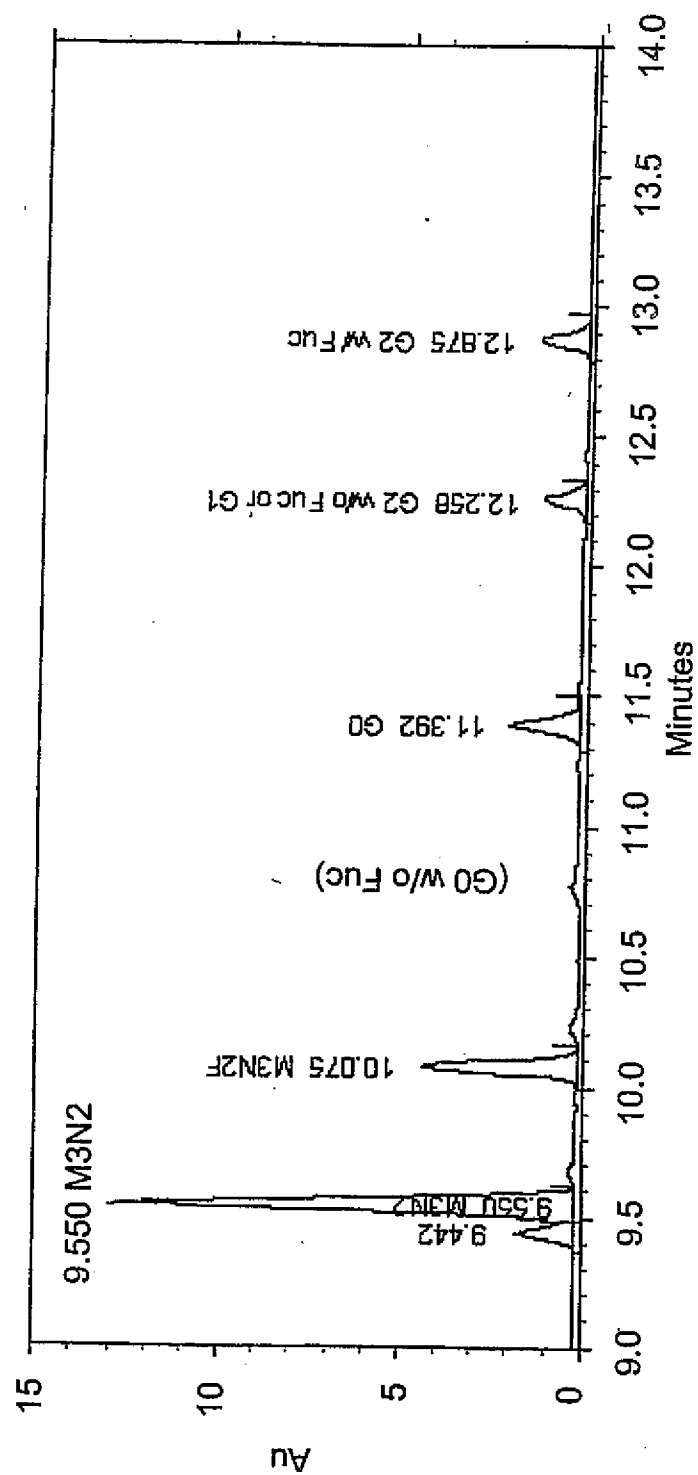


FIG. 100A

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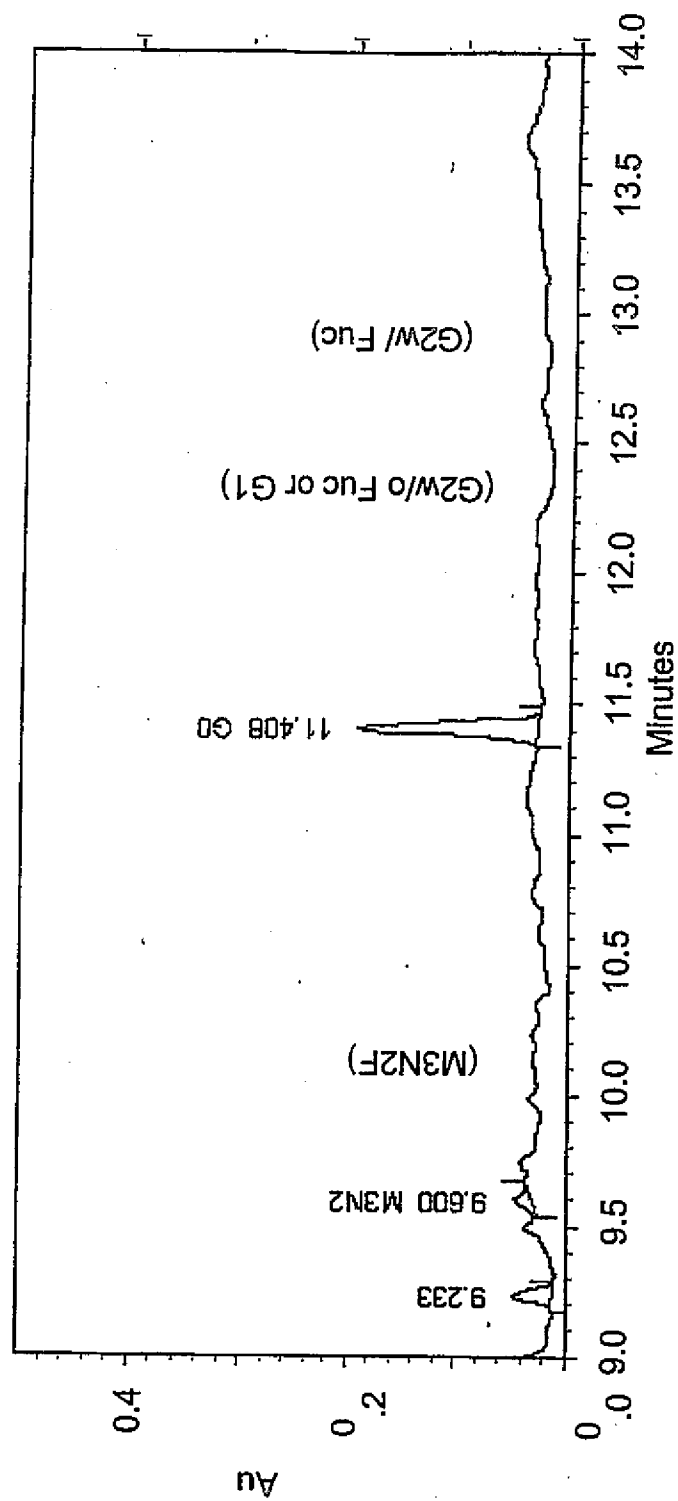


FIG. 100B

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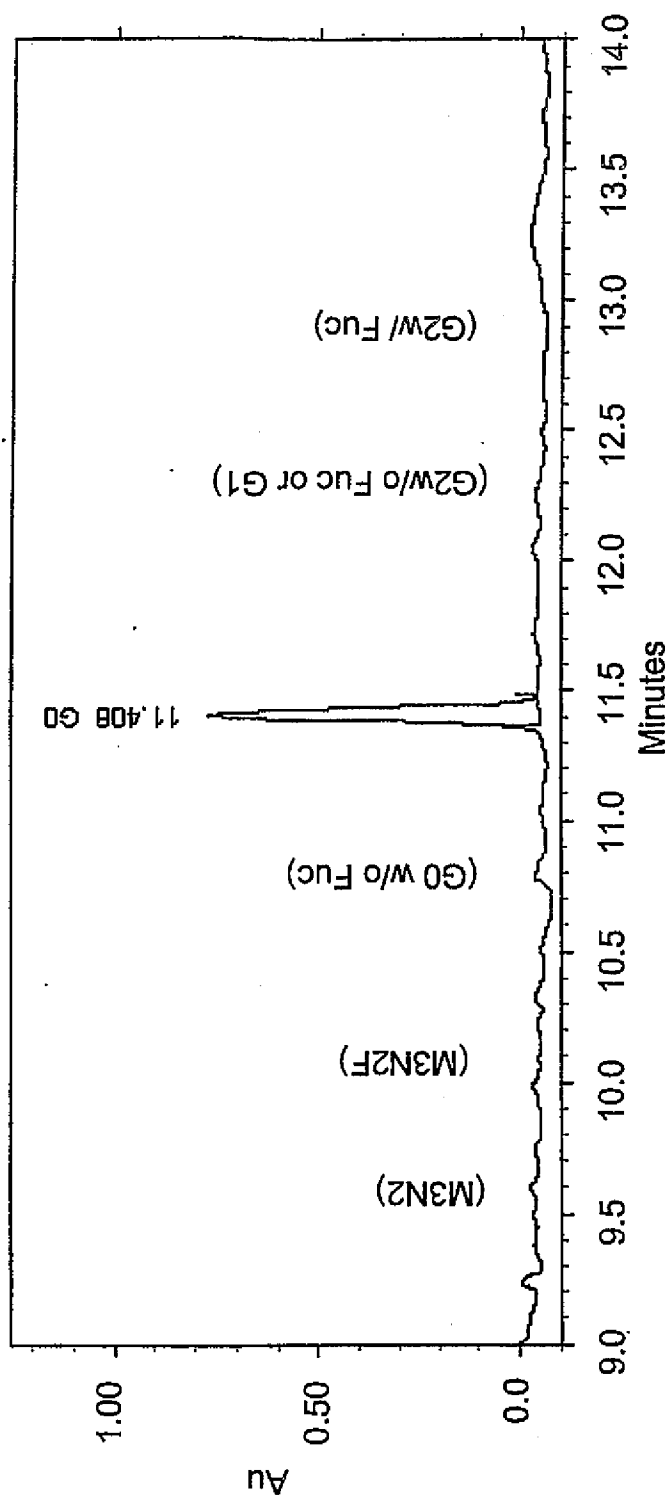


FIG. 100D

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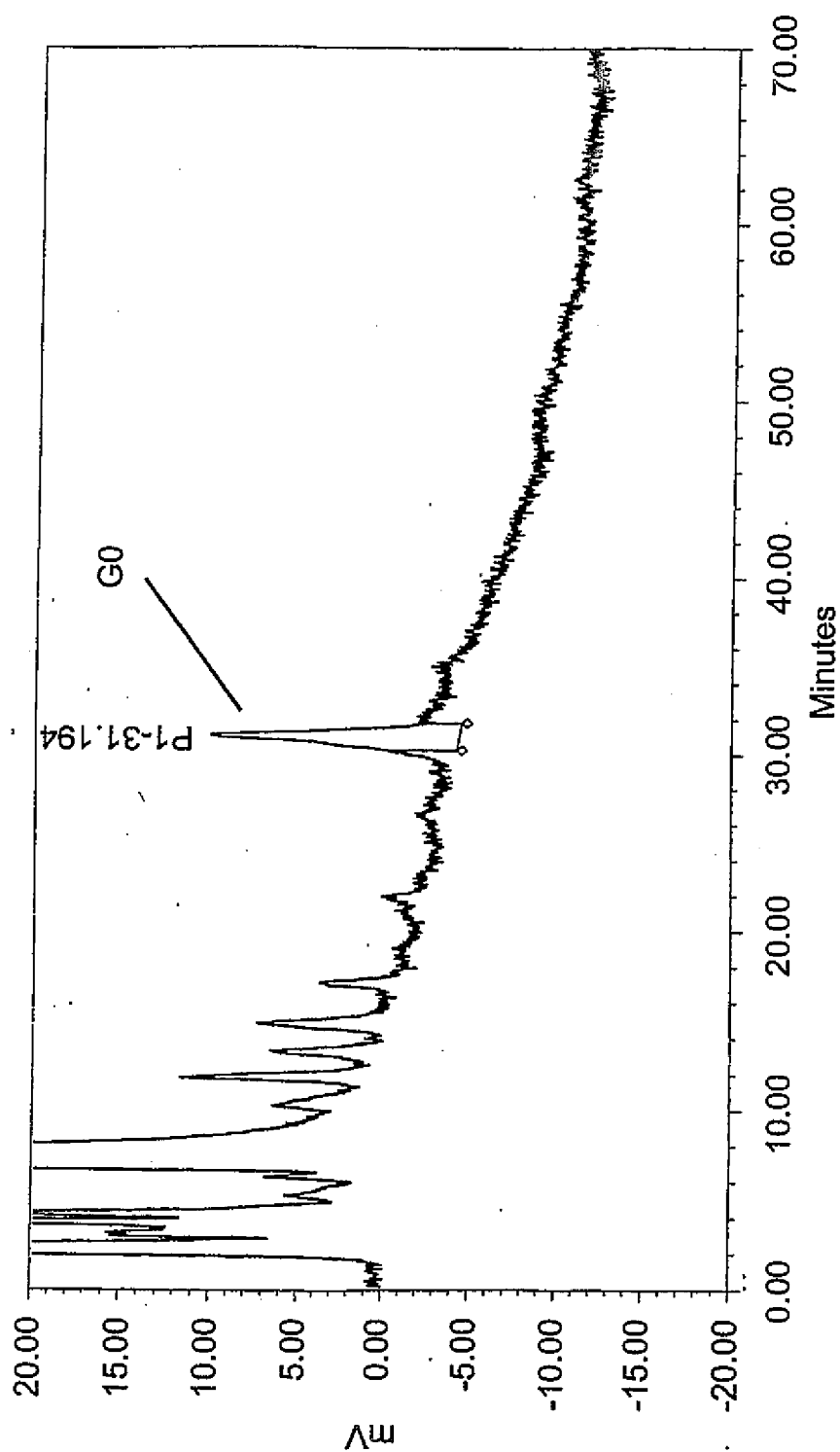


FIG. 101A

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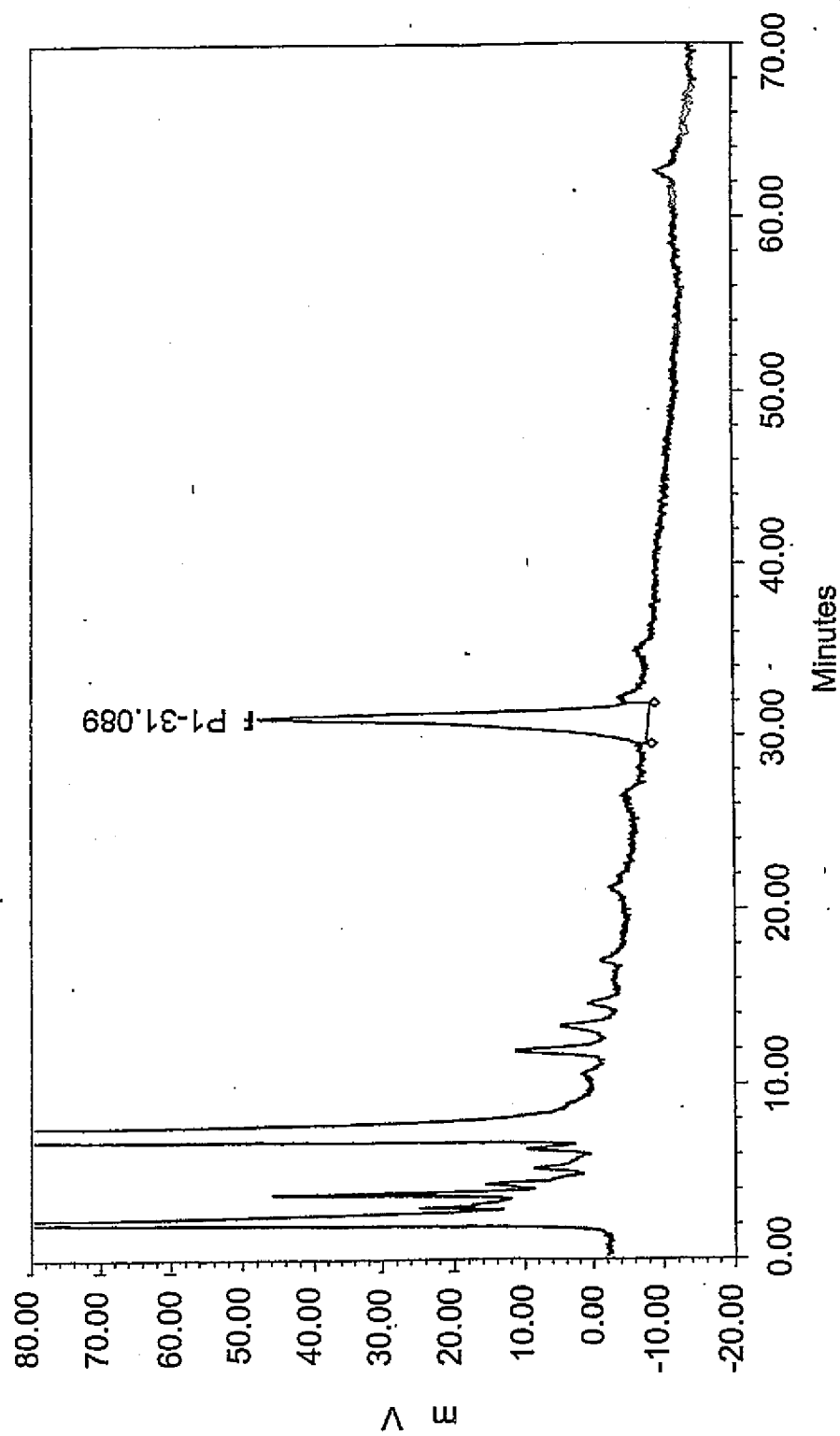


FIG. 101B

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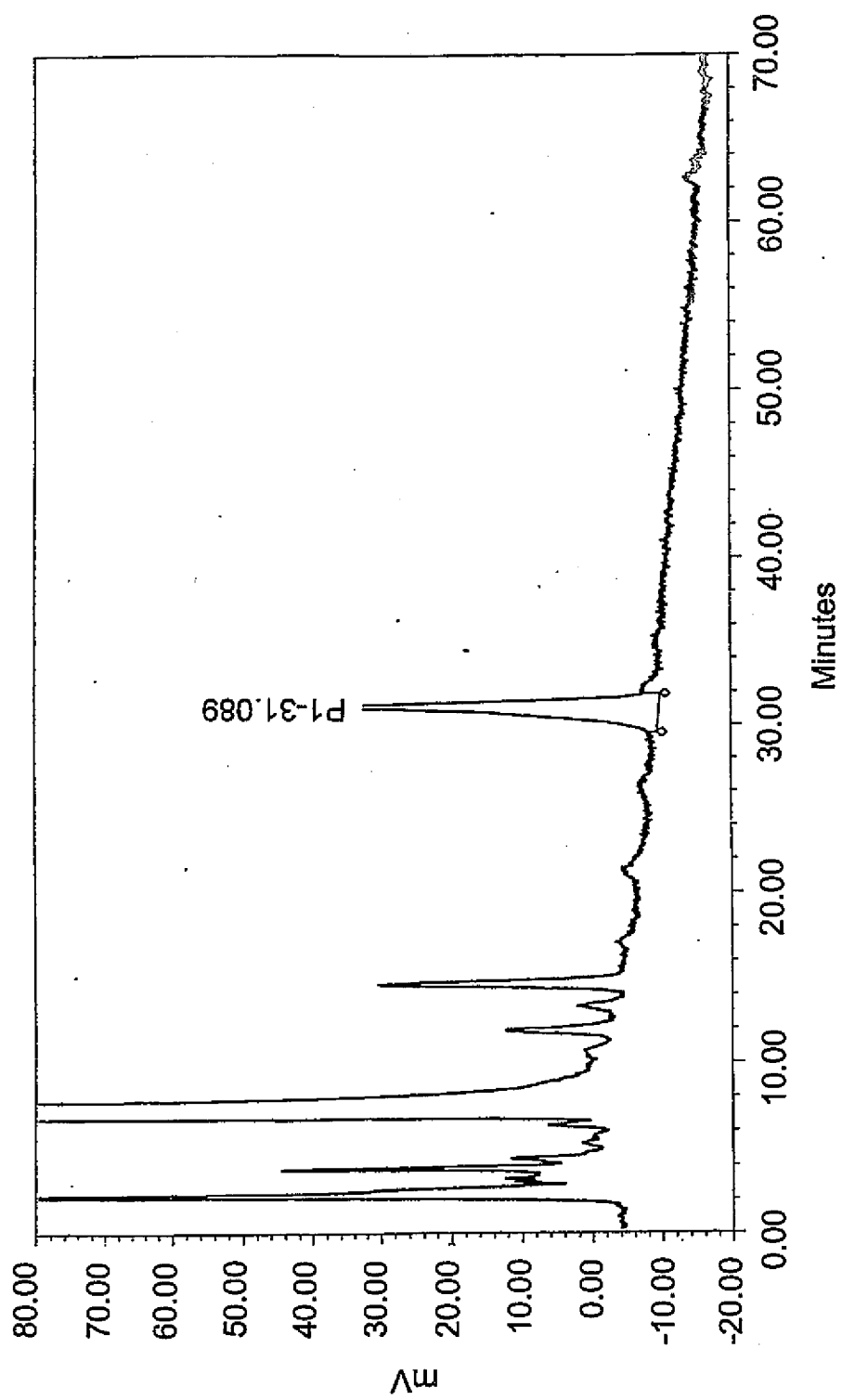


FIG. 101C

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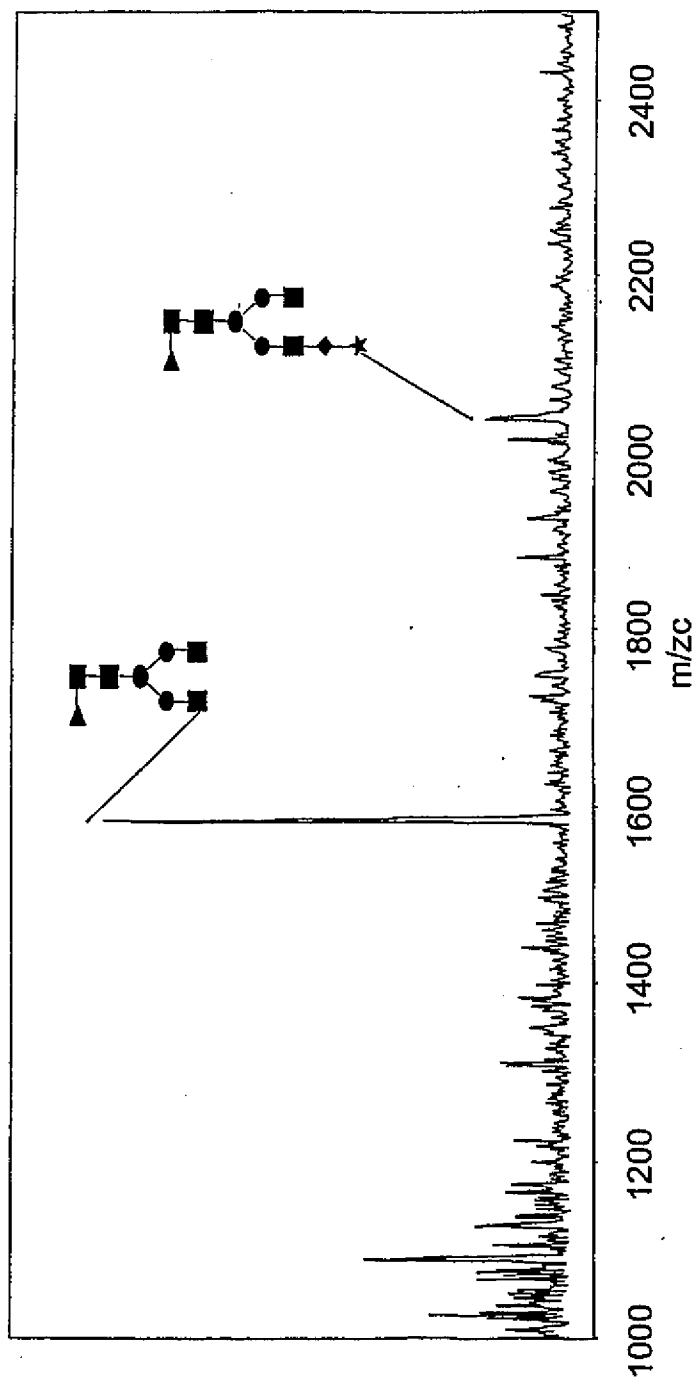
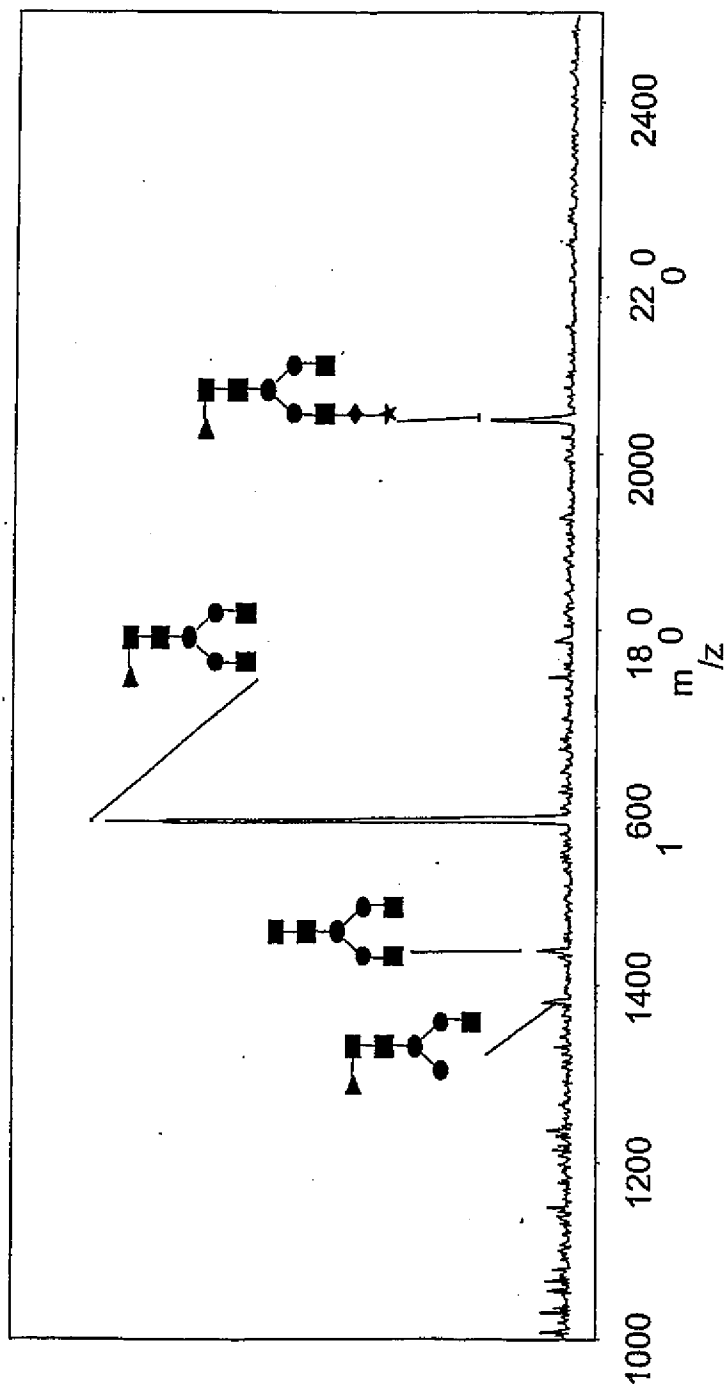


FIG. 102A

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FIG. 102^B

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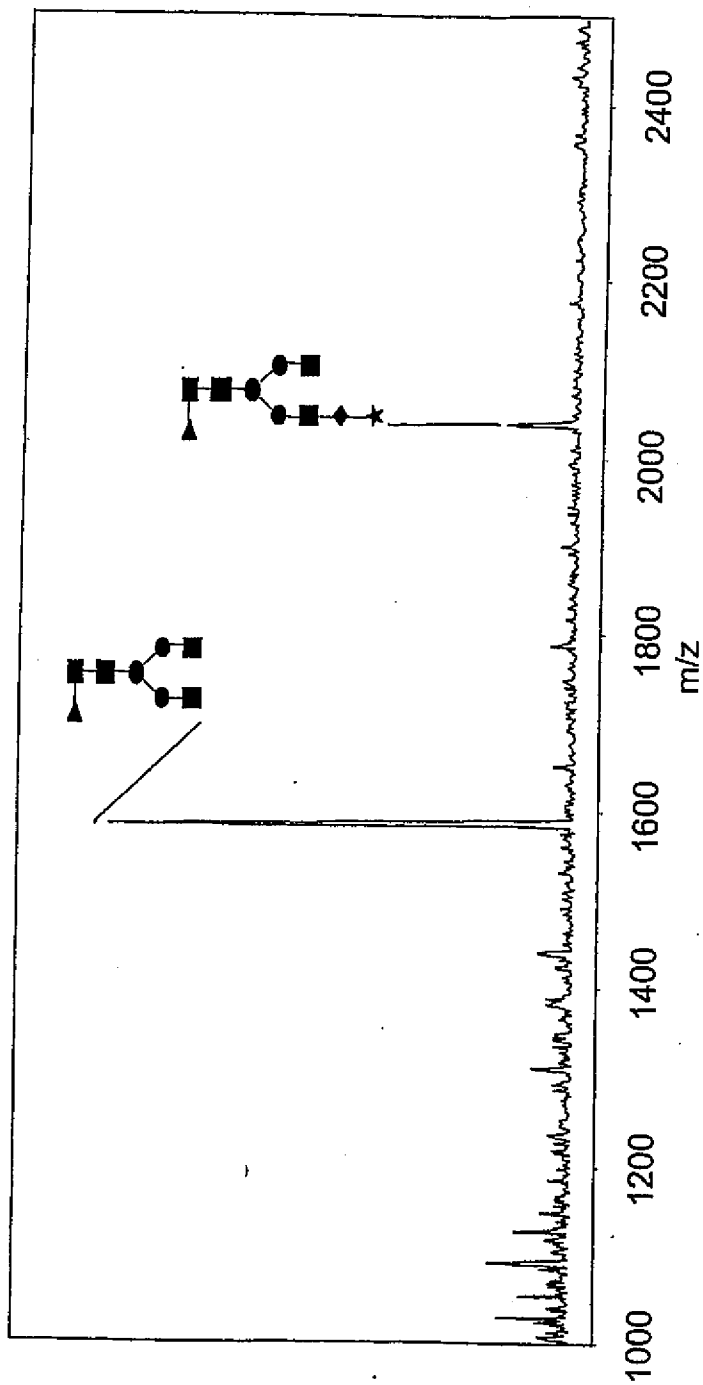


FIG. 102C

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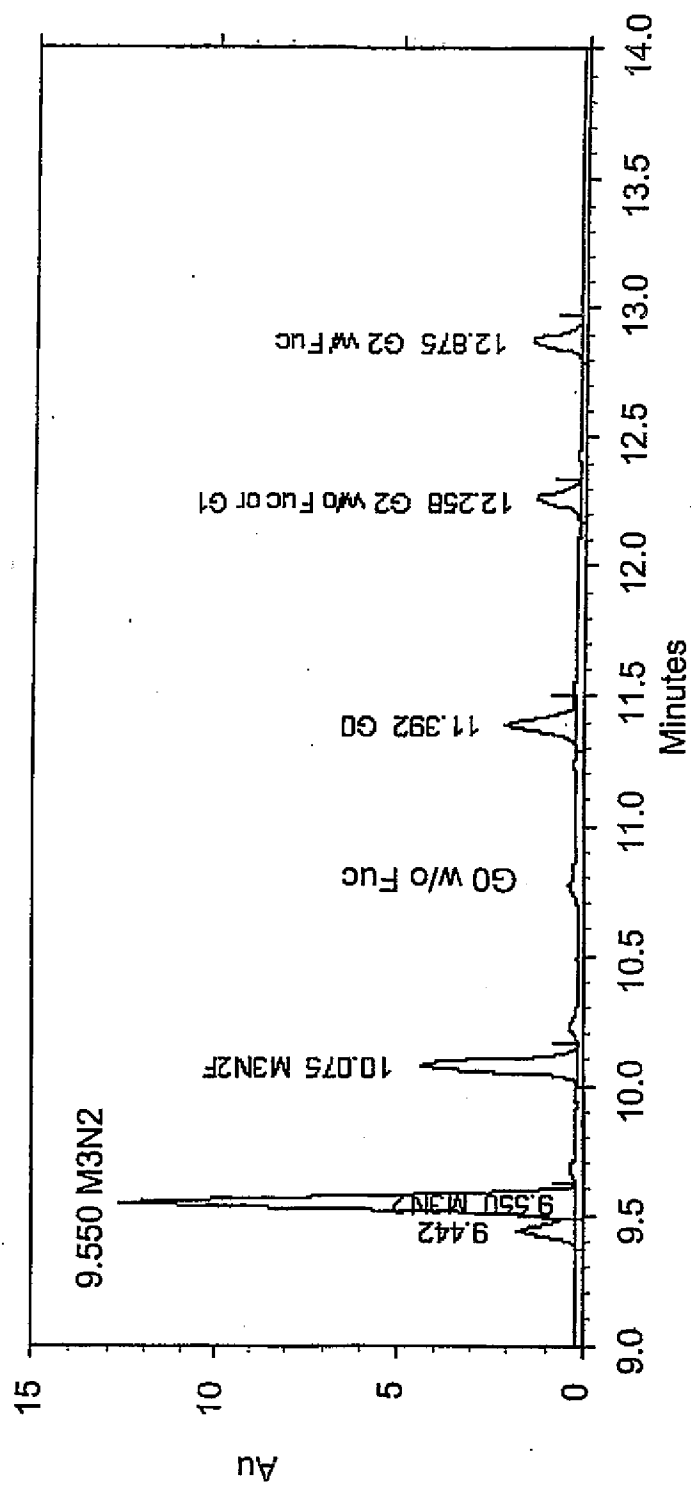


FIG. 103A

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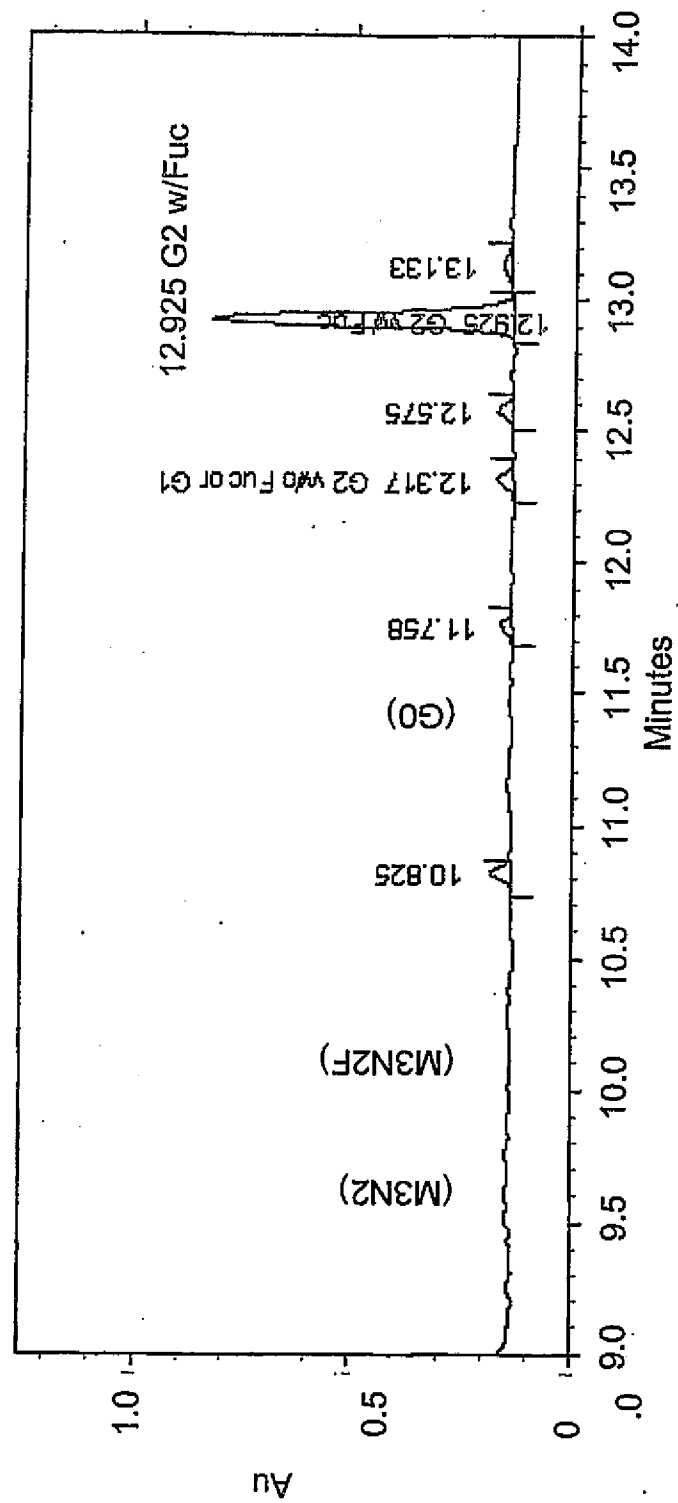


FIG. 103B

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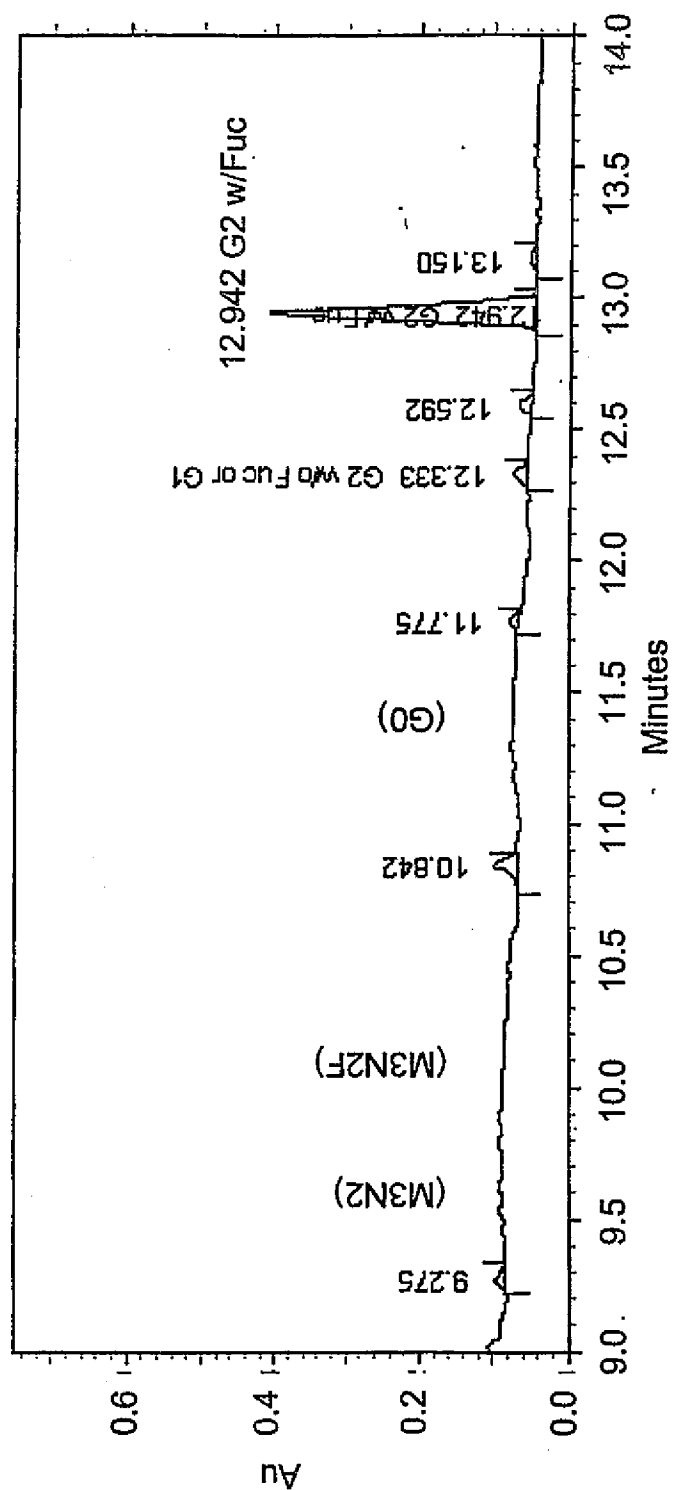


FIG. 103C

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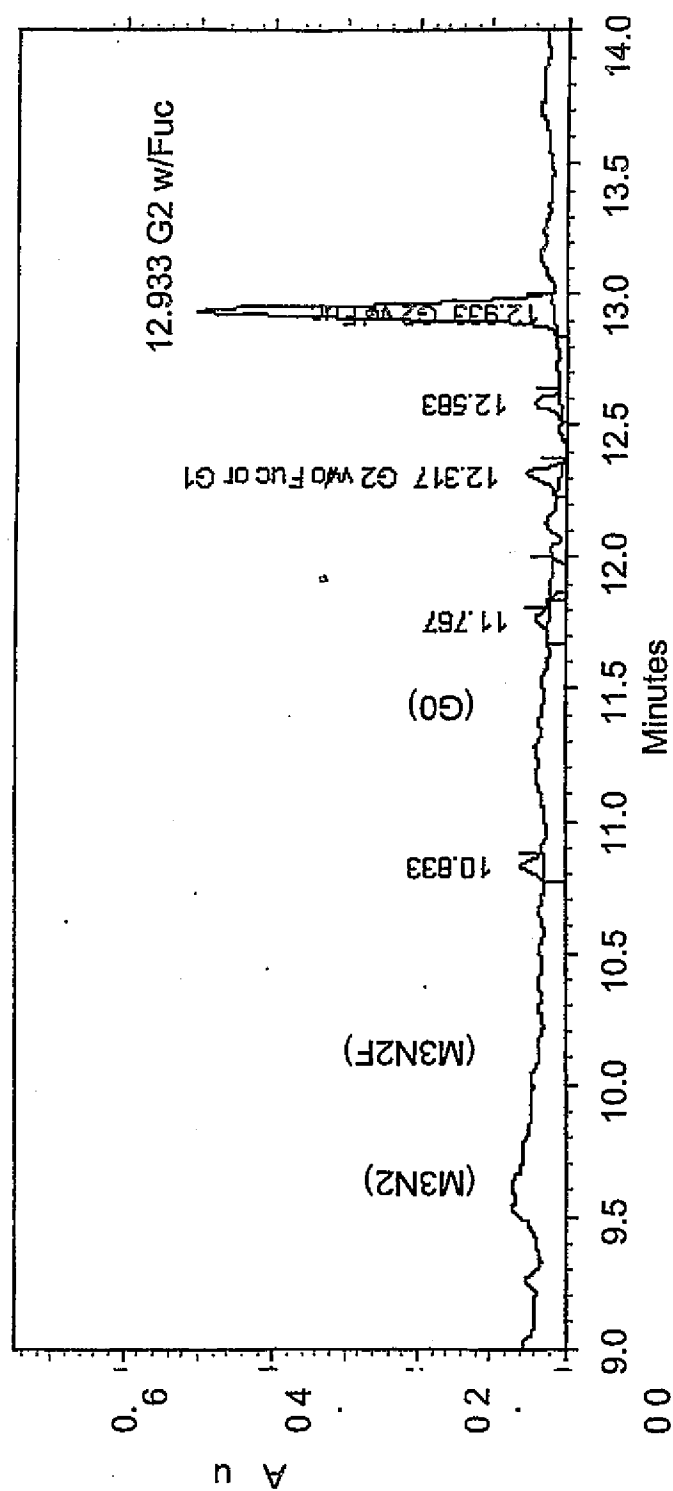


FIG. 103D

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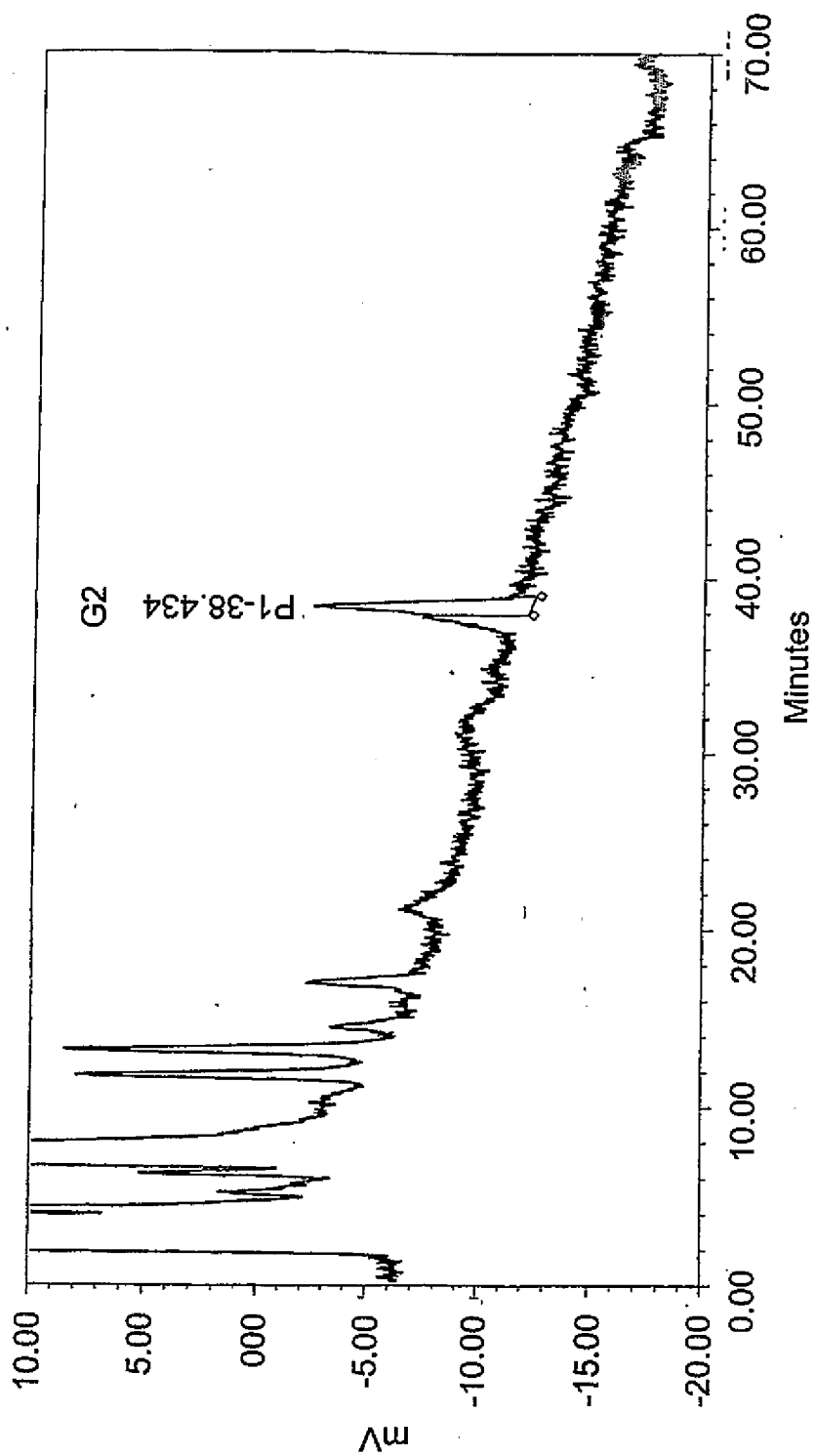


FIG. 104A

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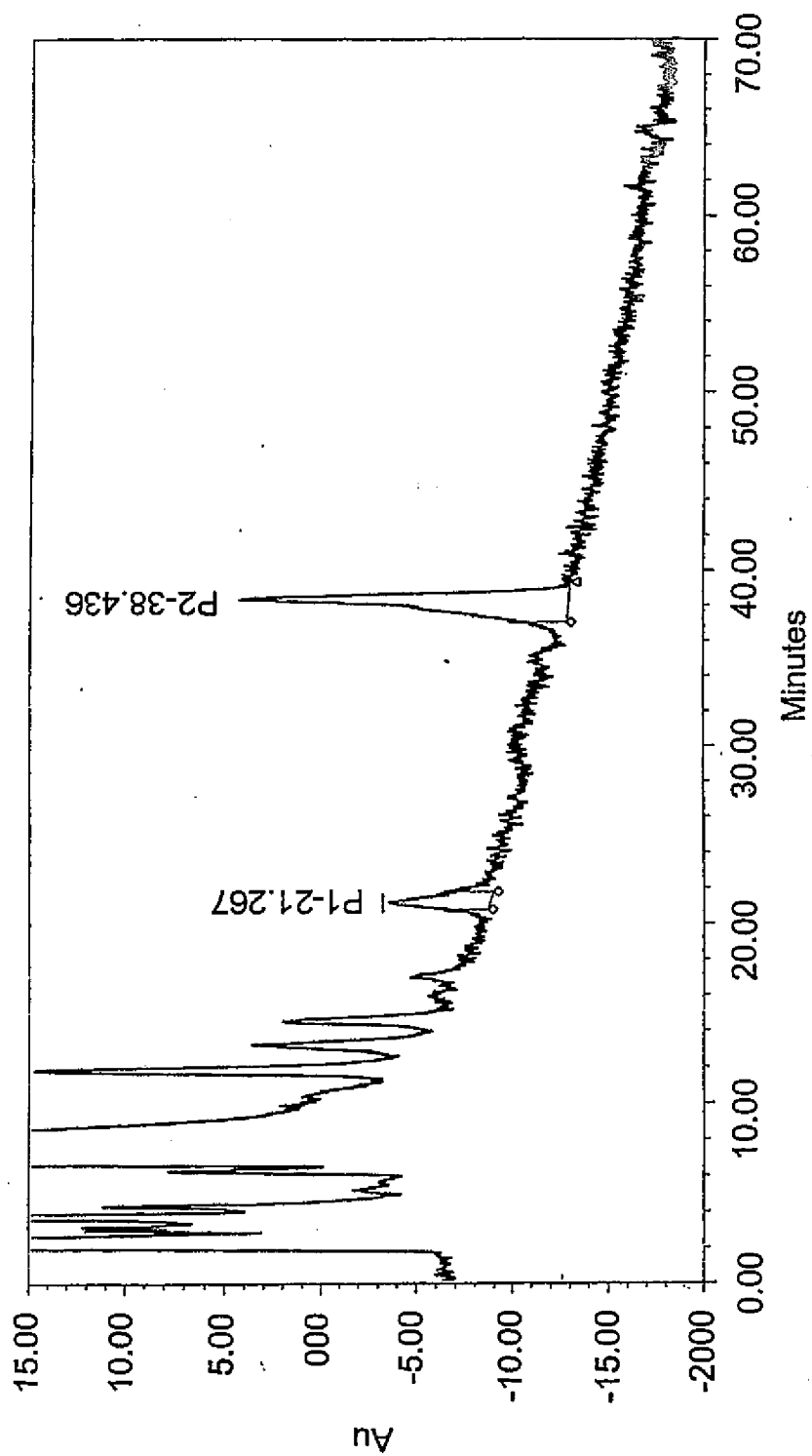


FIG. 104B

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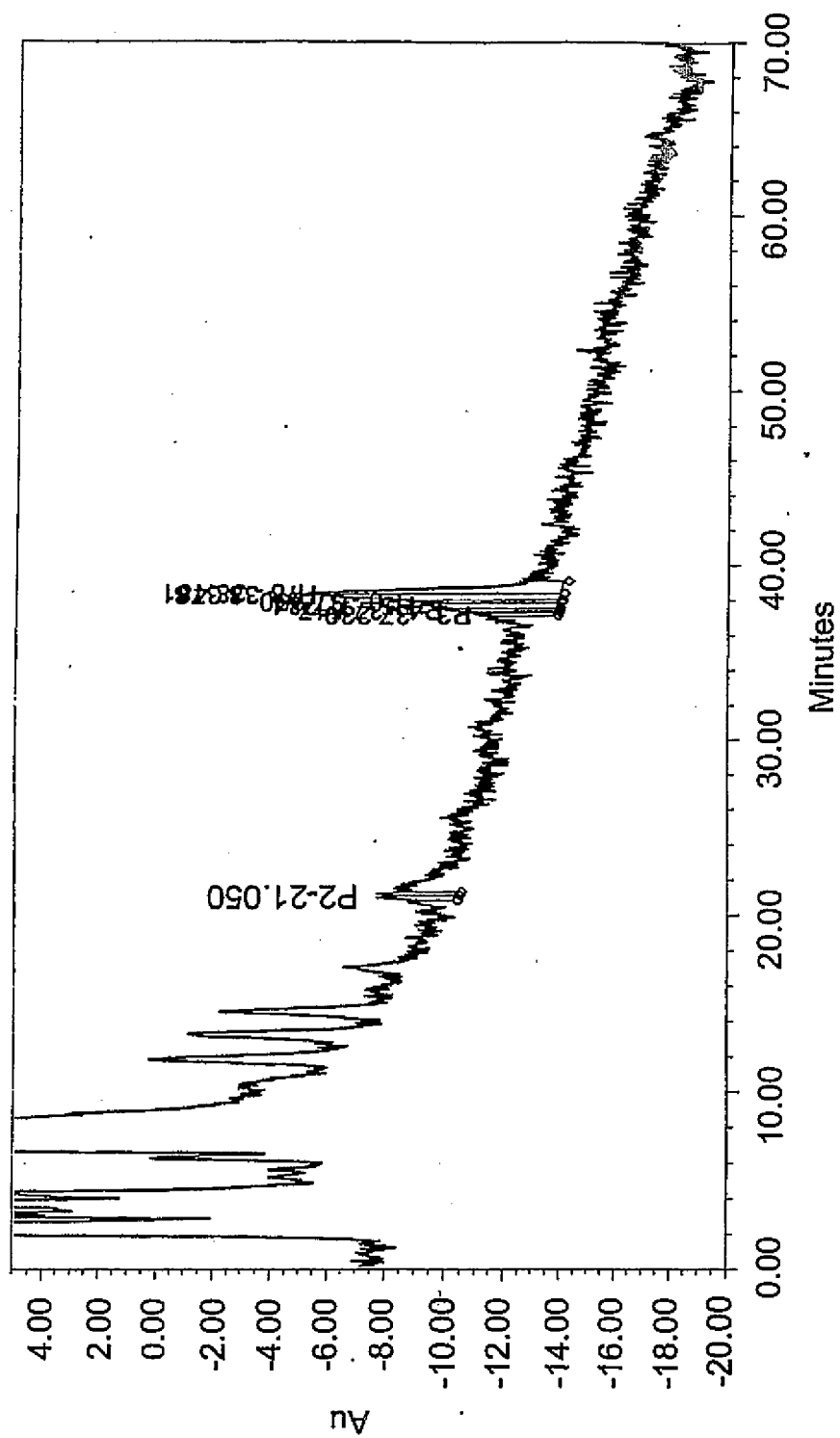


FIG. 104C

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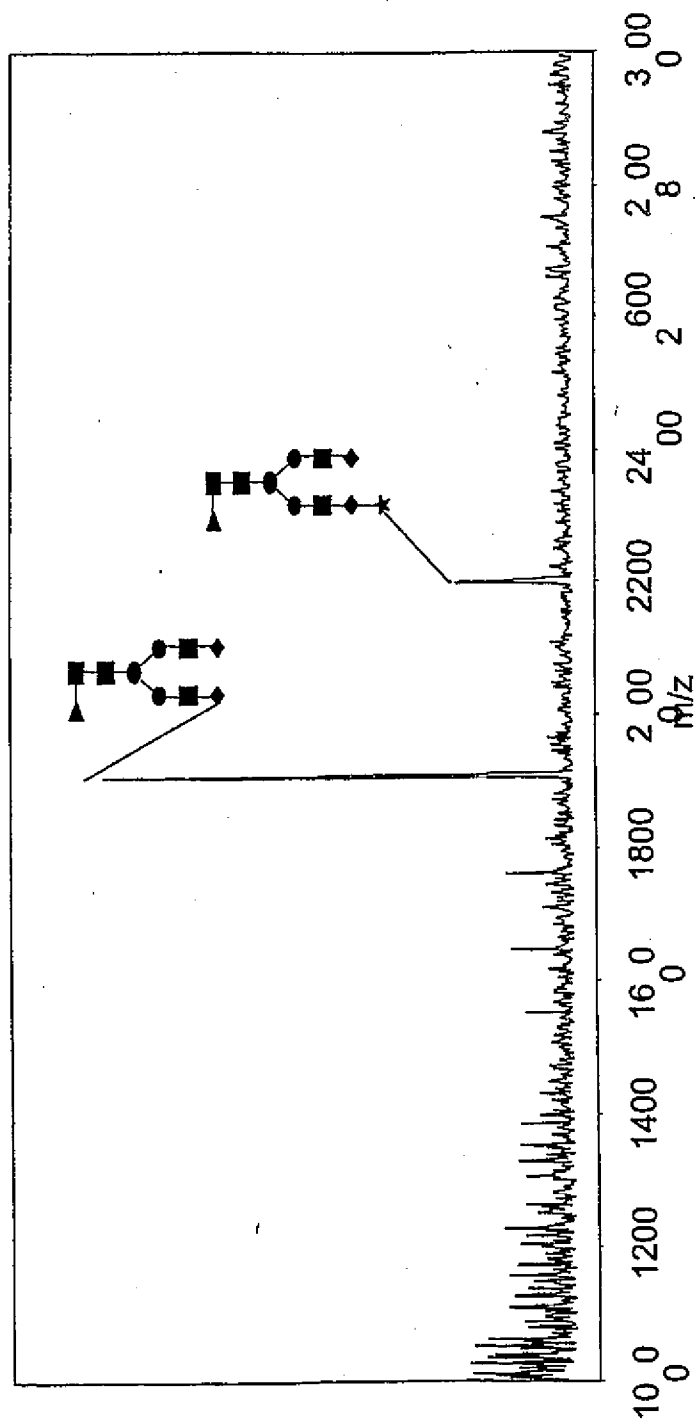


FIG. 105A

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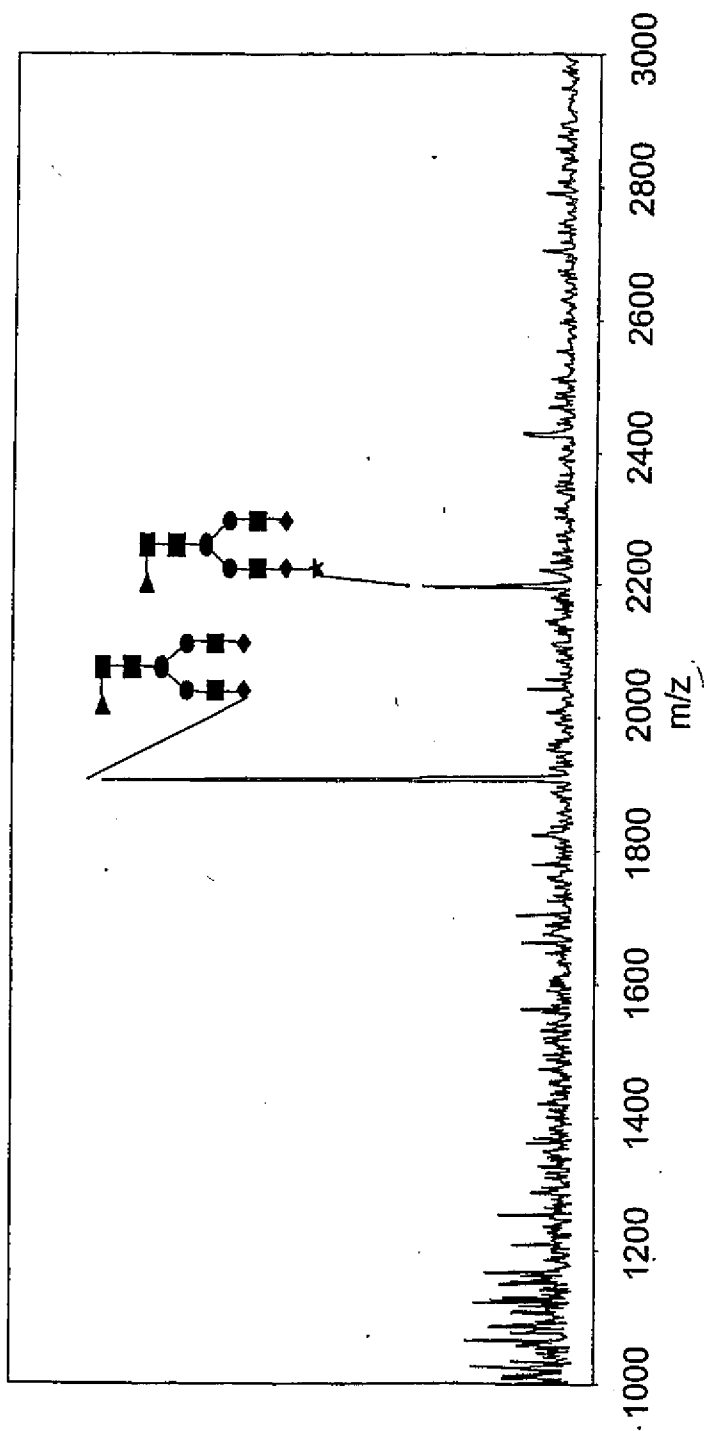


FIG. 105B

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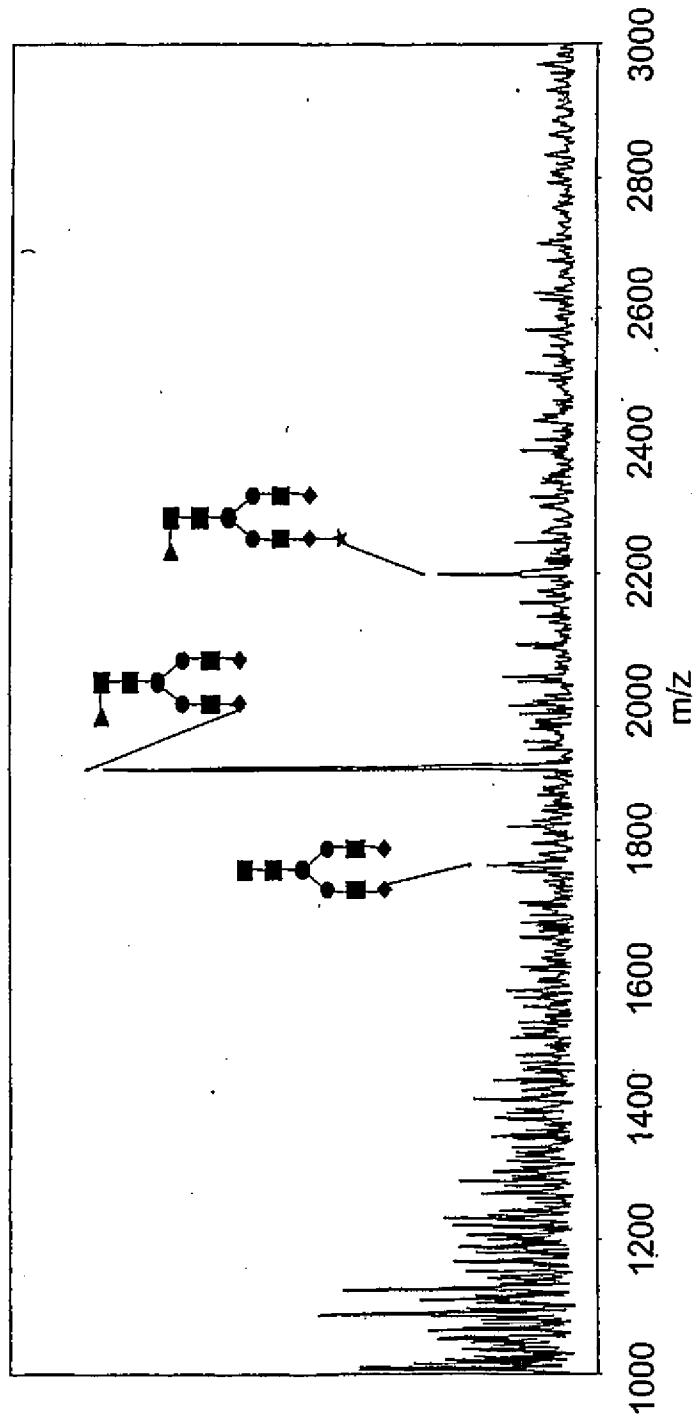


FIG. 105C

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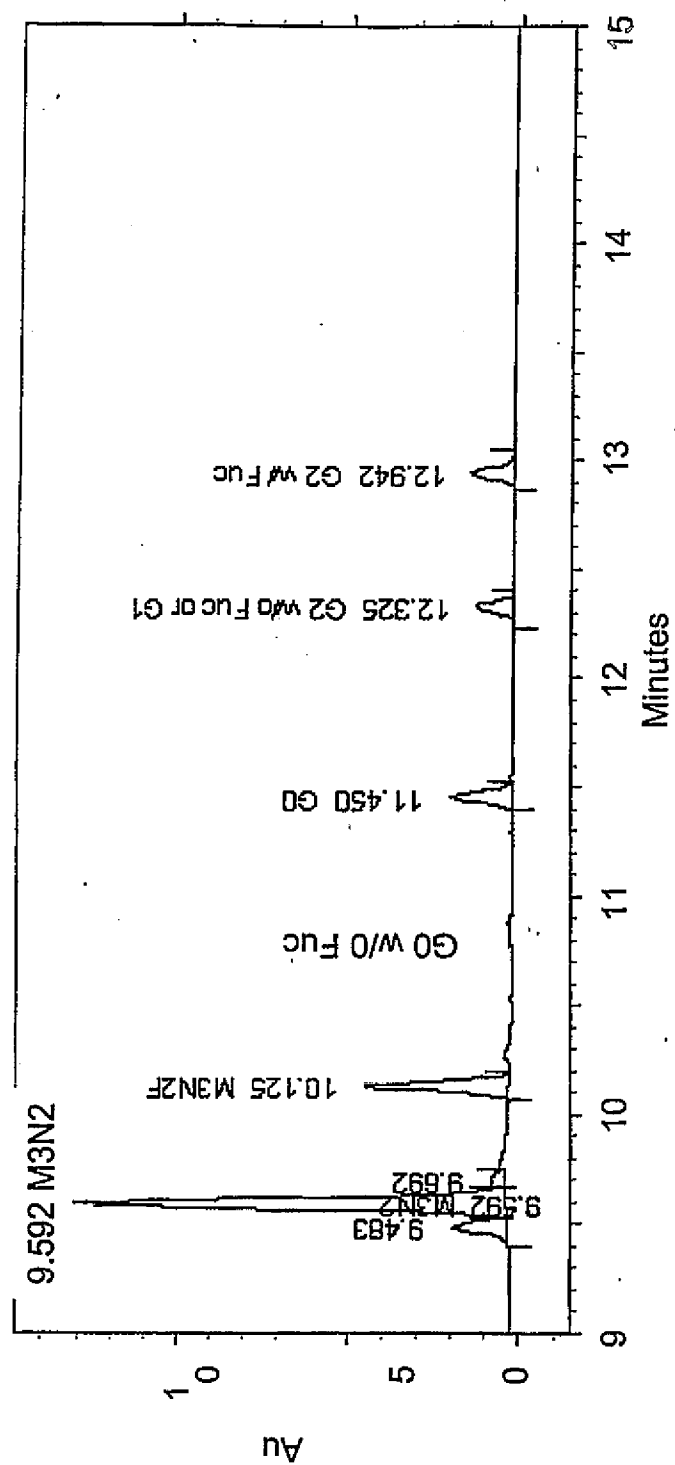


FIG. 106A

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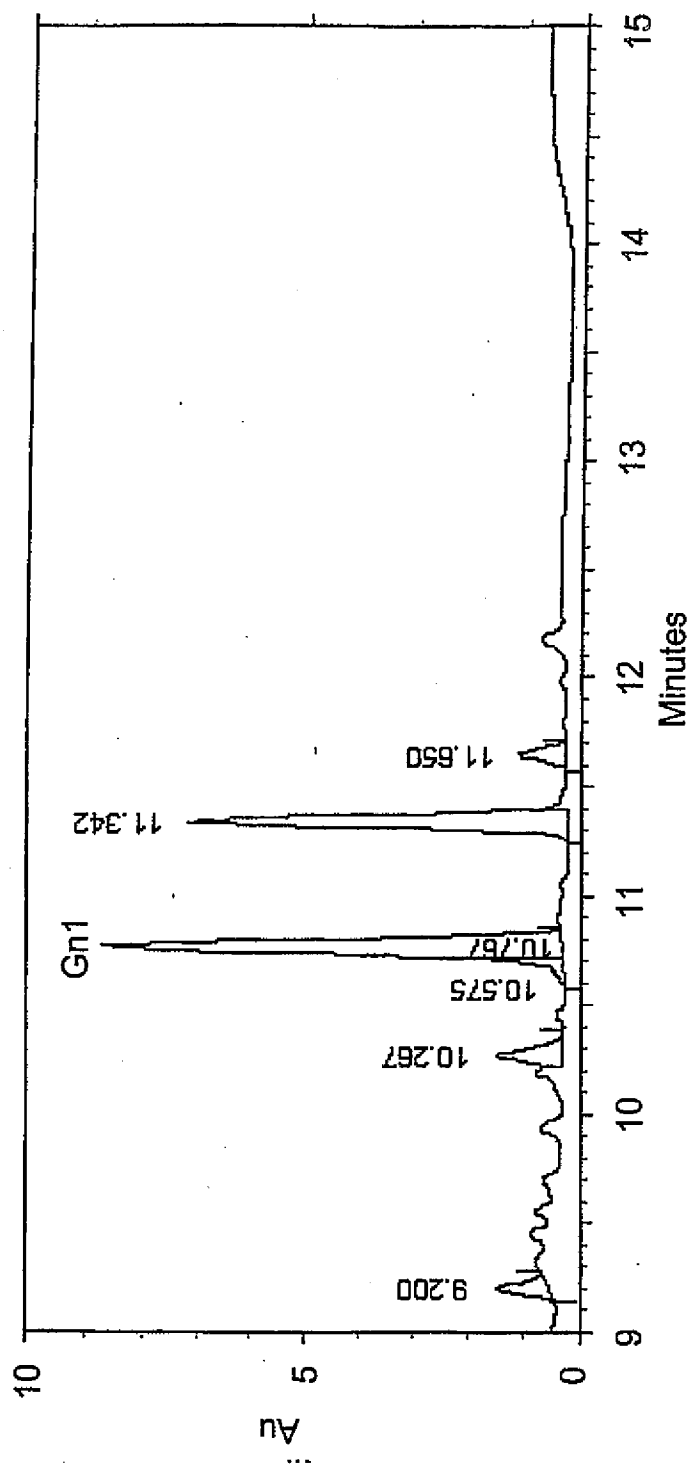


FIG. 106B

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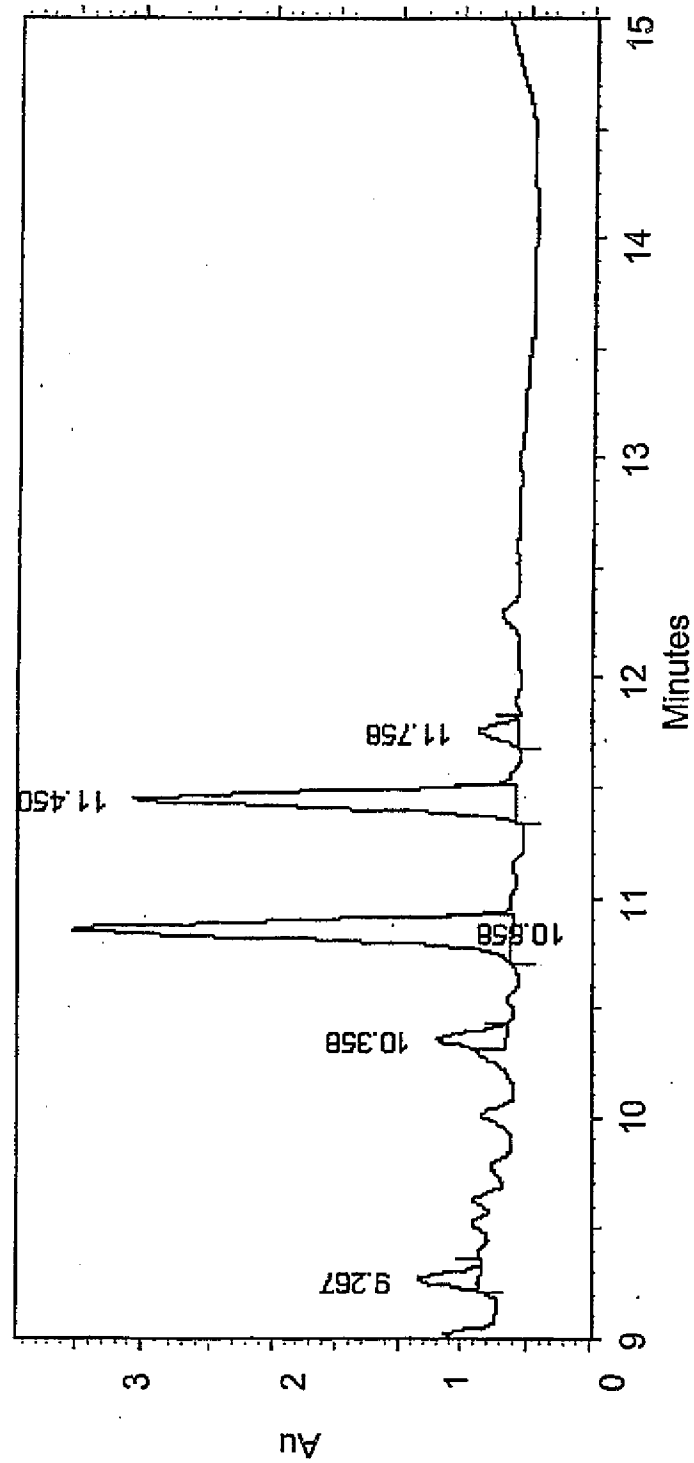


FIG. 106C

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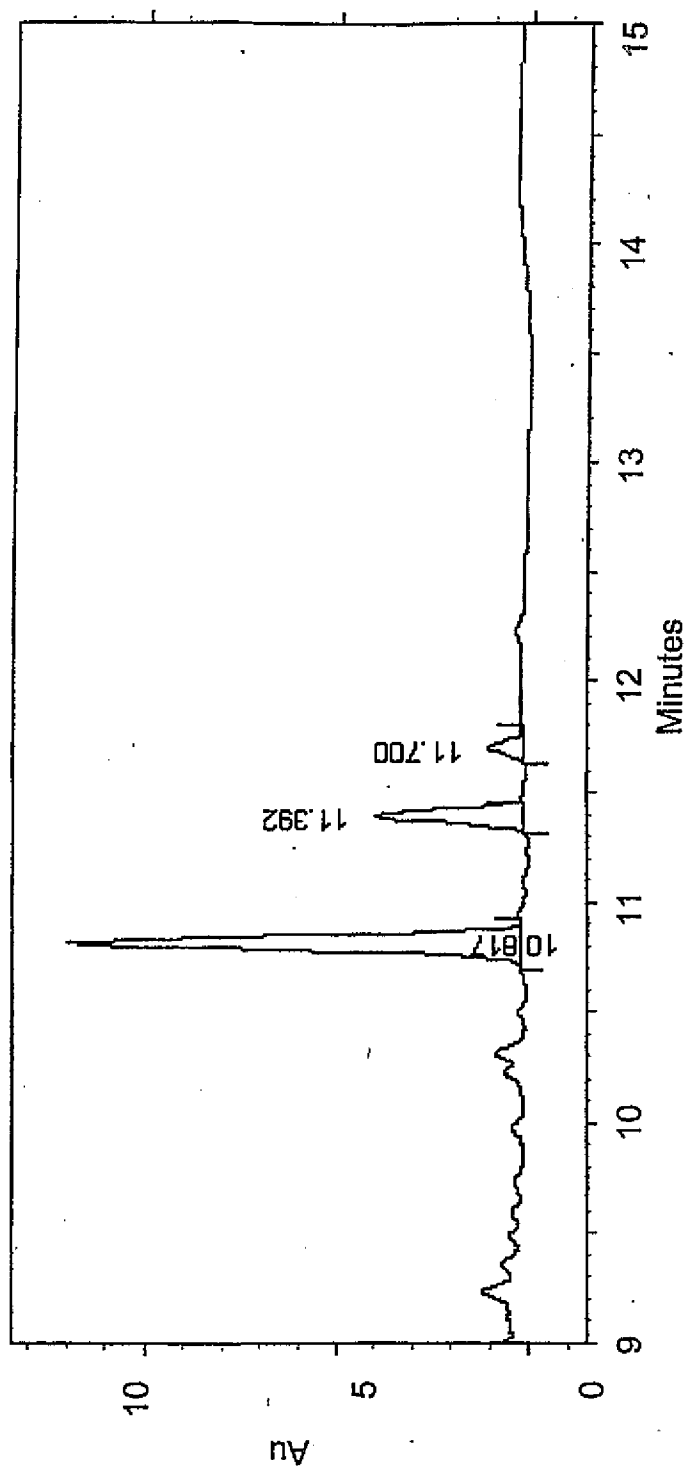


FIG. 106D

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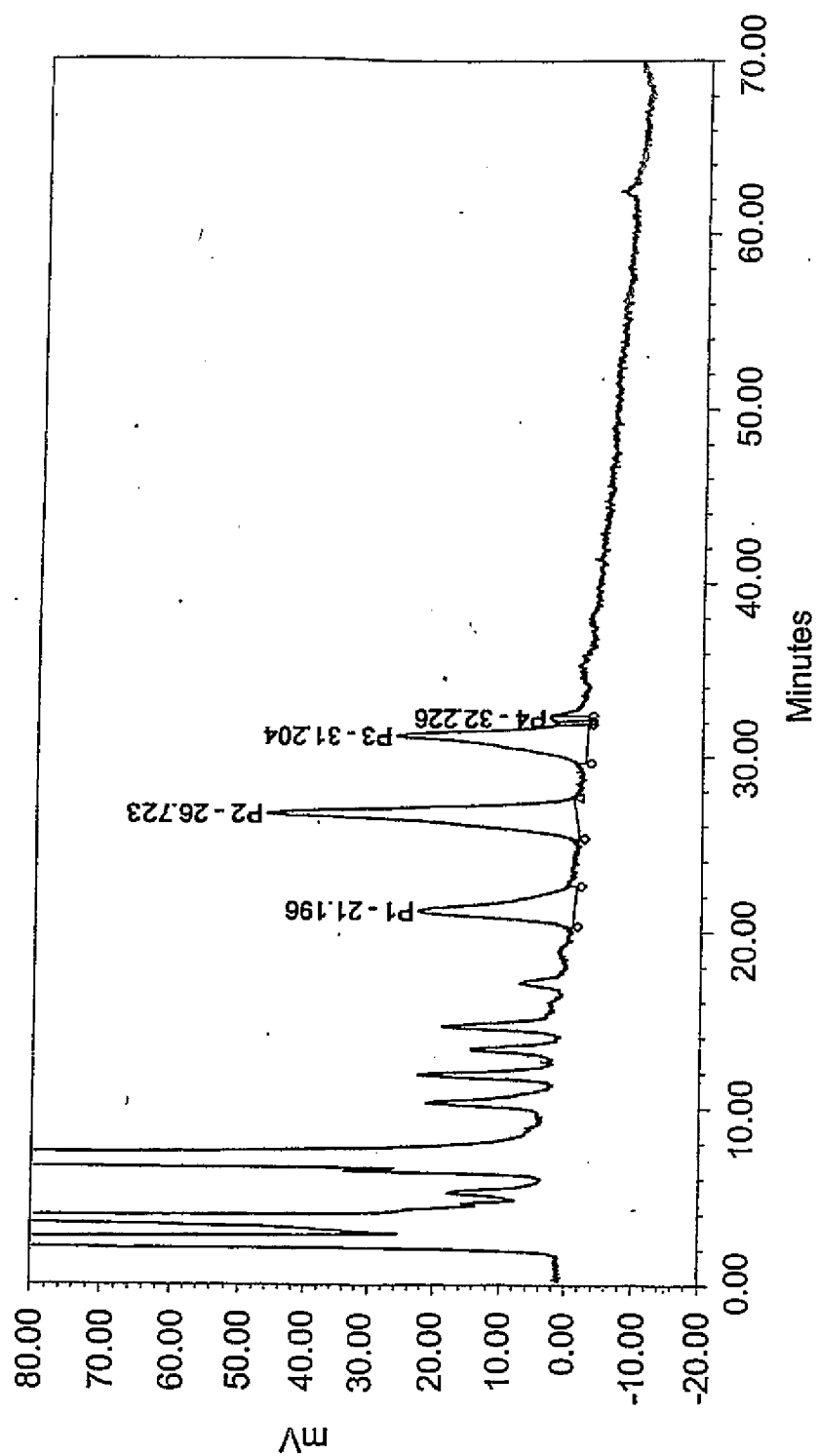


FIG. 107A

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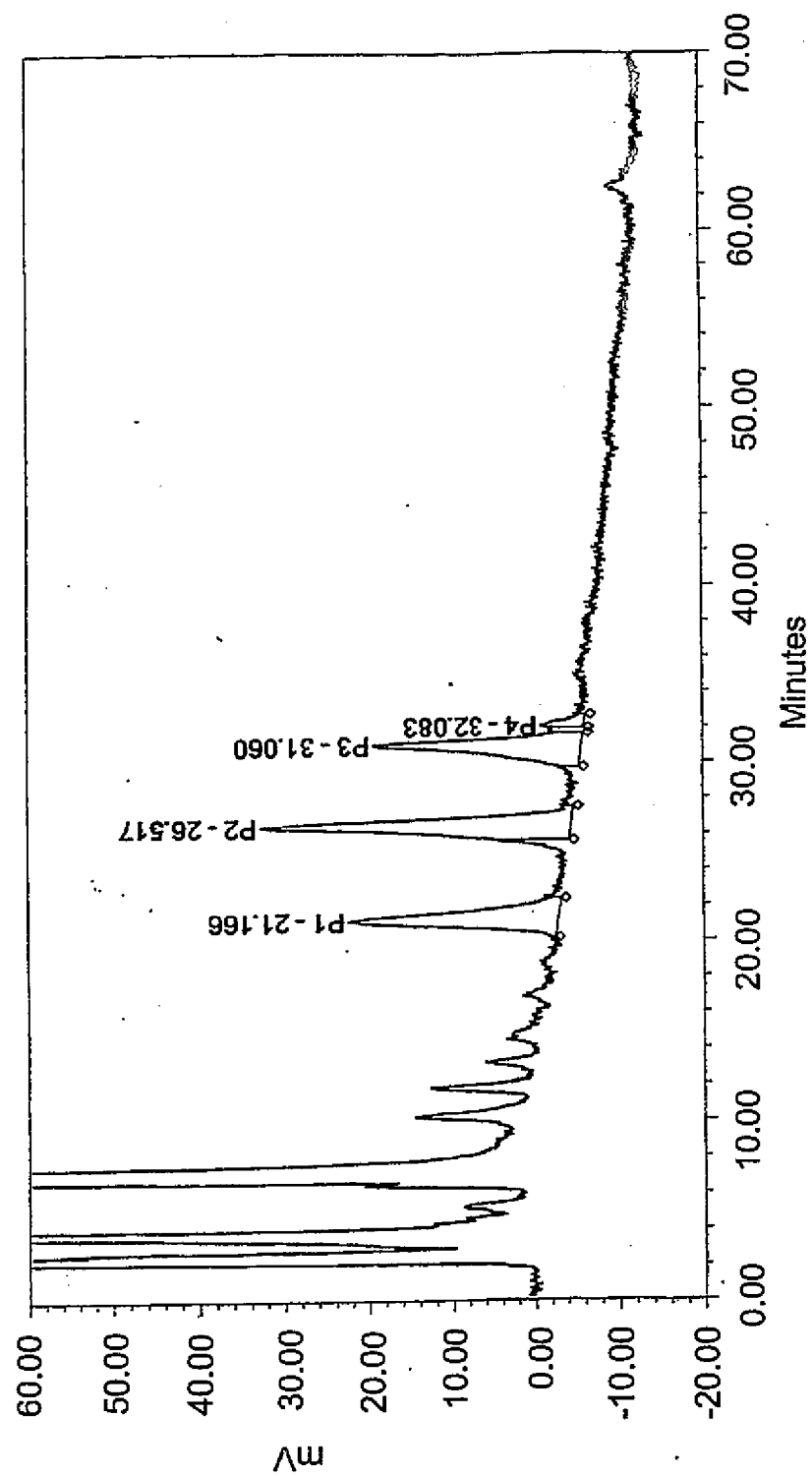


FIG. 107B

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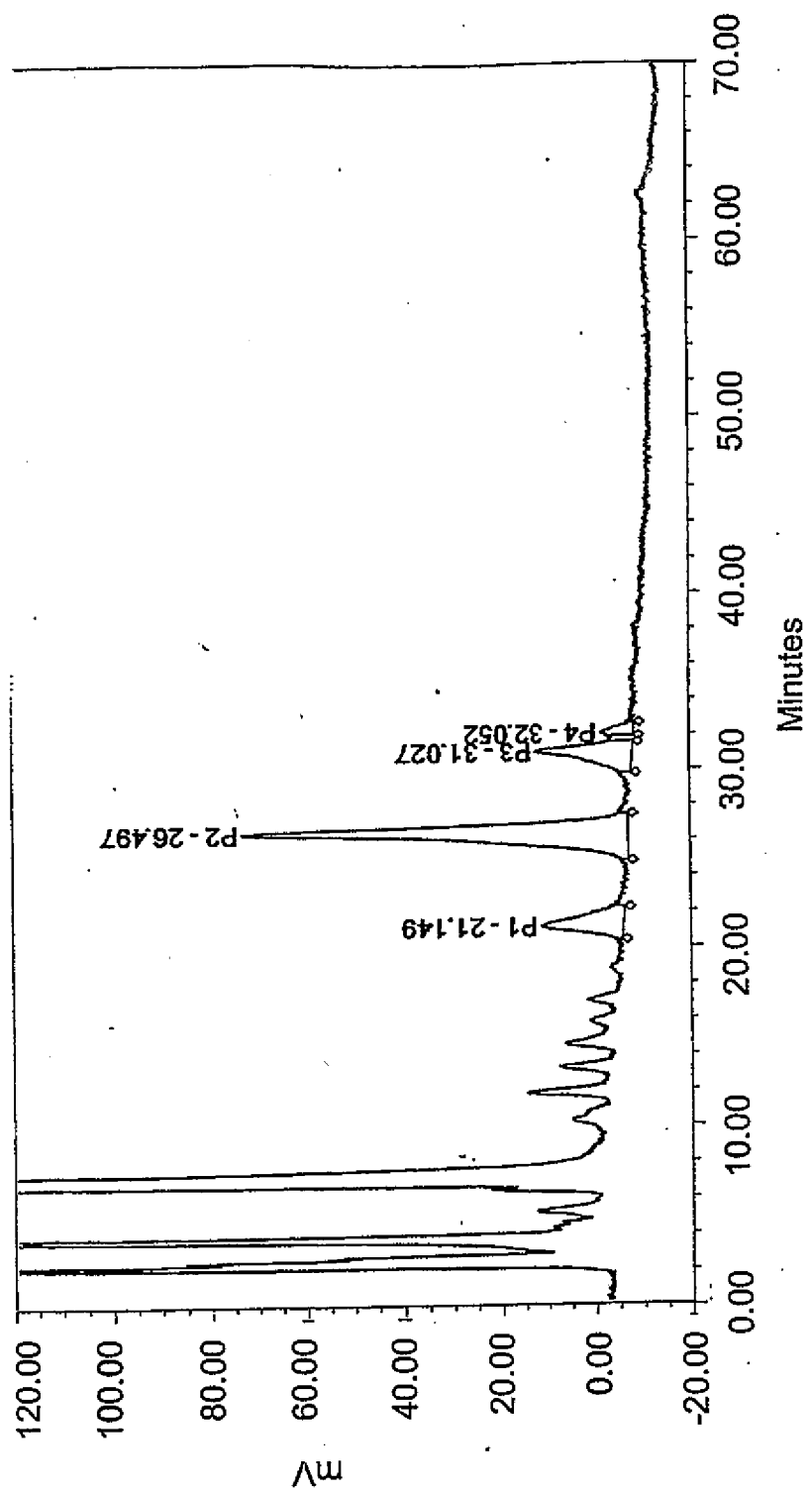


FIG. 107C

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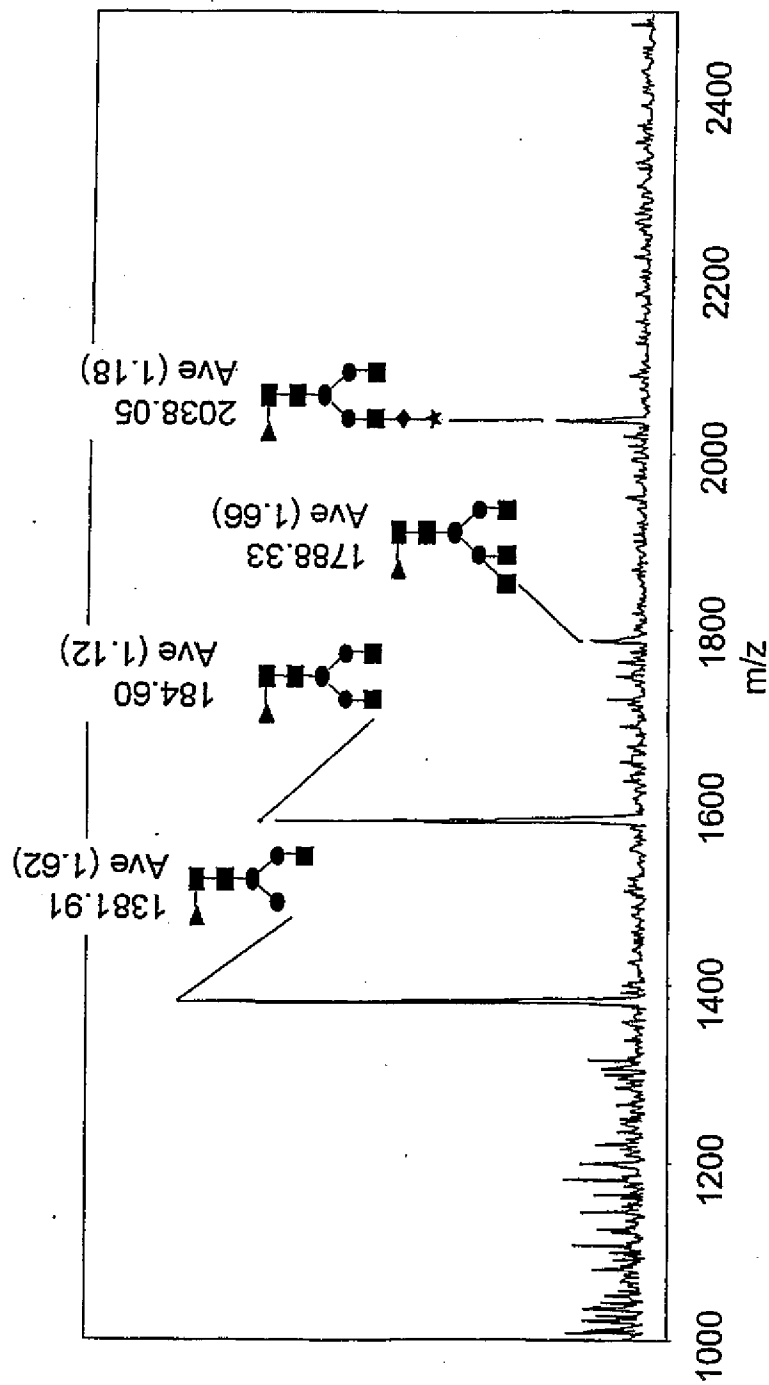
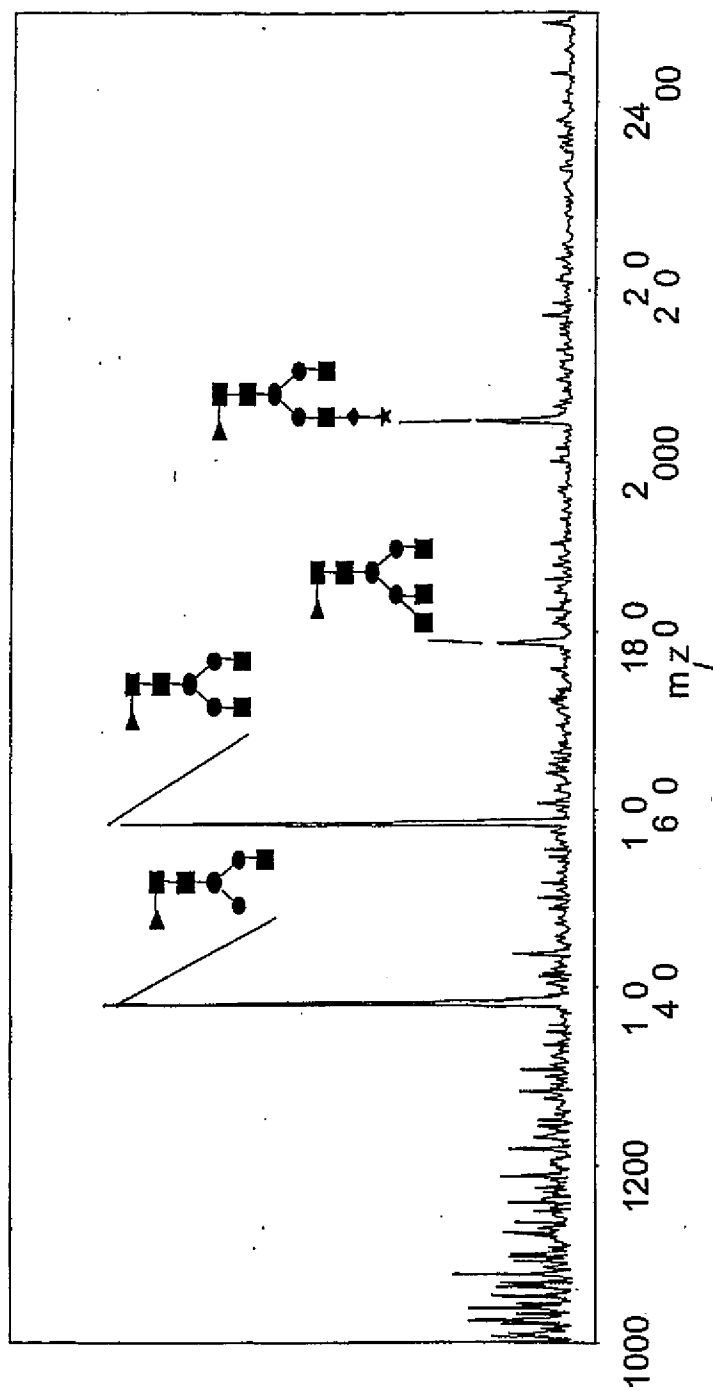


FIG. 108A

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FI . 10⁸B
G

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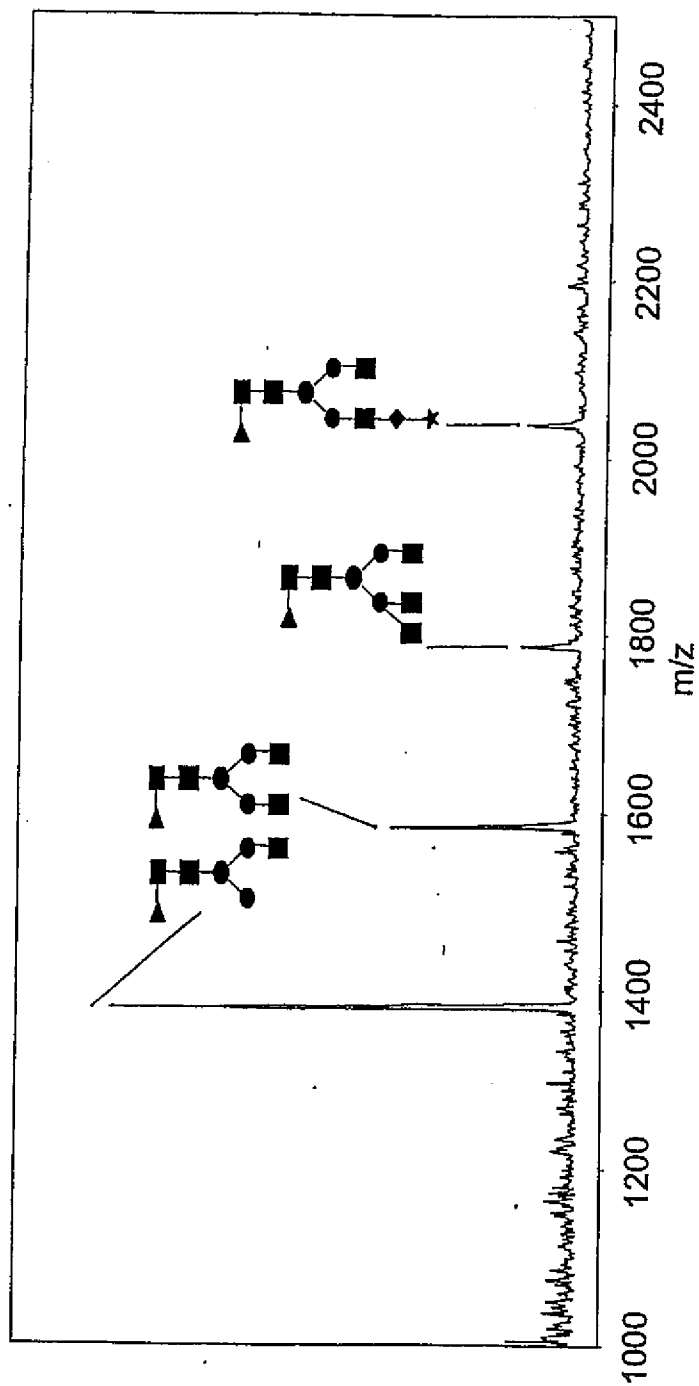


FIG. 108C

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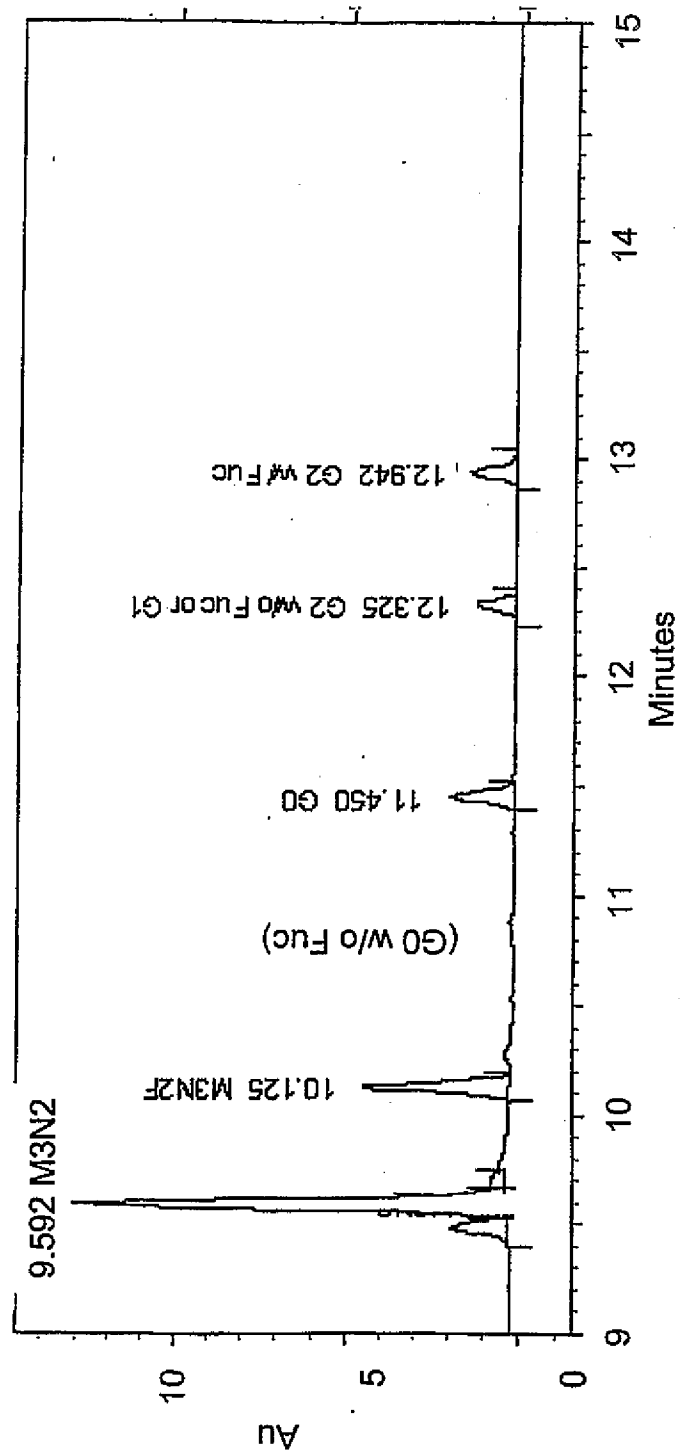


FIG. 109A

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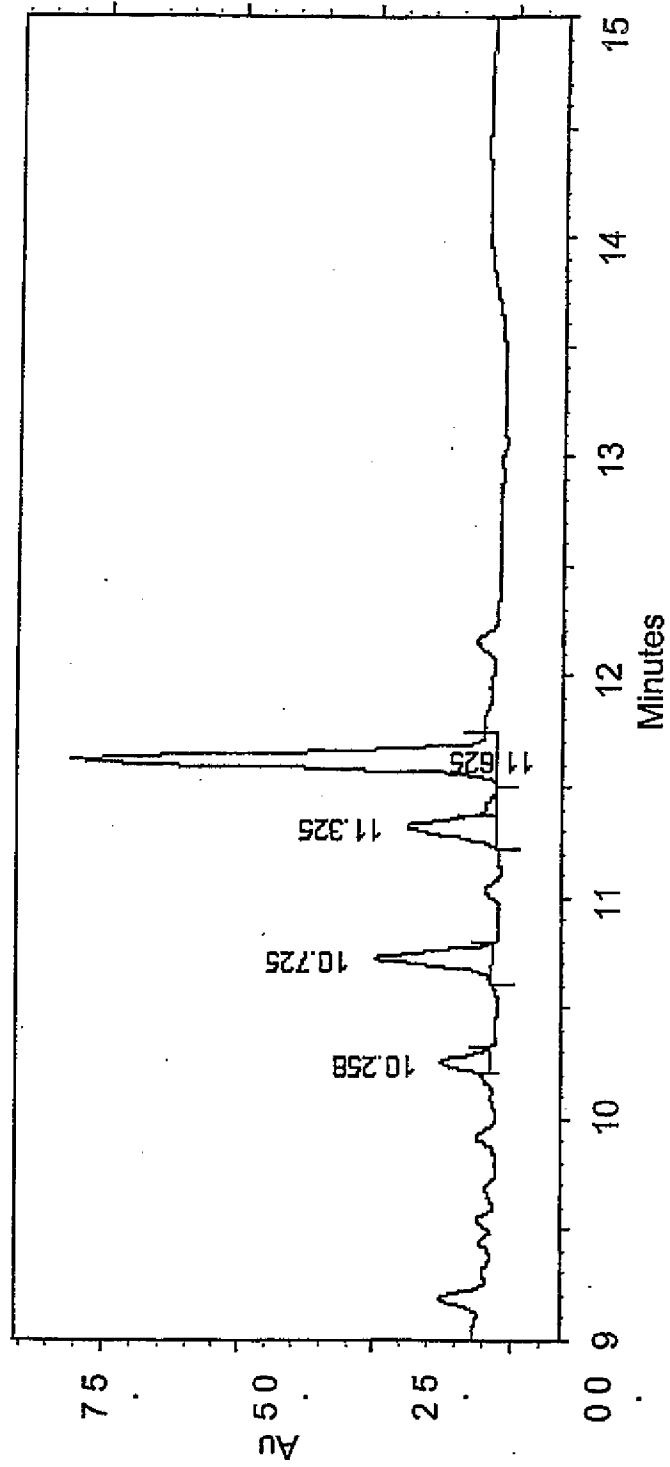


FIG. 109B

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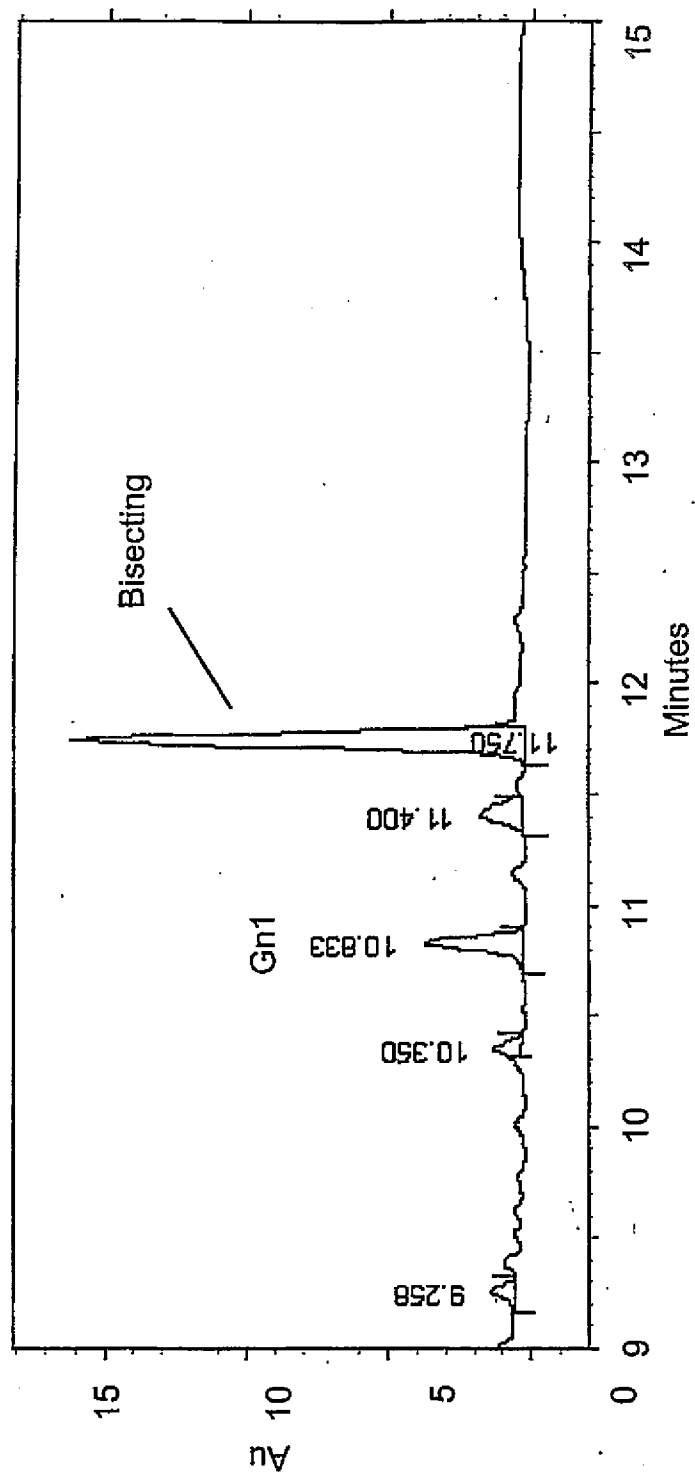


FIG. 109C

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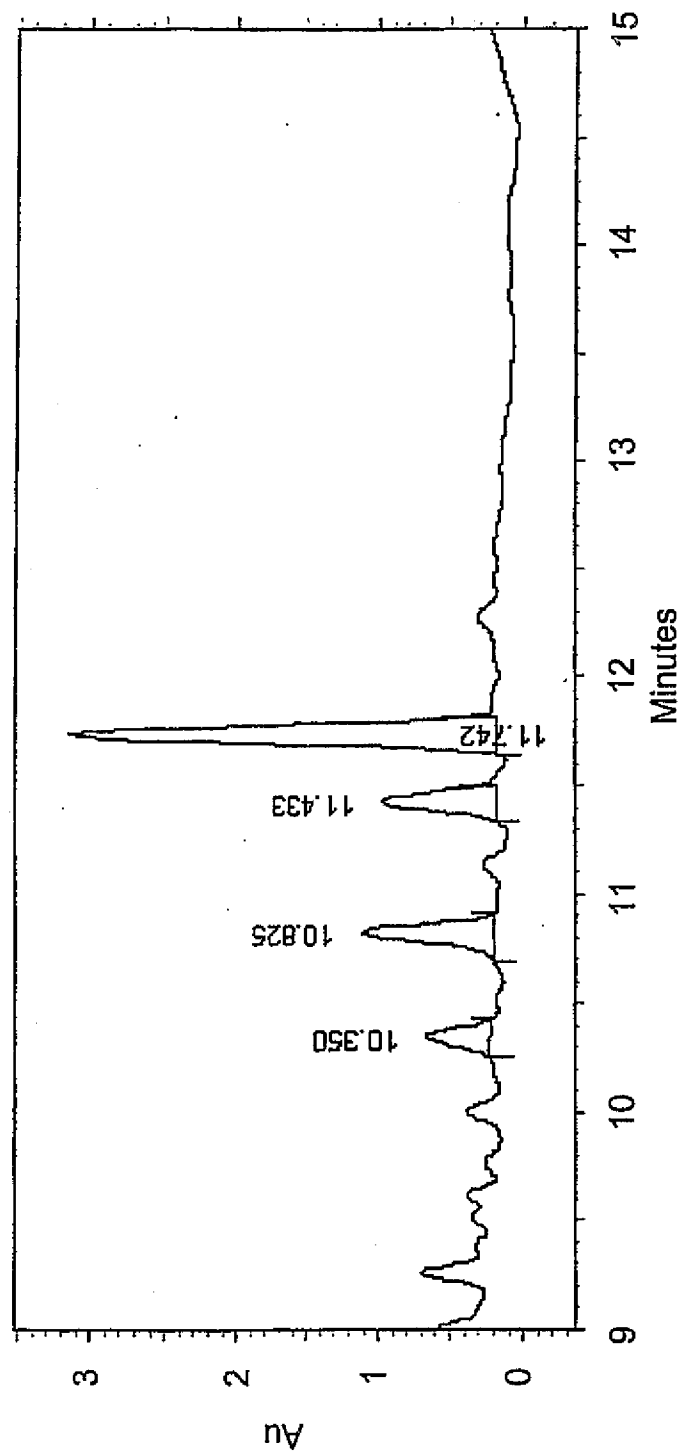


FIG. 109D

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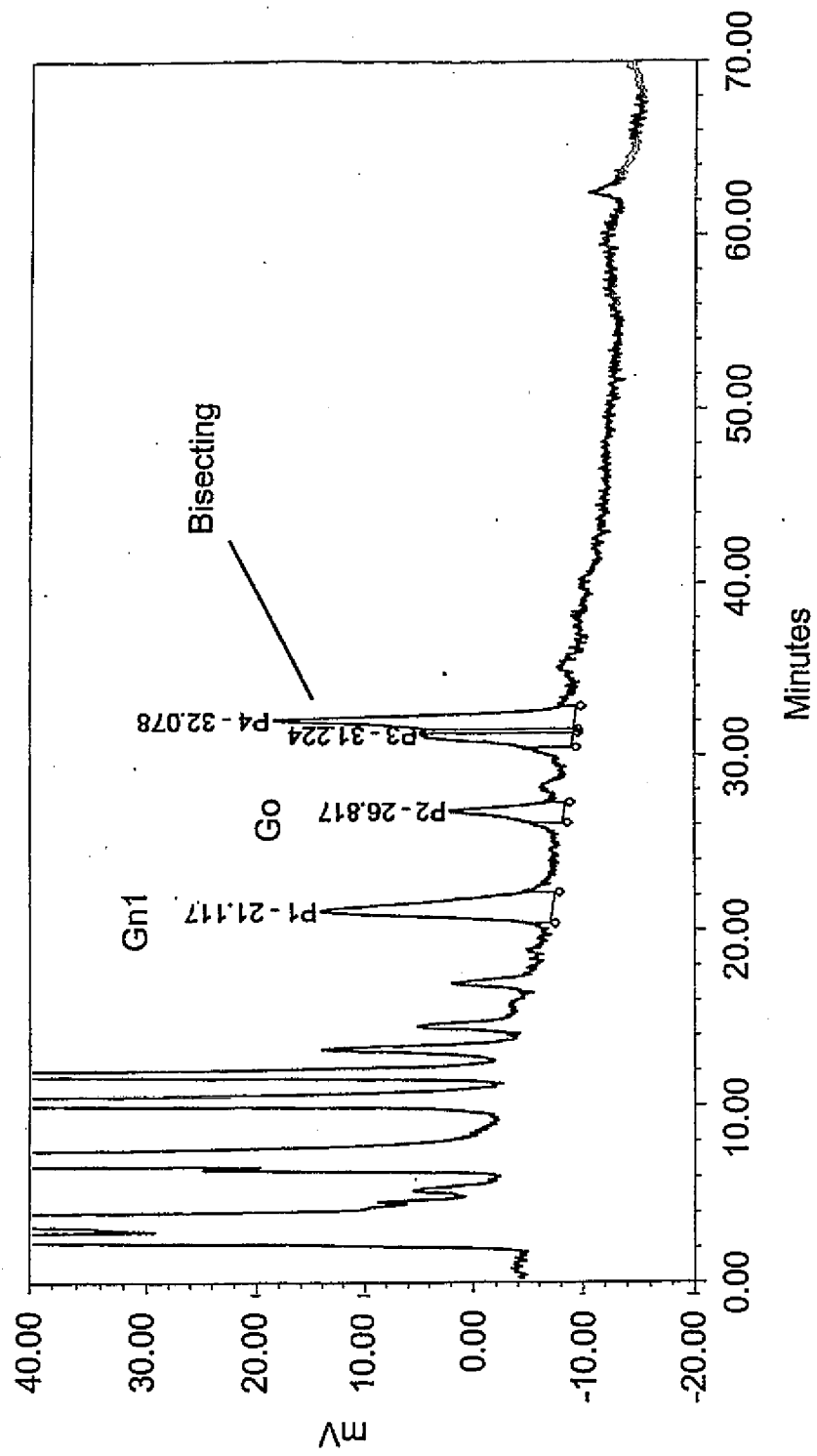


FIG. 110A

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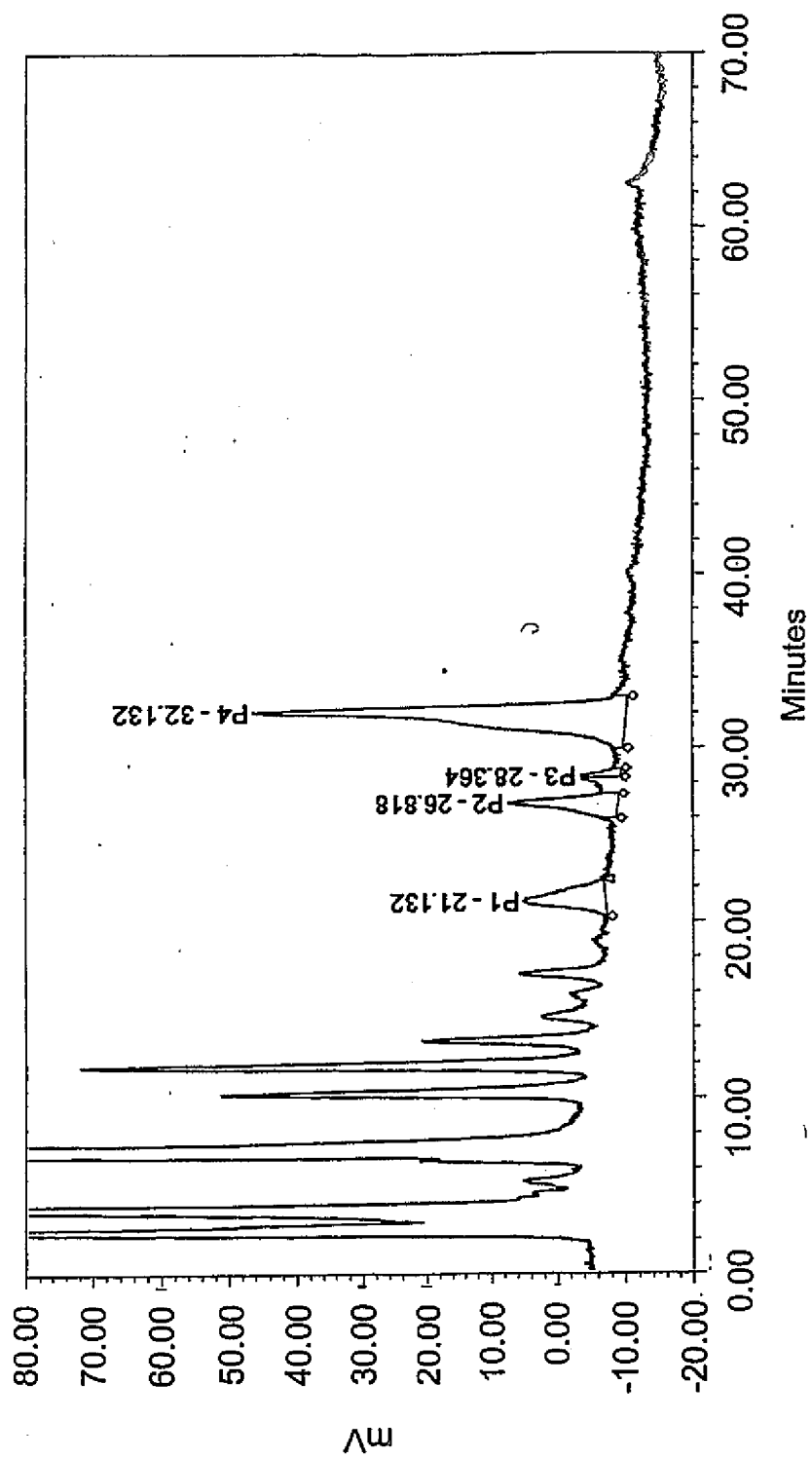


FIG. 110B

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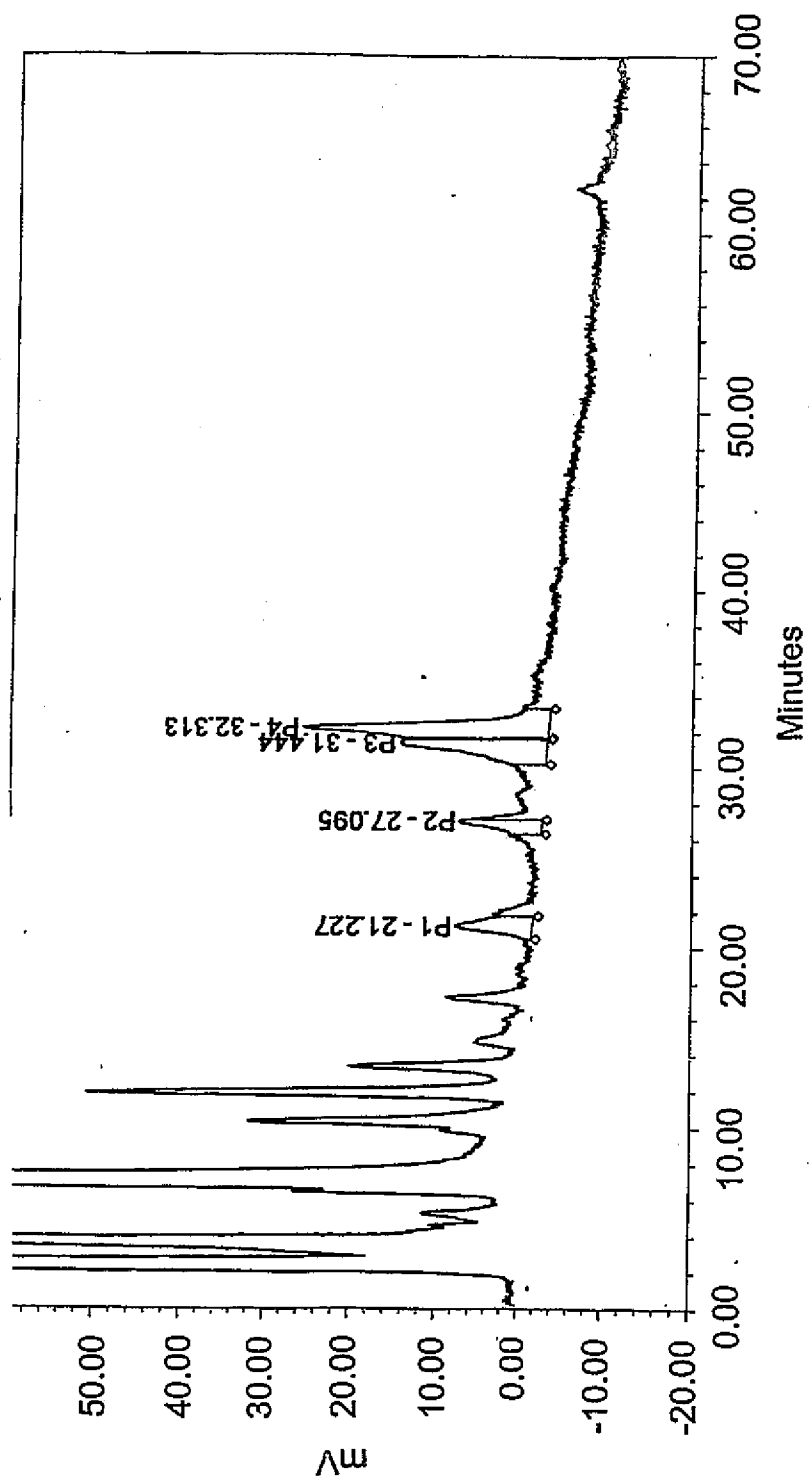


FIG. 110C

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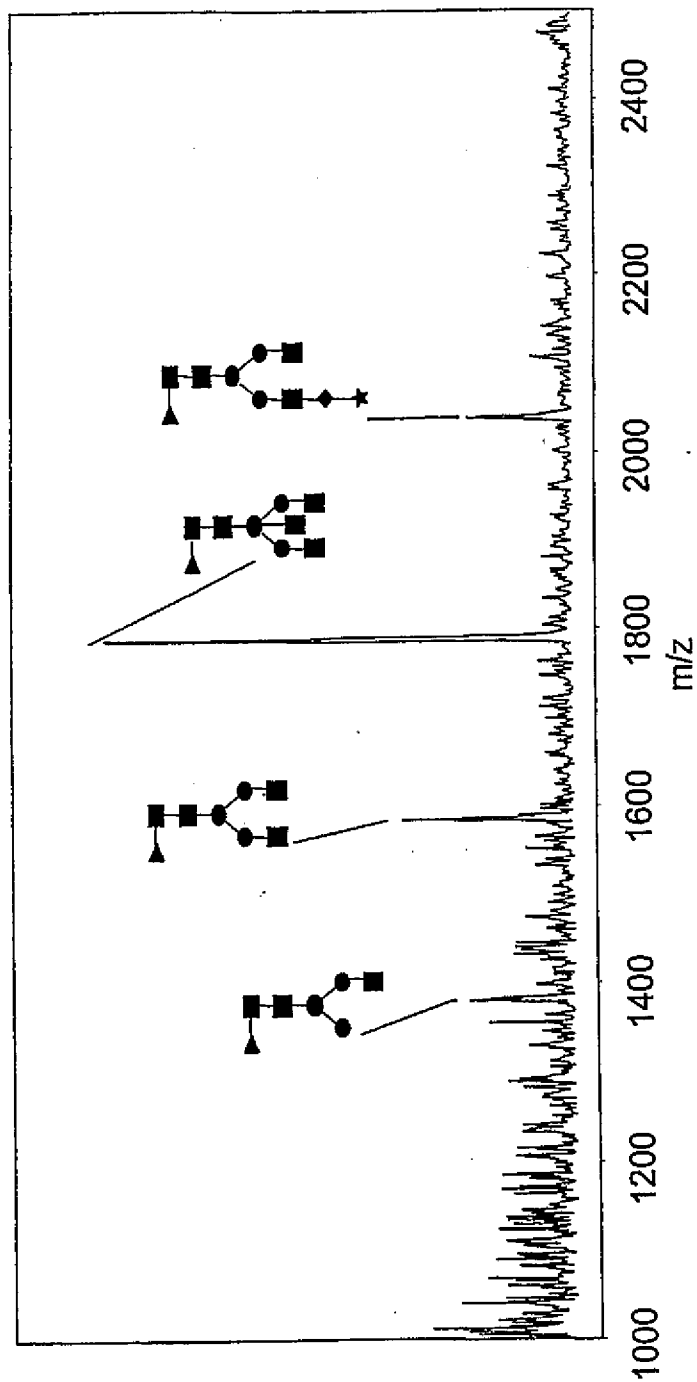


FIG. 111A

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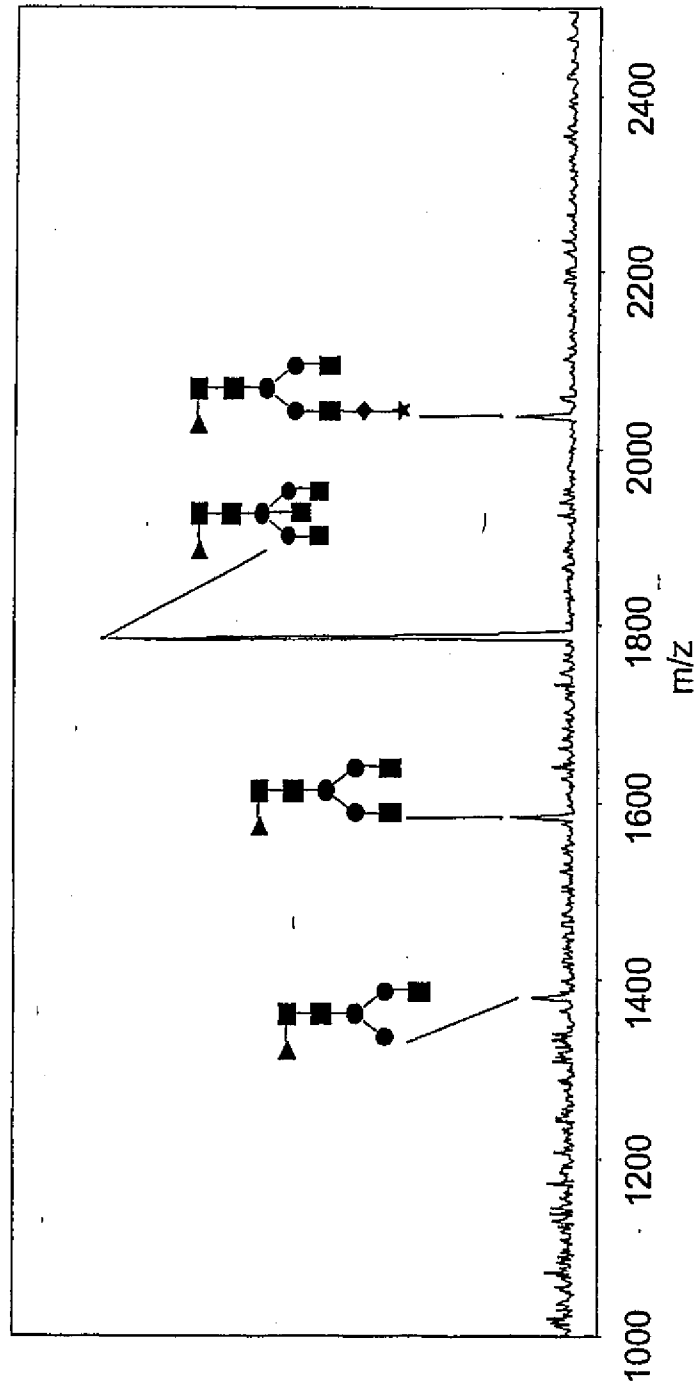


FIG. 111B

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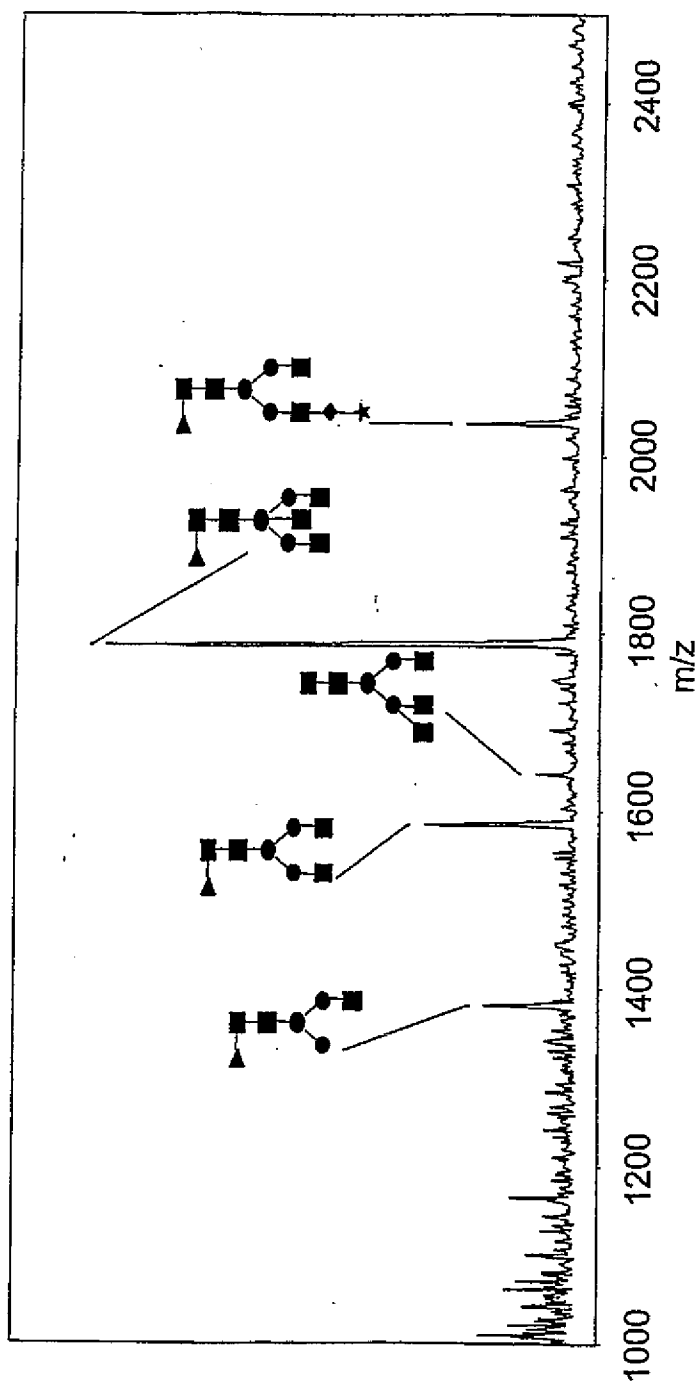


FIG. 111C

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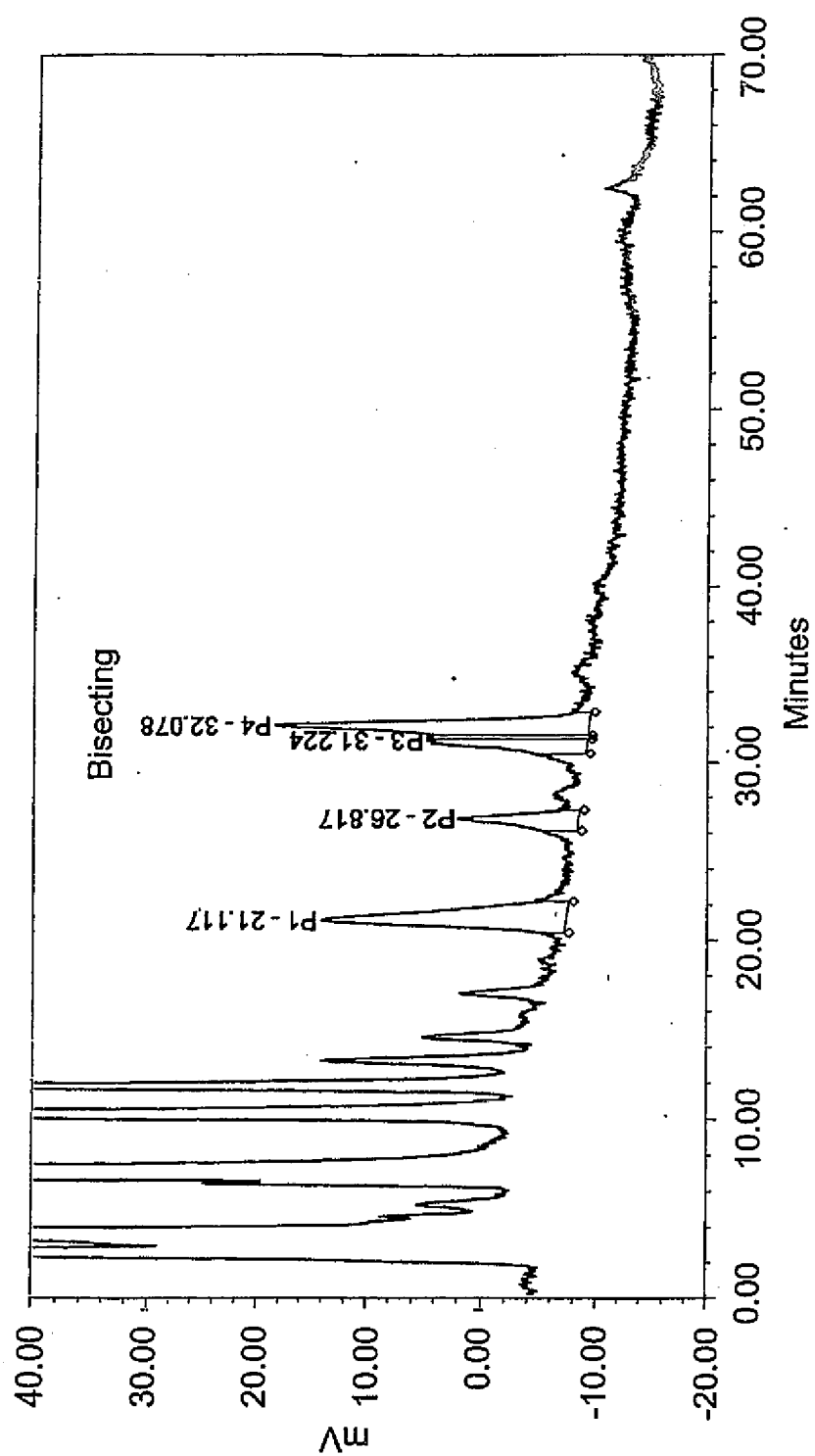


FIG. 112A

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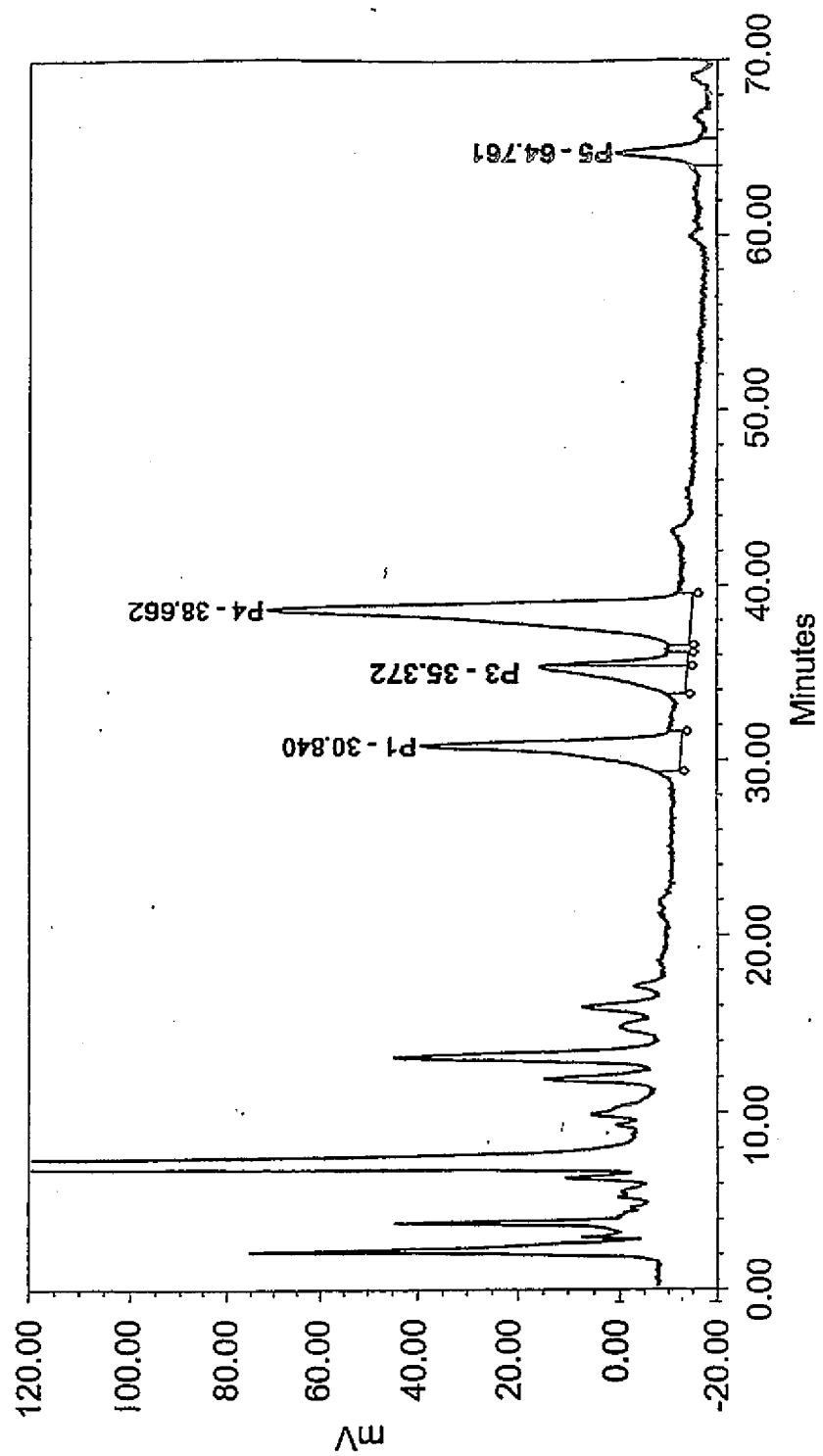


FIG. 112B

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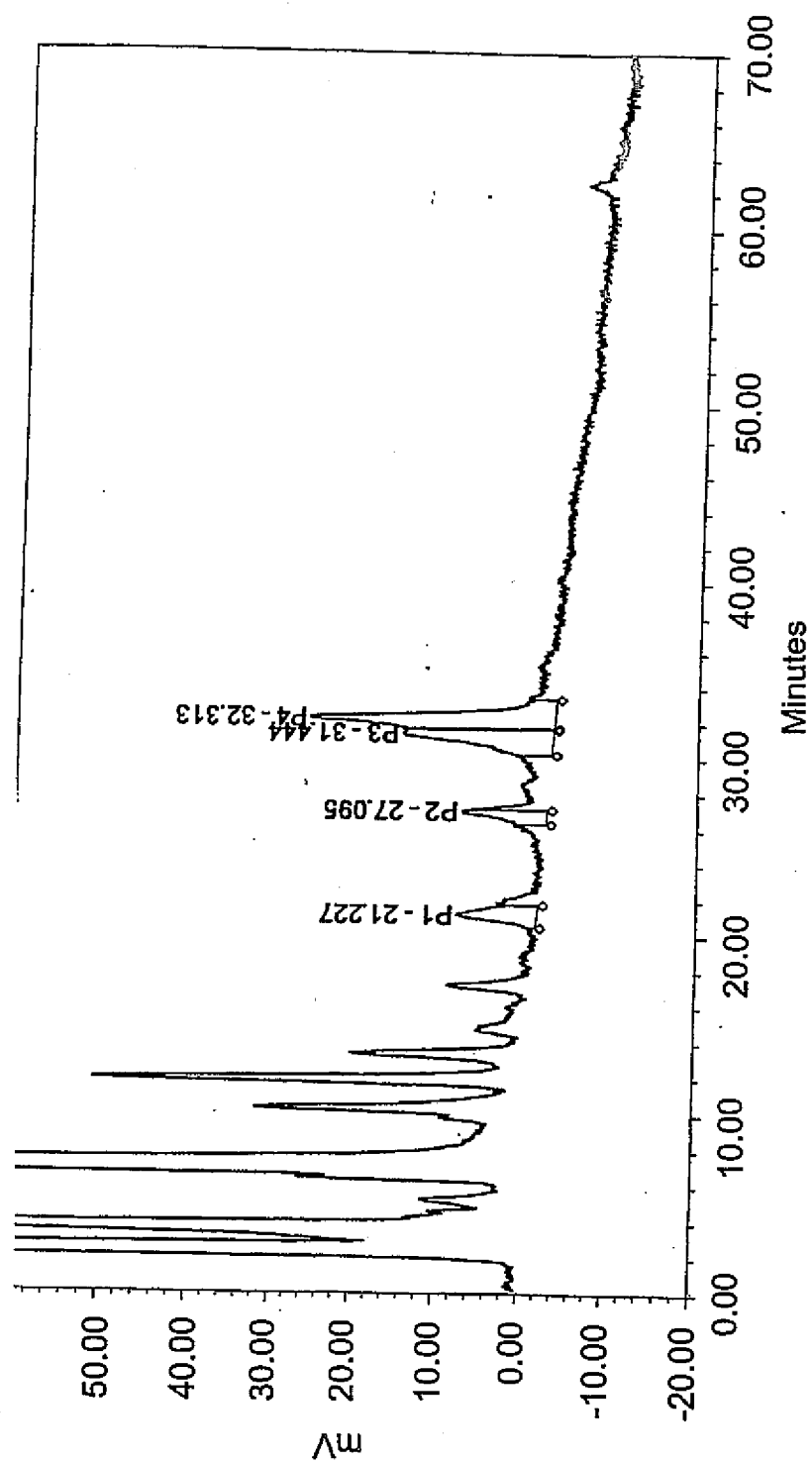


FIG. 112C

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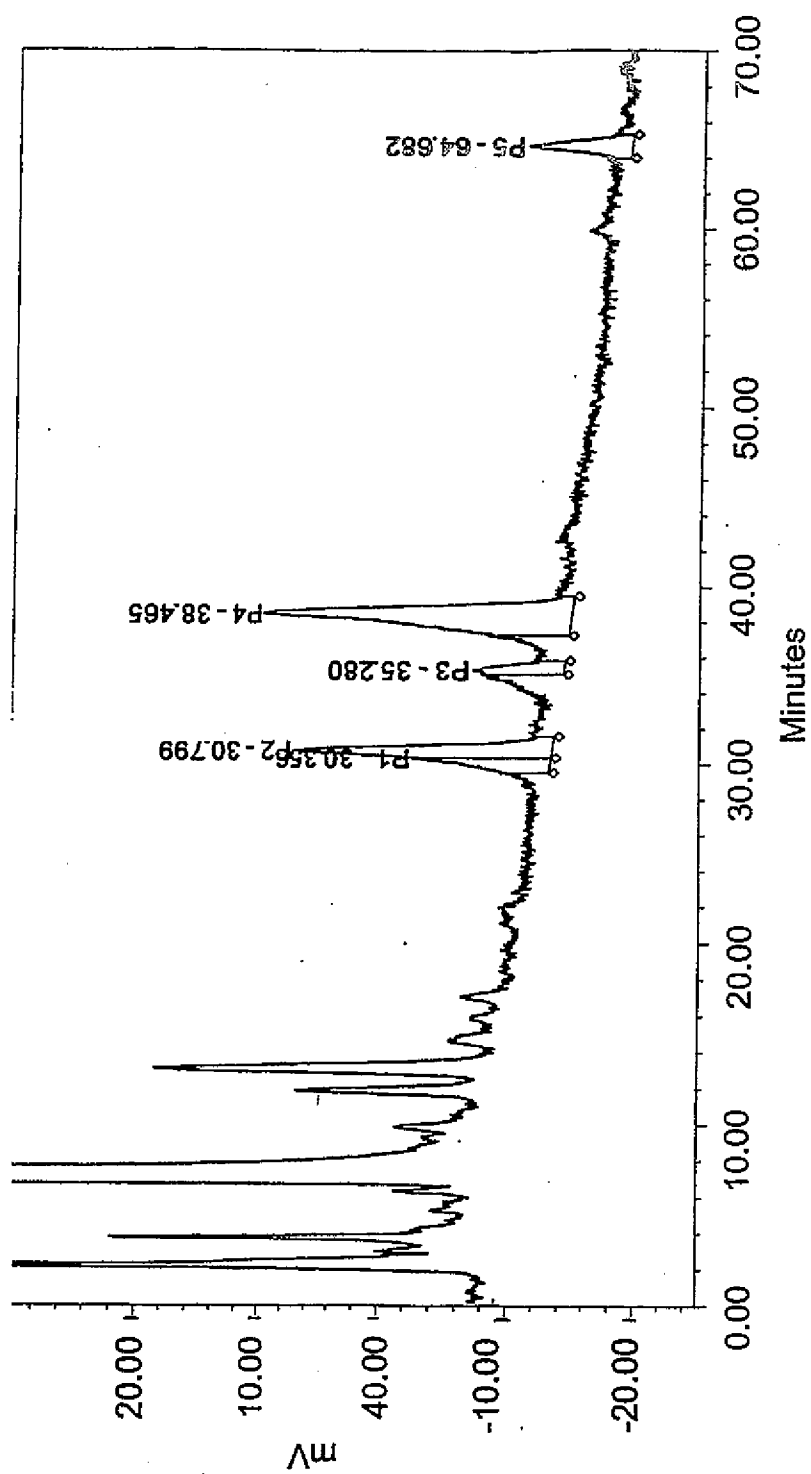


FIG. 112D

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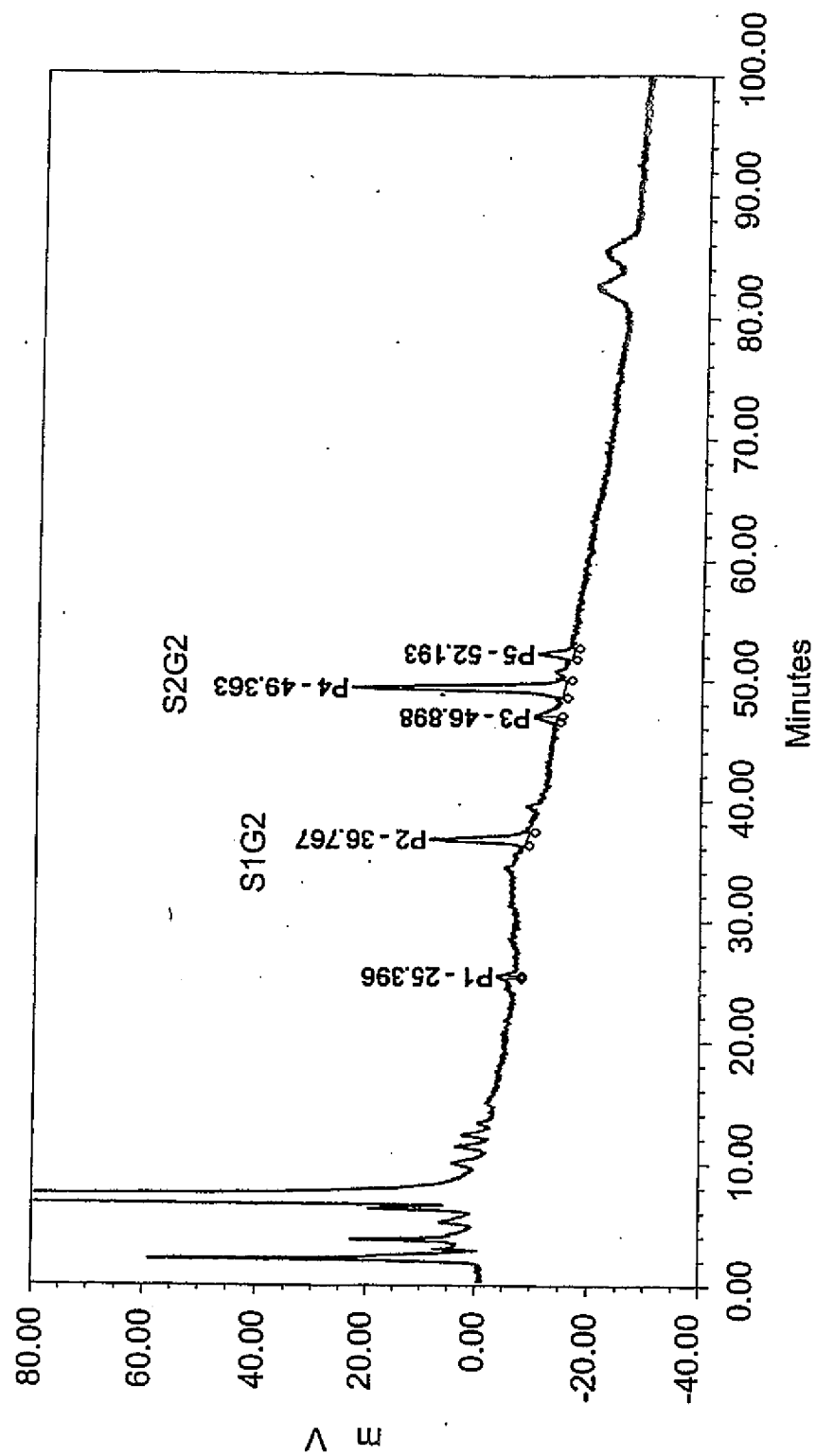


FIG. 113A

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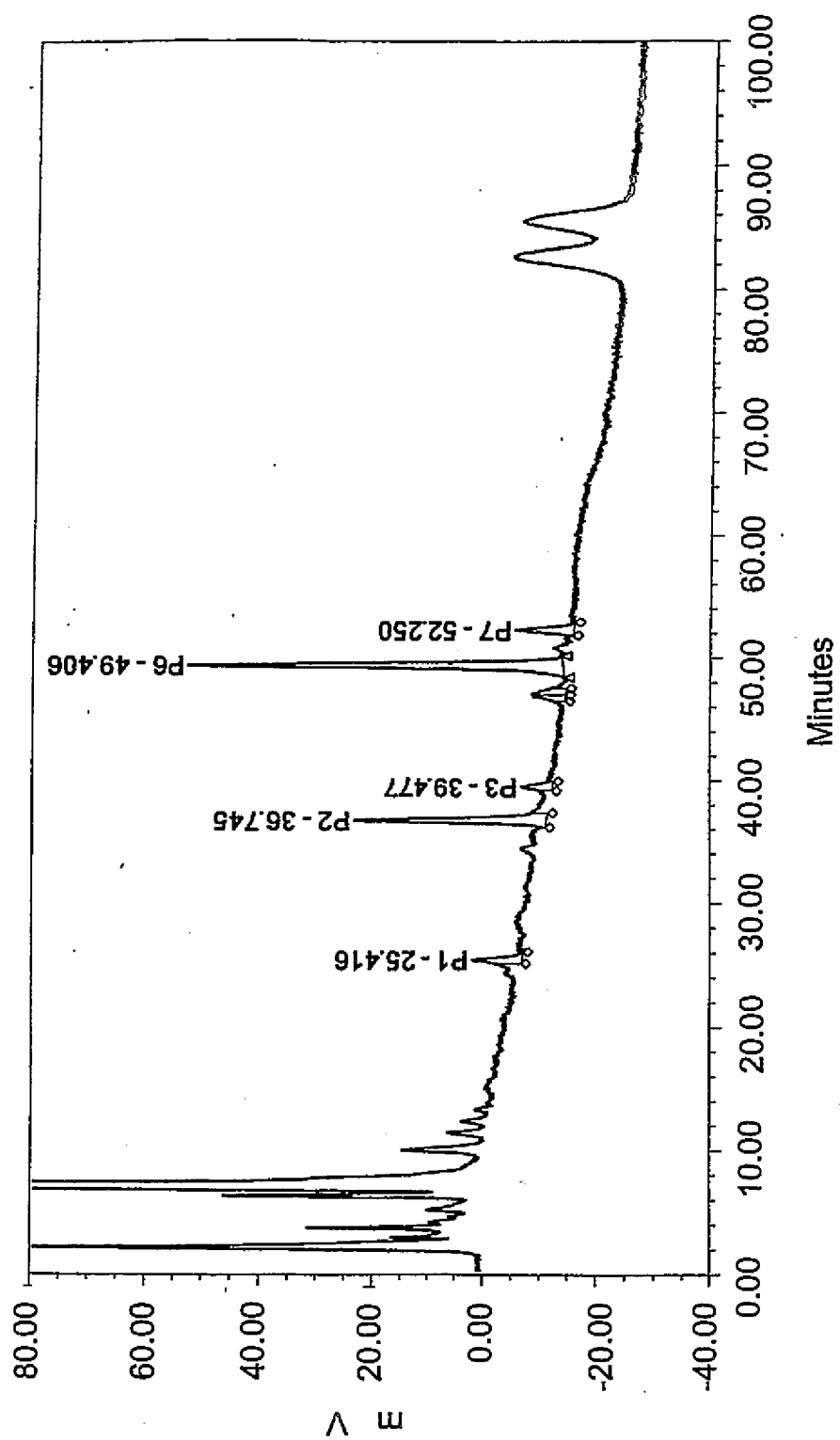


FIG. 113B

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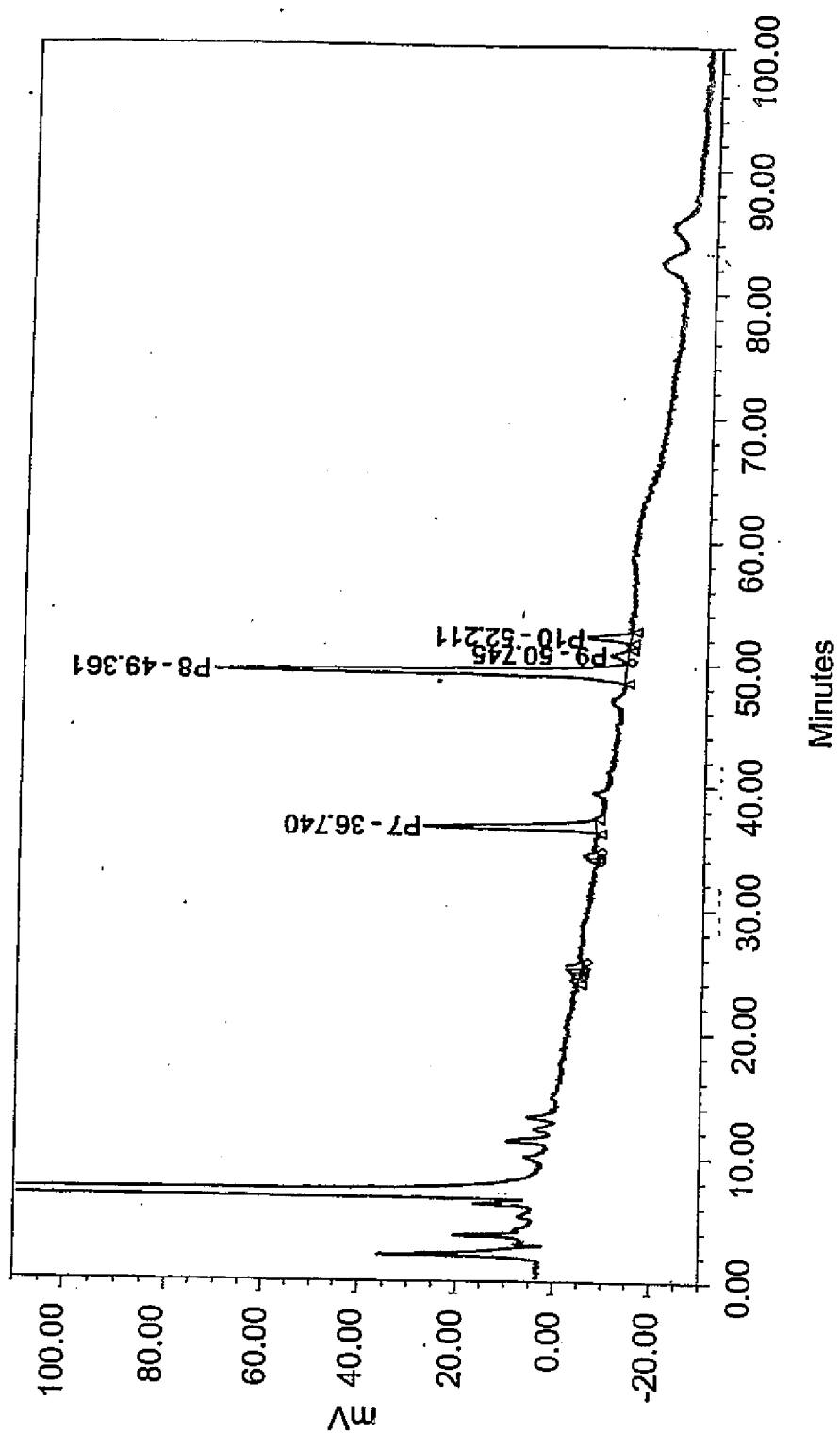


FIG. 113C

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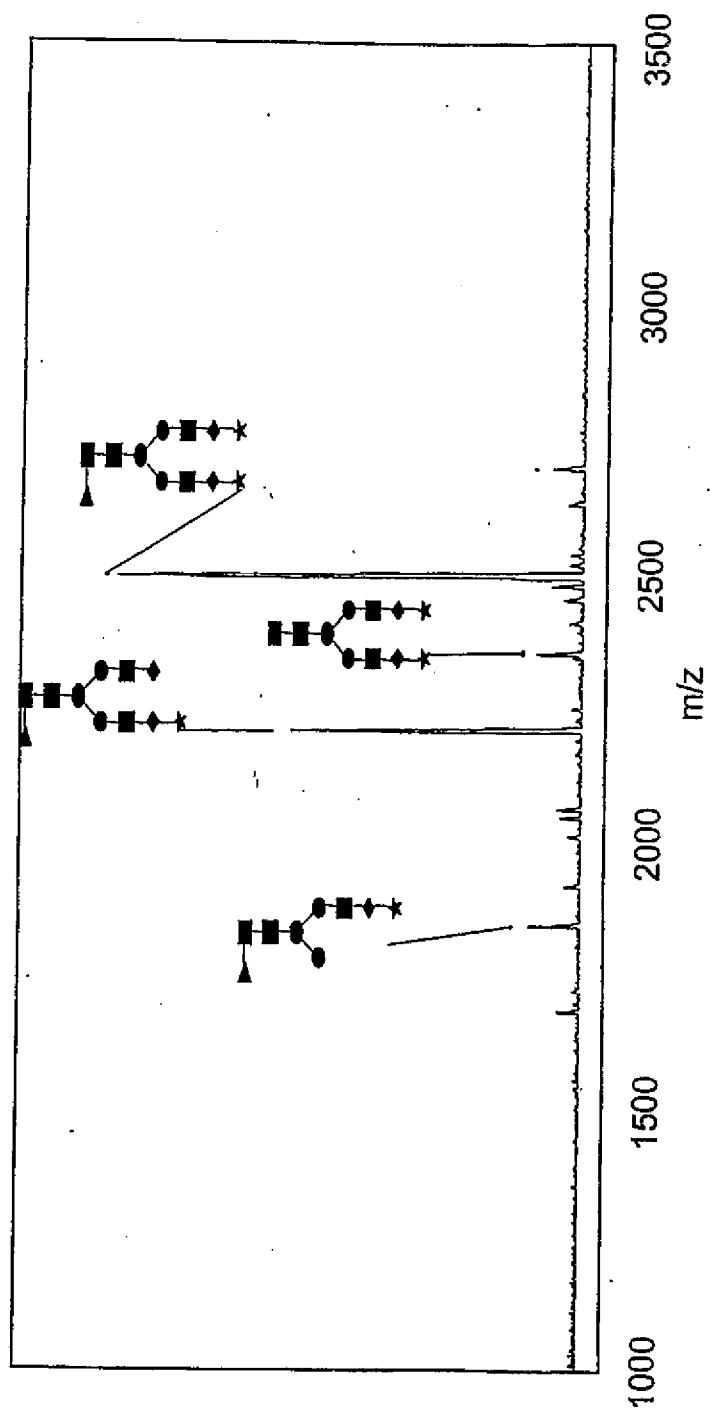
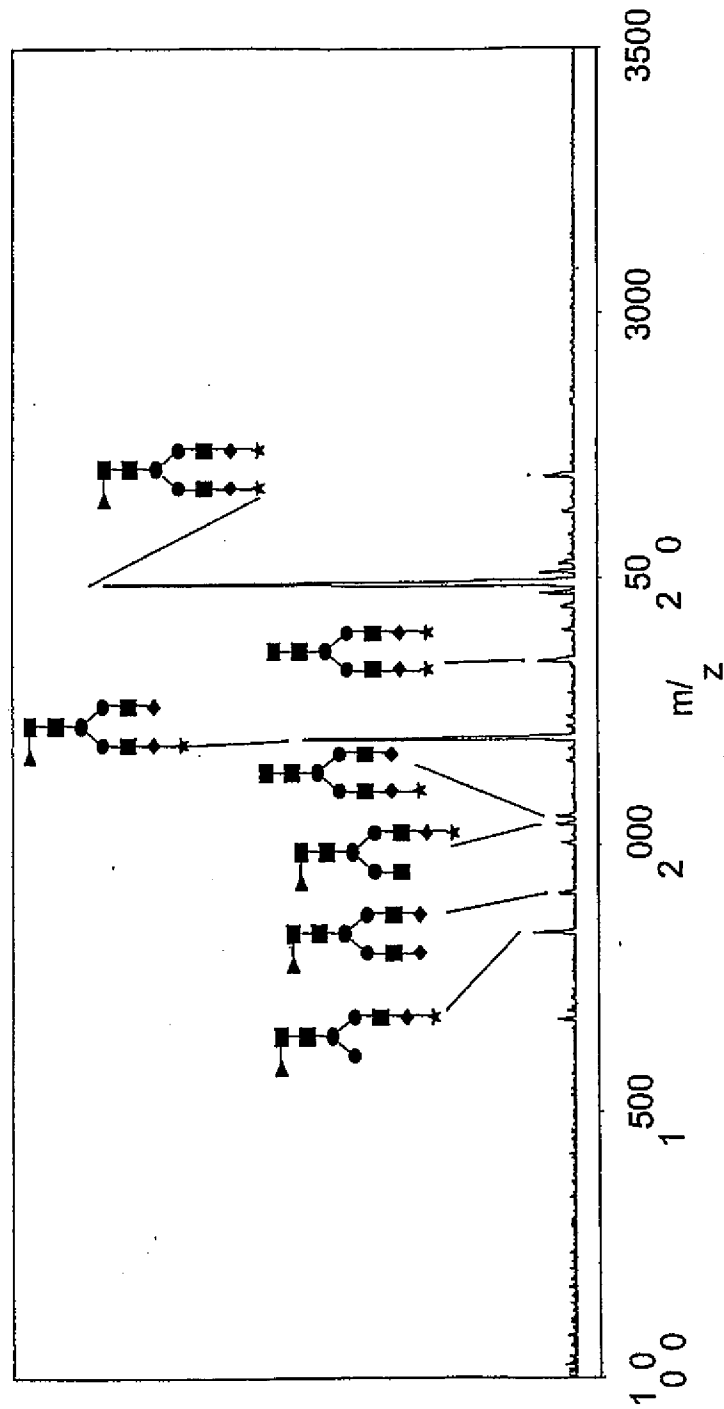
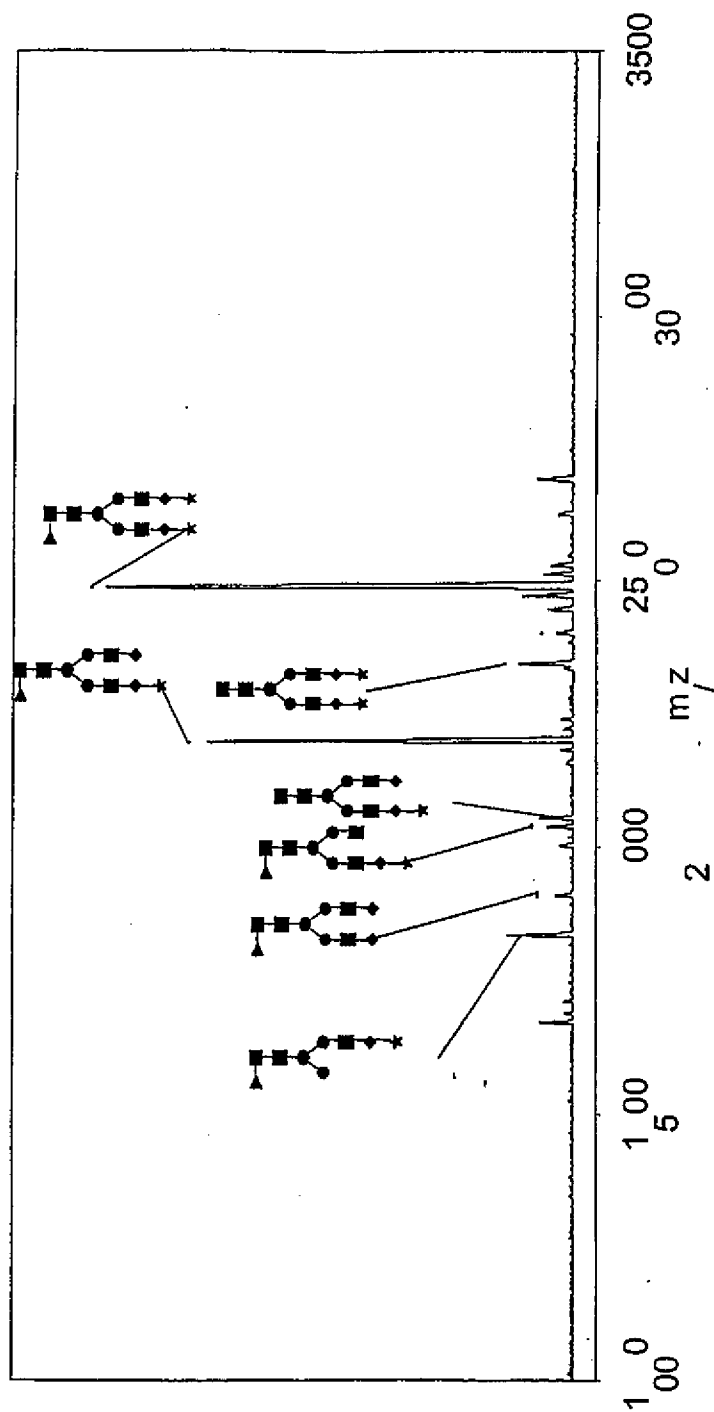


FIG. 114A

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FIG. 1₄B

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F¹G.114C

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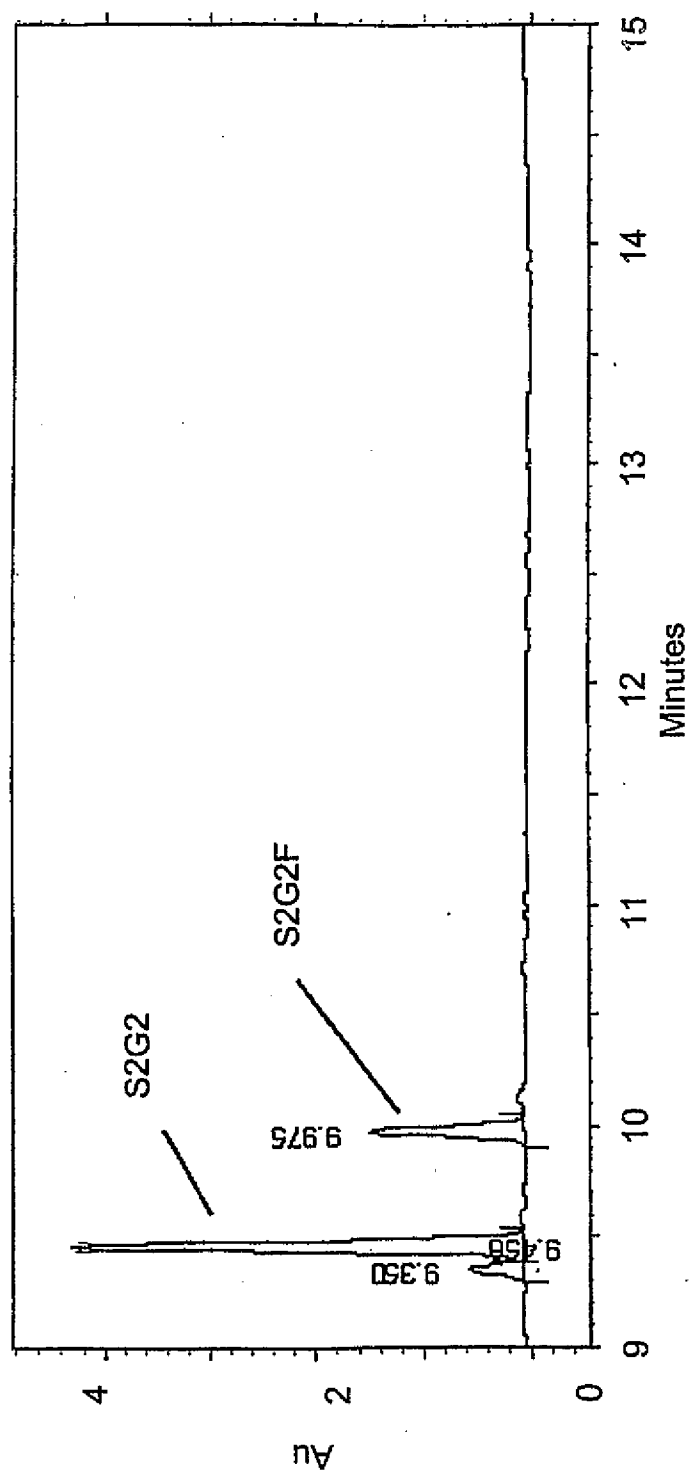


FIG. 115A

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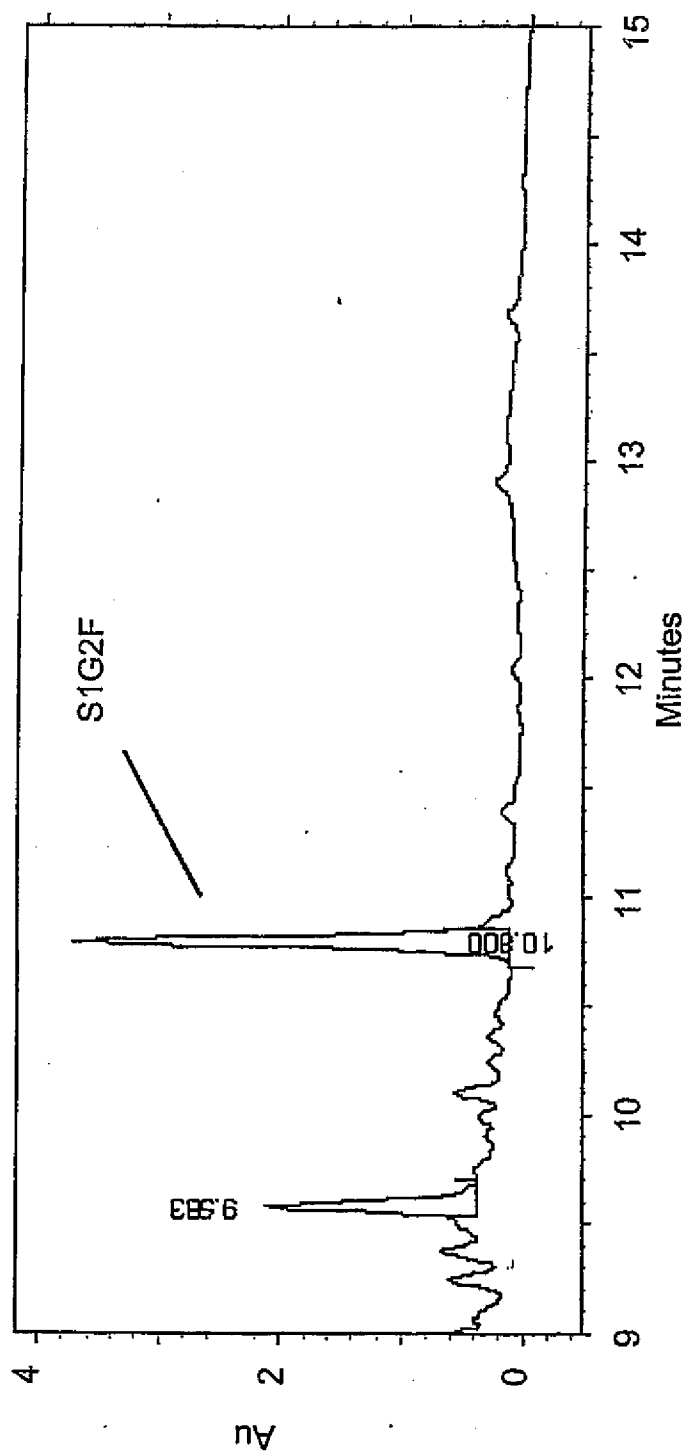


FIG. 115B

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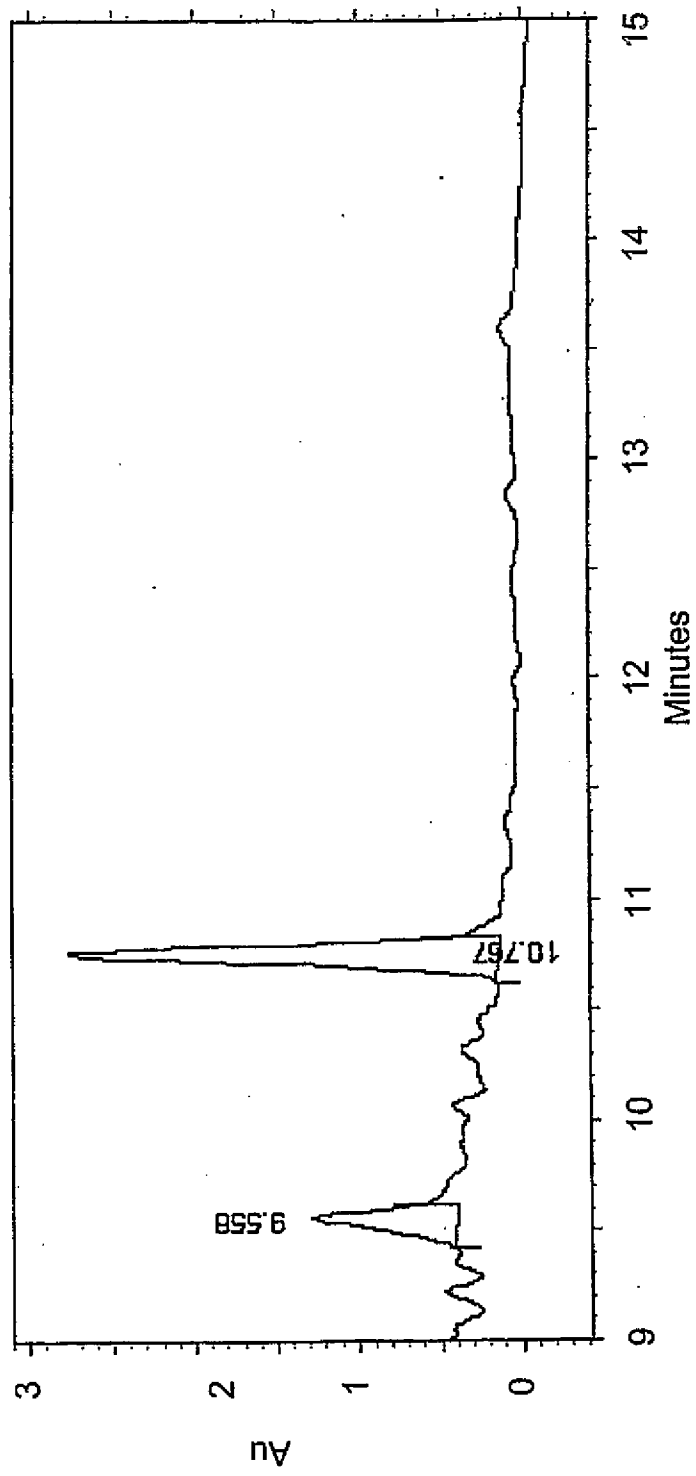


FIG. 115C

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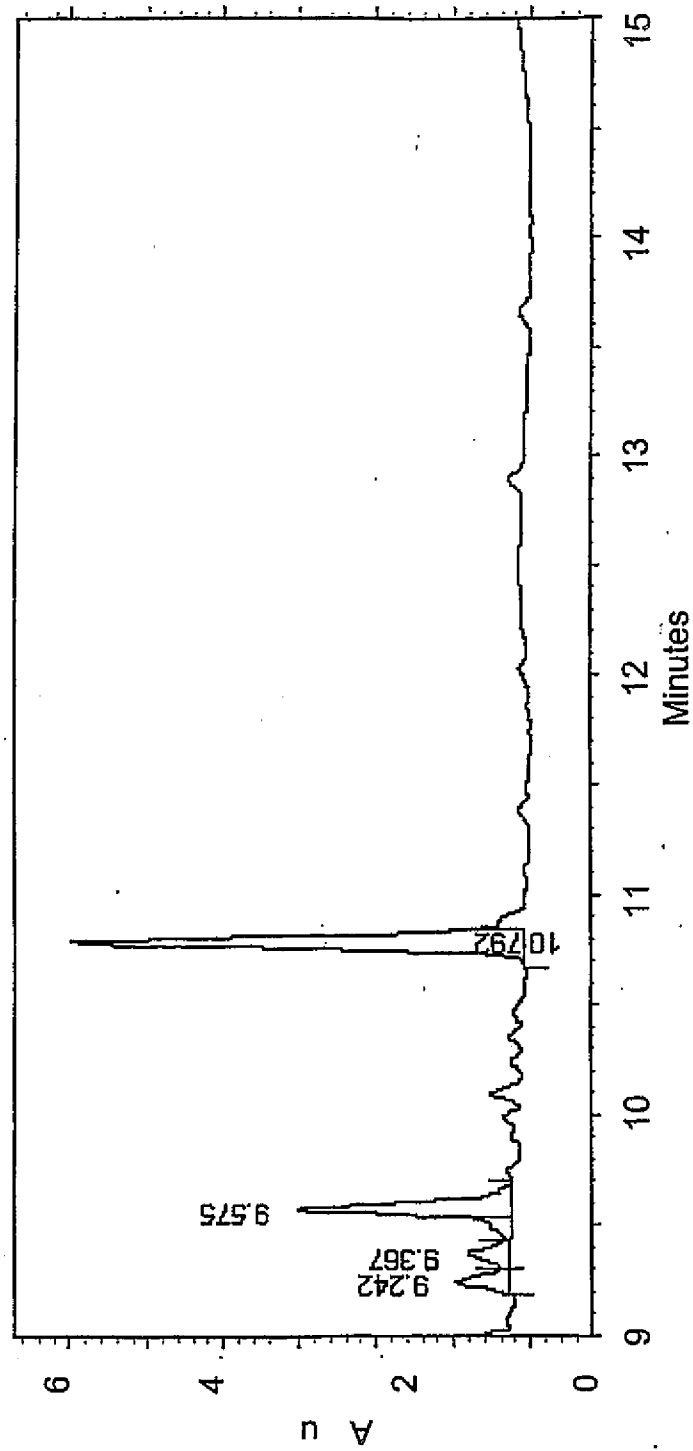


FIG. 115D

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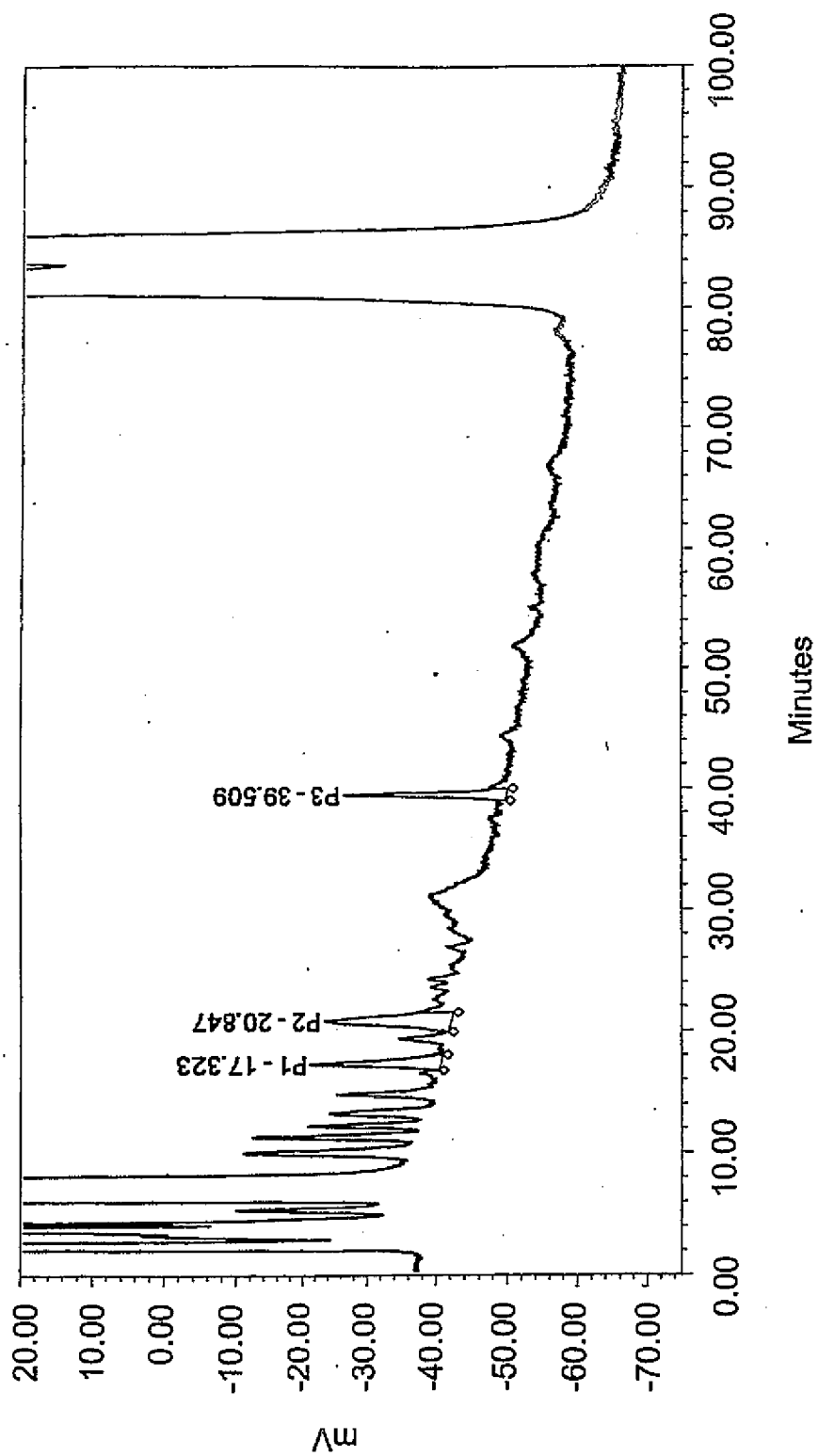


FIG. 116A

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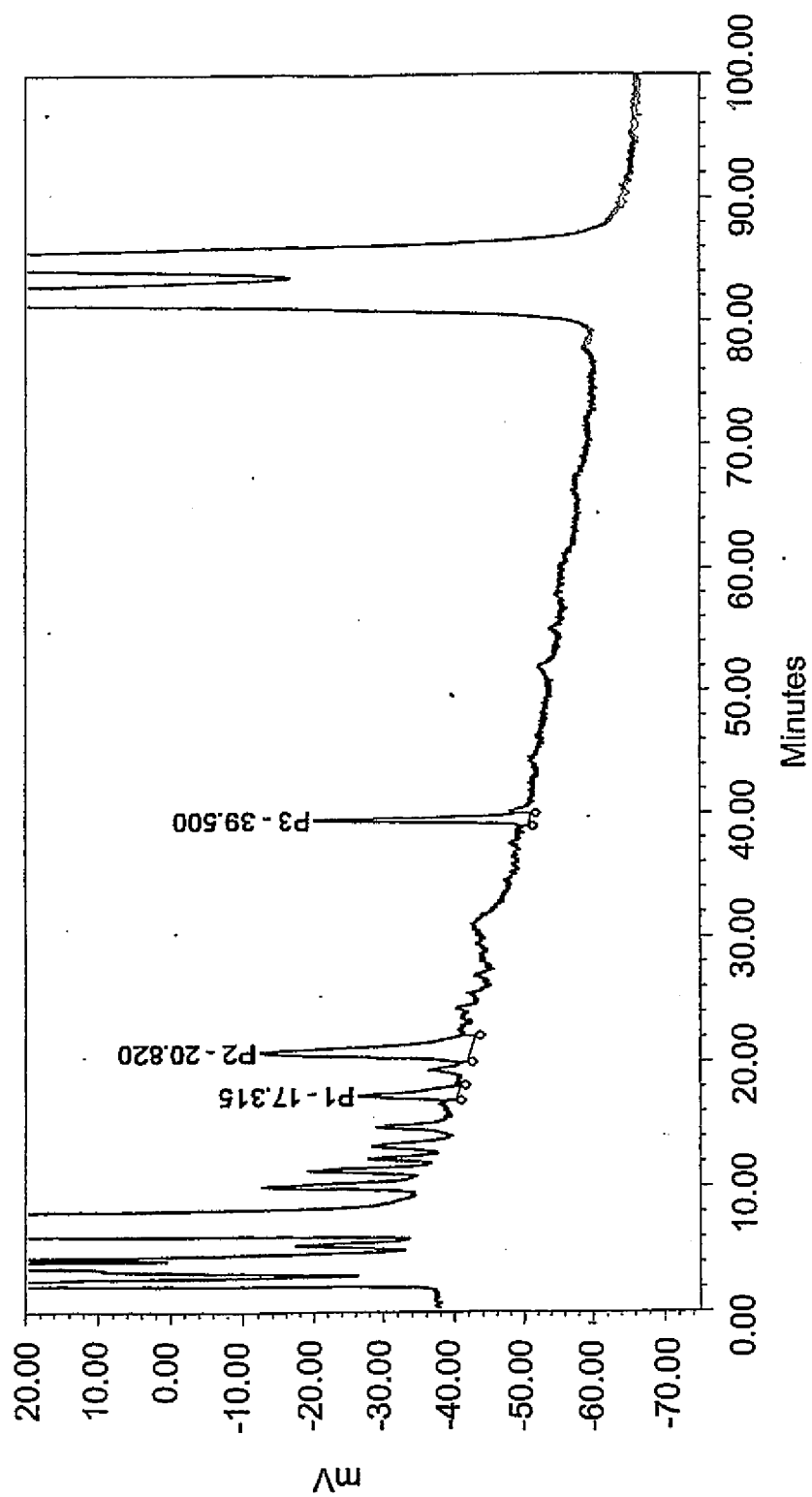


FIG. 116B

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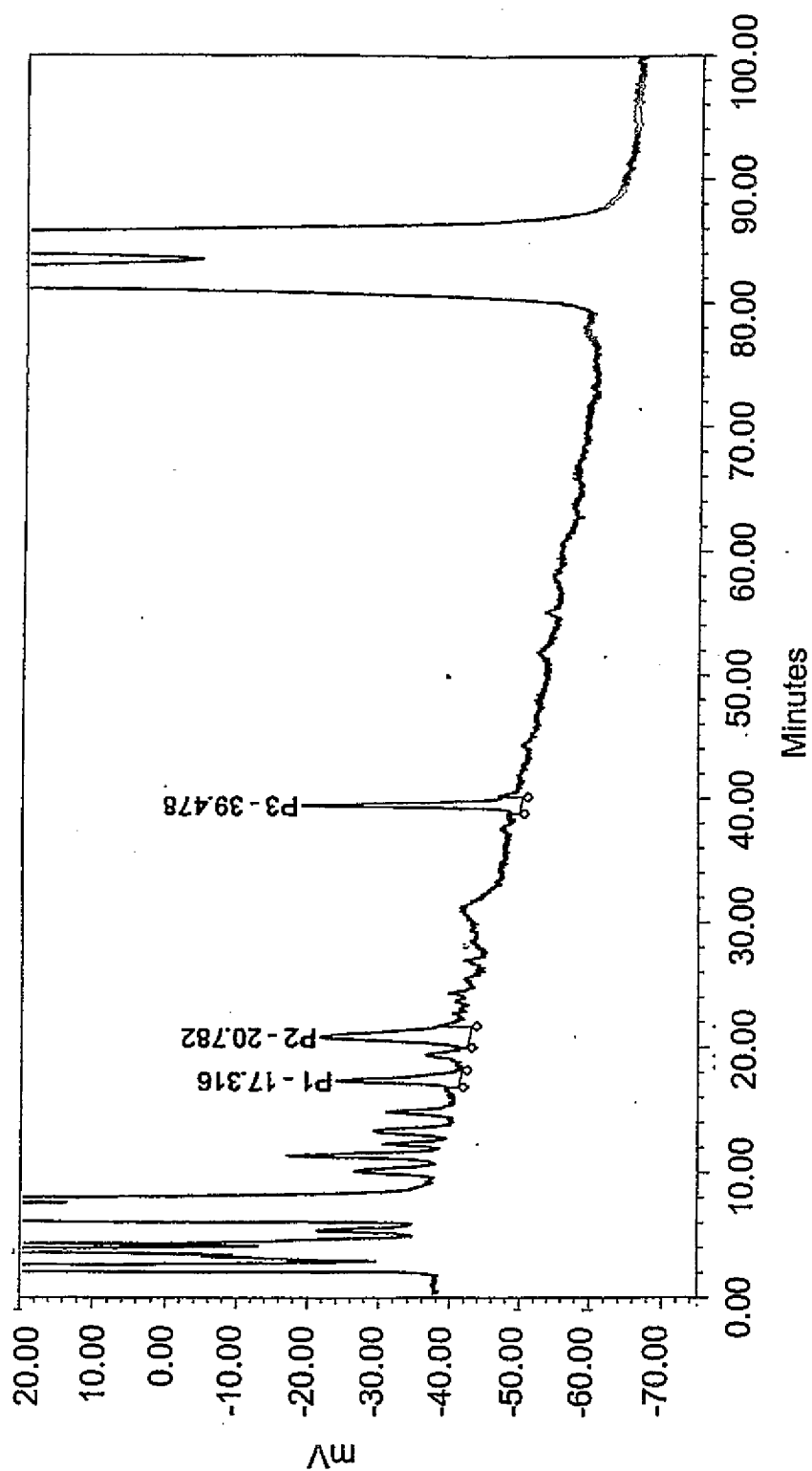


FIG. 116C

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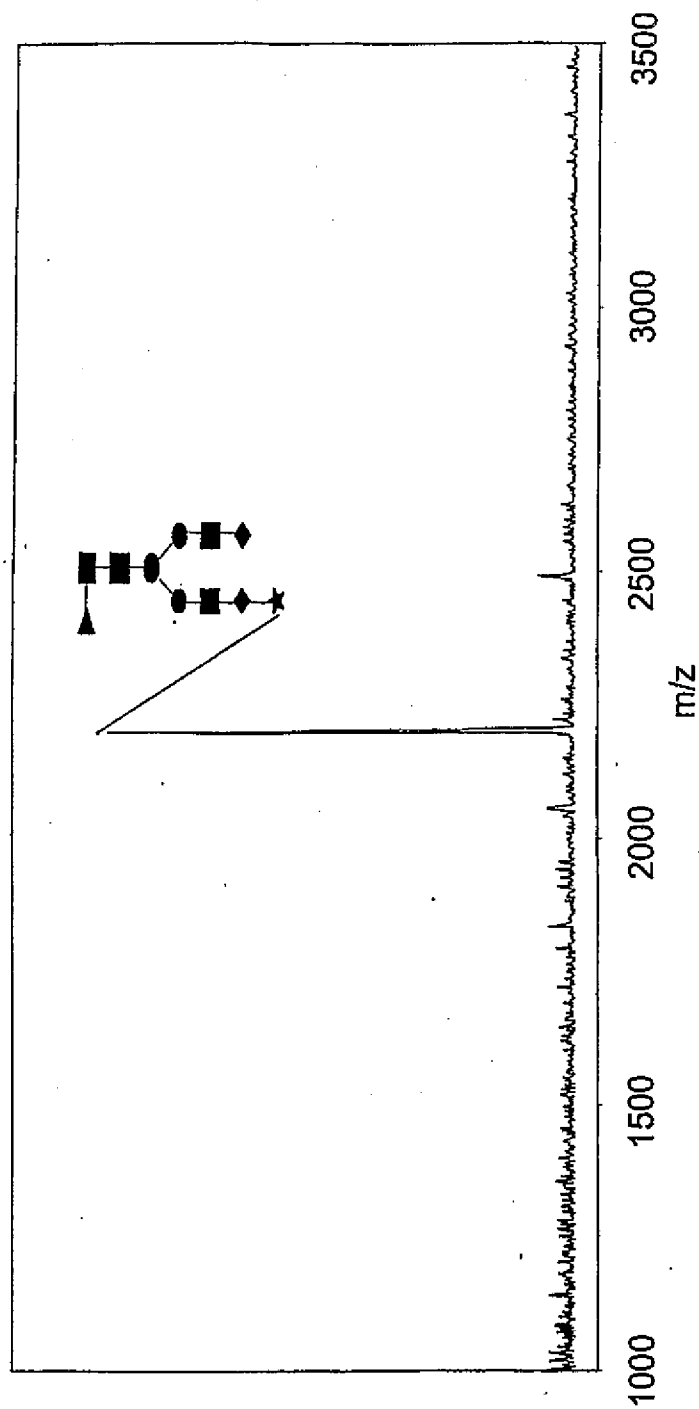


FIG. 117A

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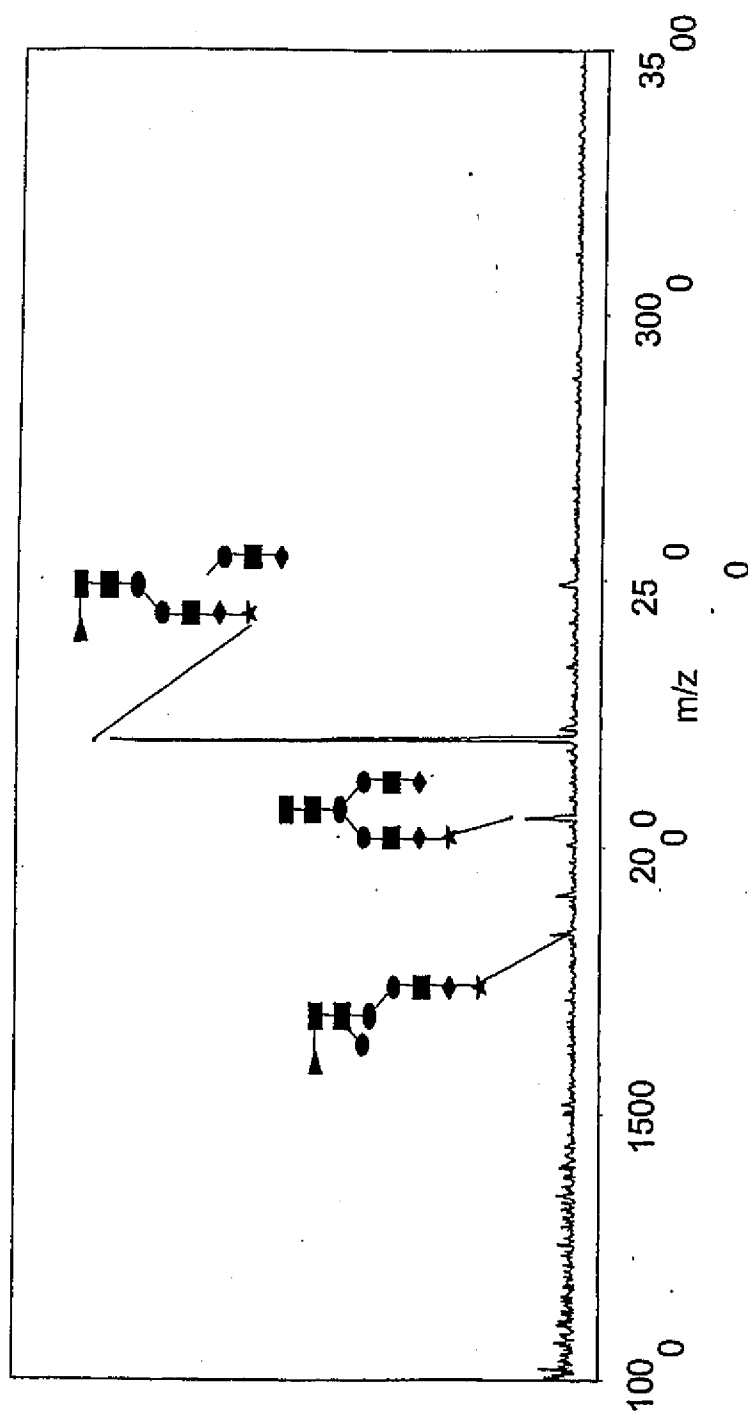


FIG. 17B

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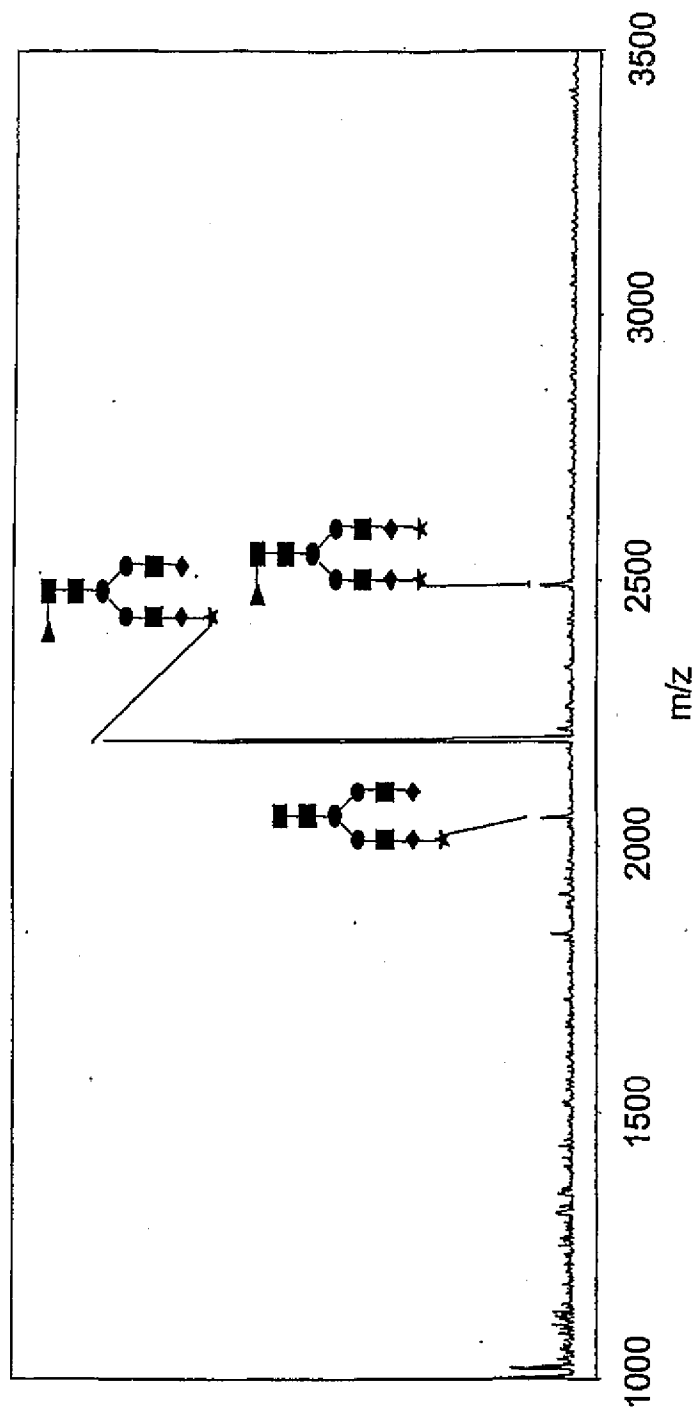


FIG. 117C

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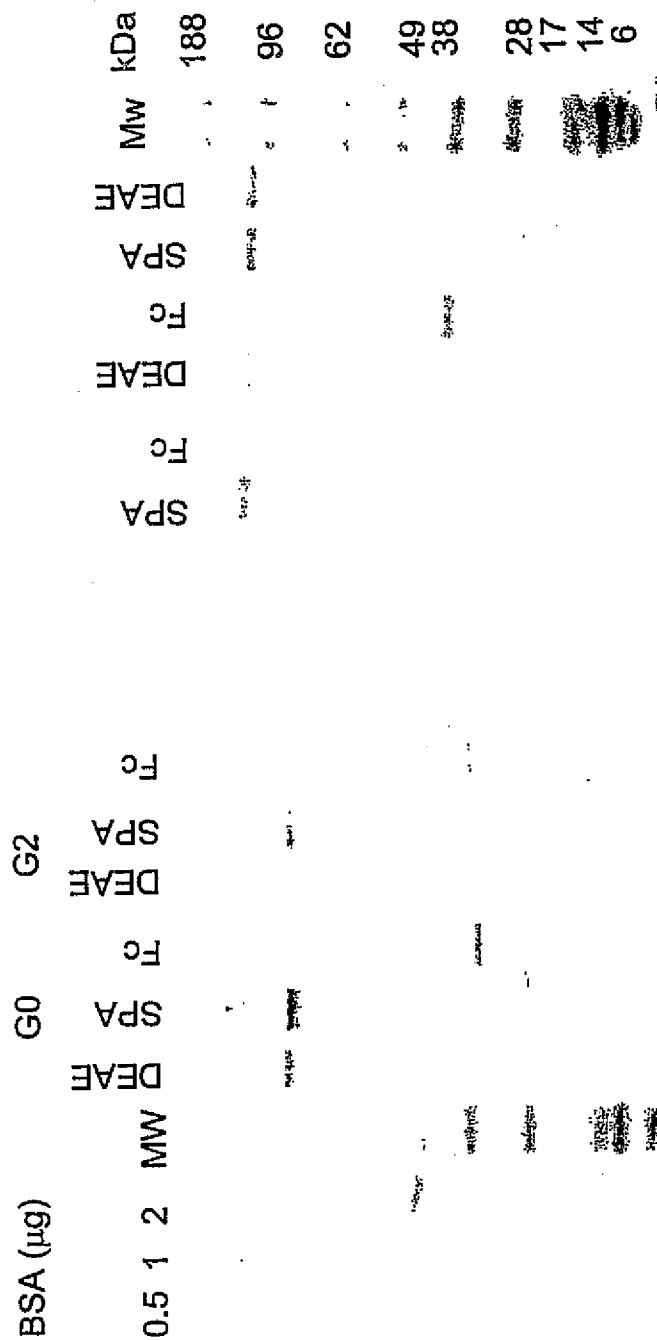


FIG. 118B

FIG. 118A

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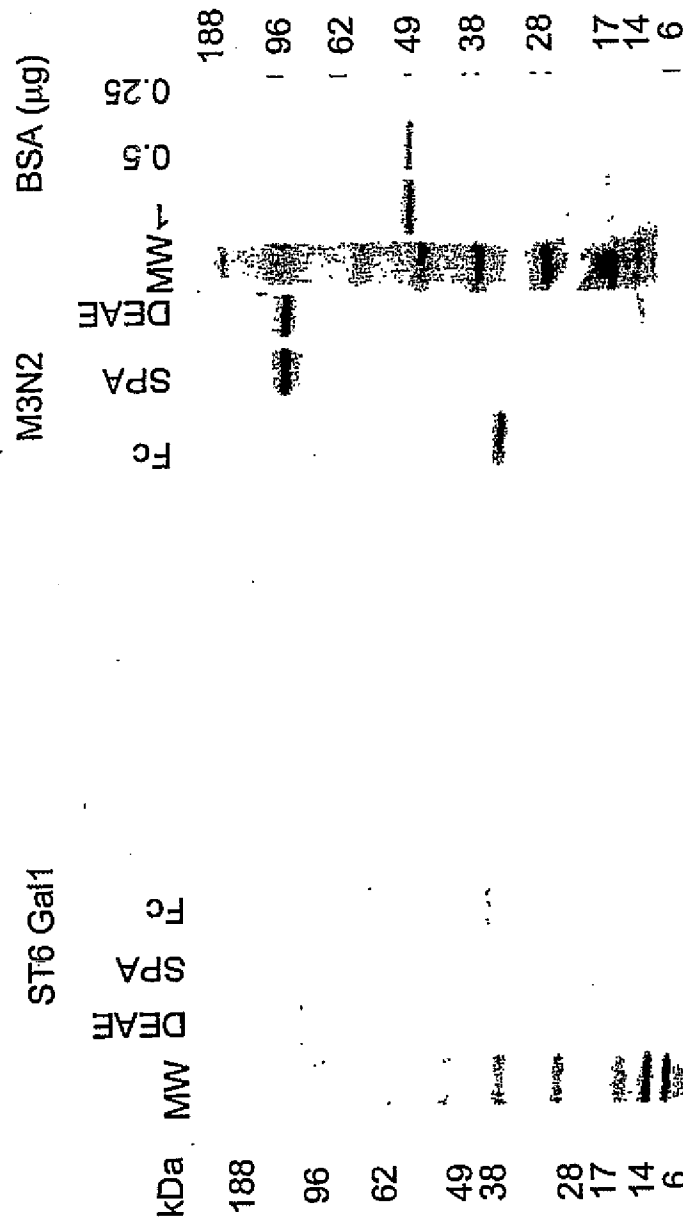


FIG. 118D

FIG. 118C

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BSA (μg)	Gal-bisecting
0	DEAE
2	Fc
5	SPA
1	

FIG 118E

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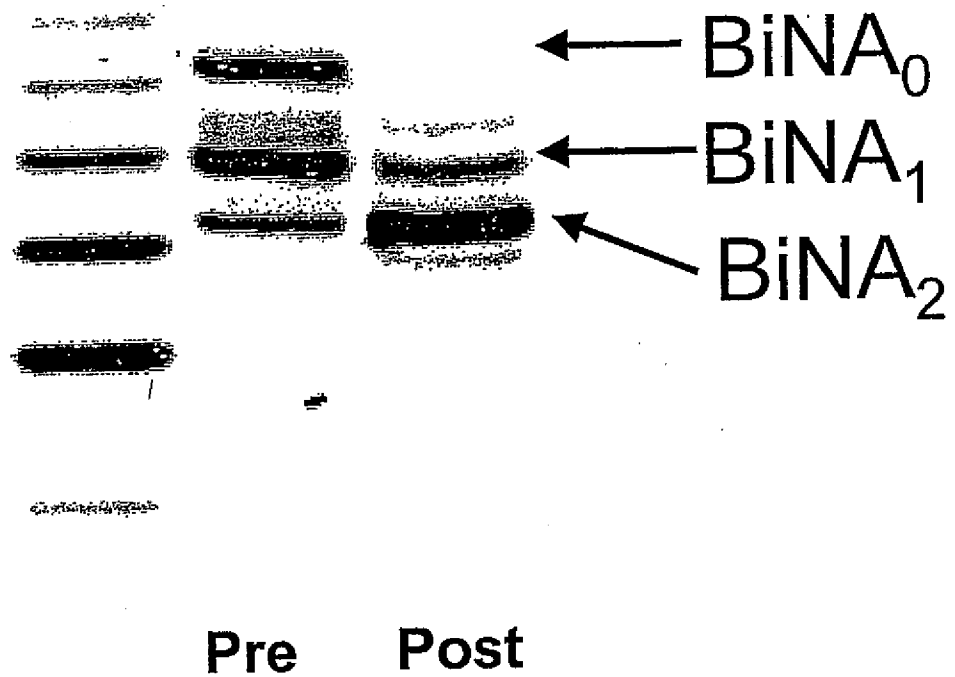


FIG. 119

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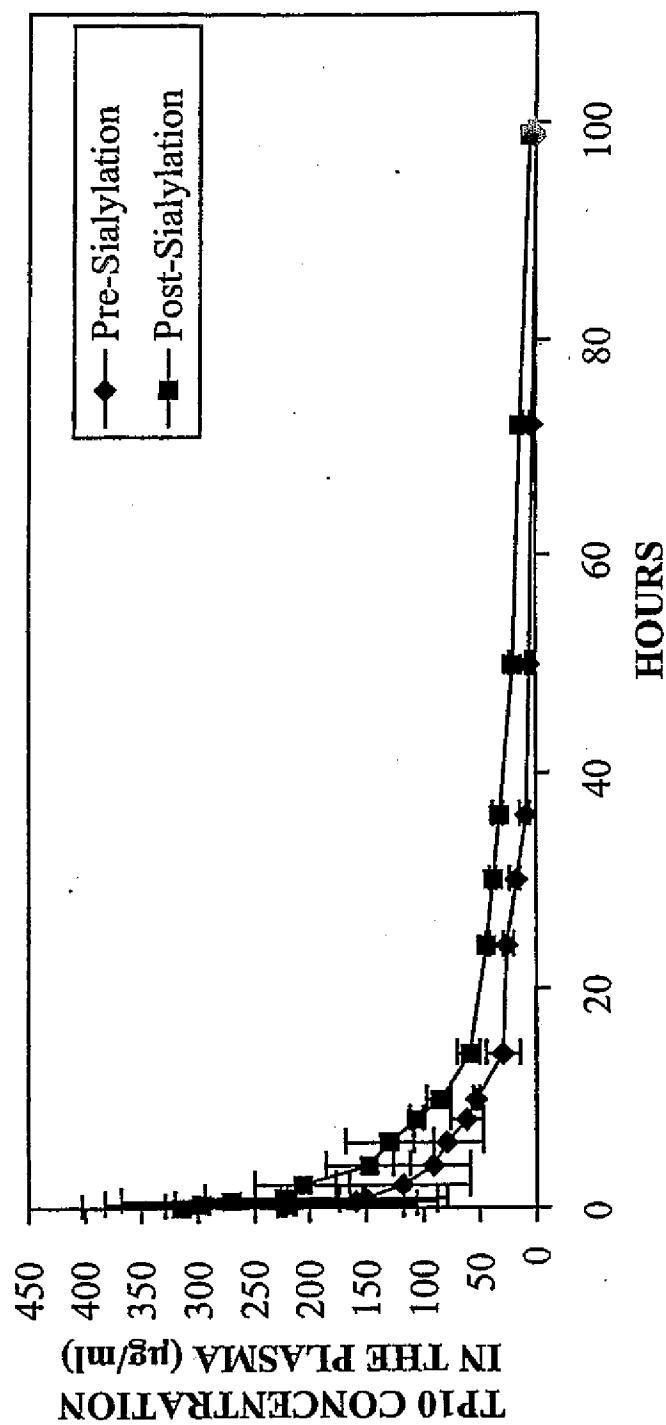


FIG. 120

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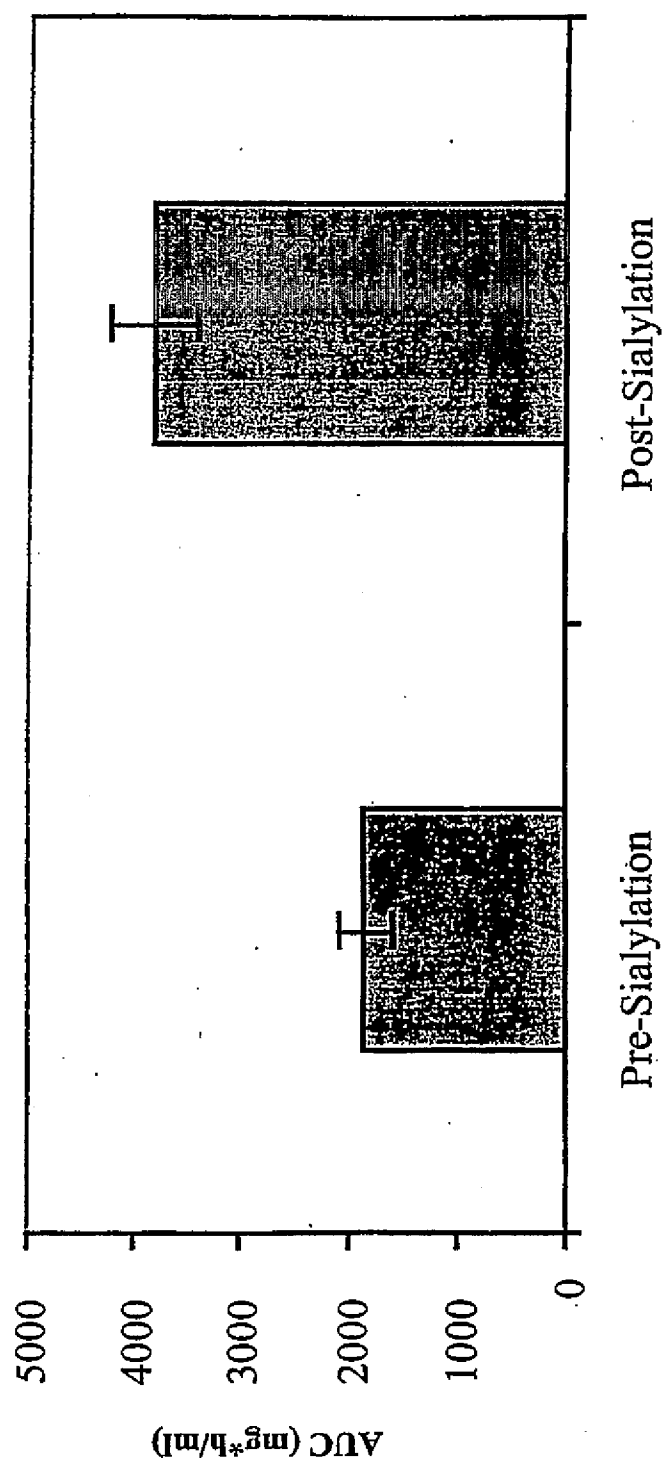


FIG. 121

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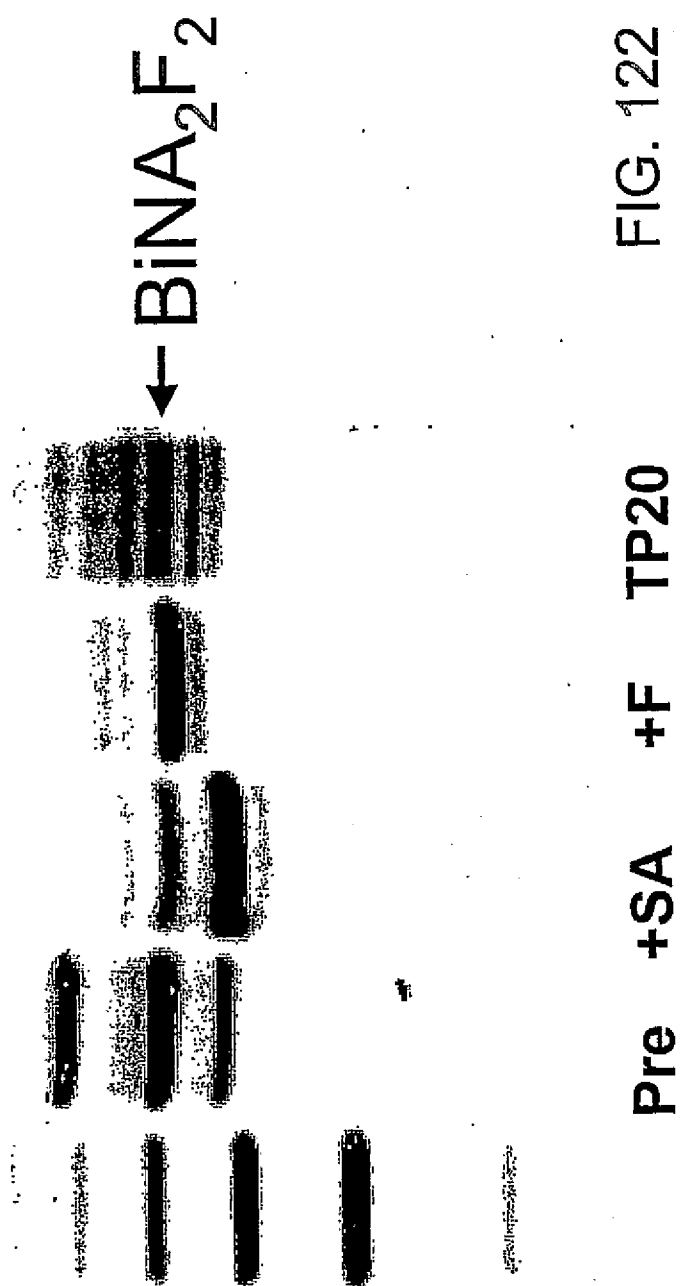


FIG. 122

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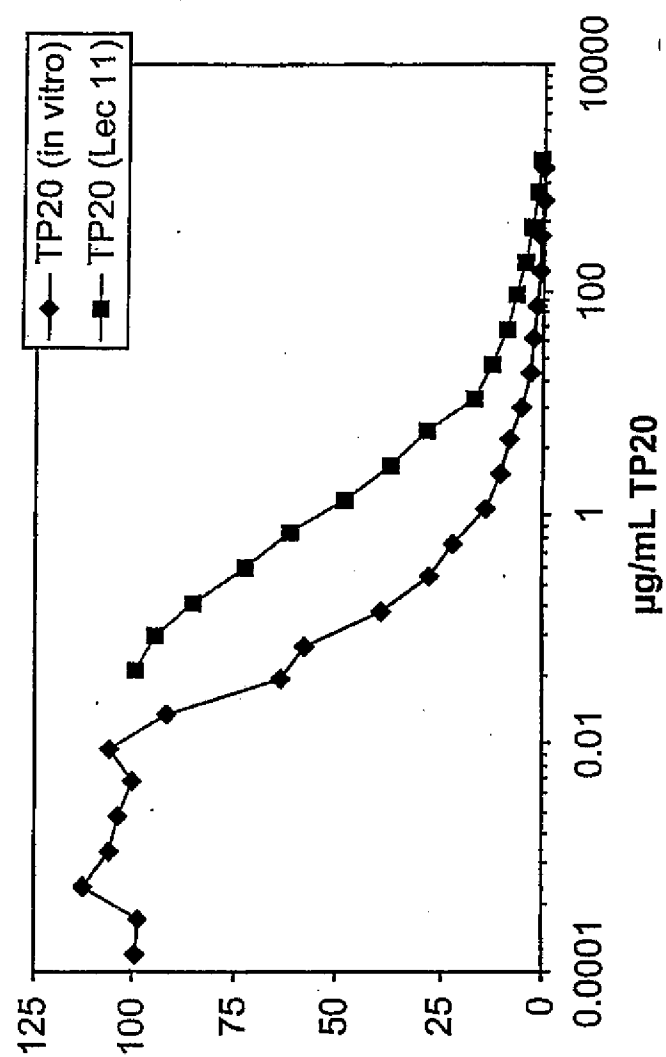


FIG. 123

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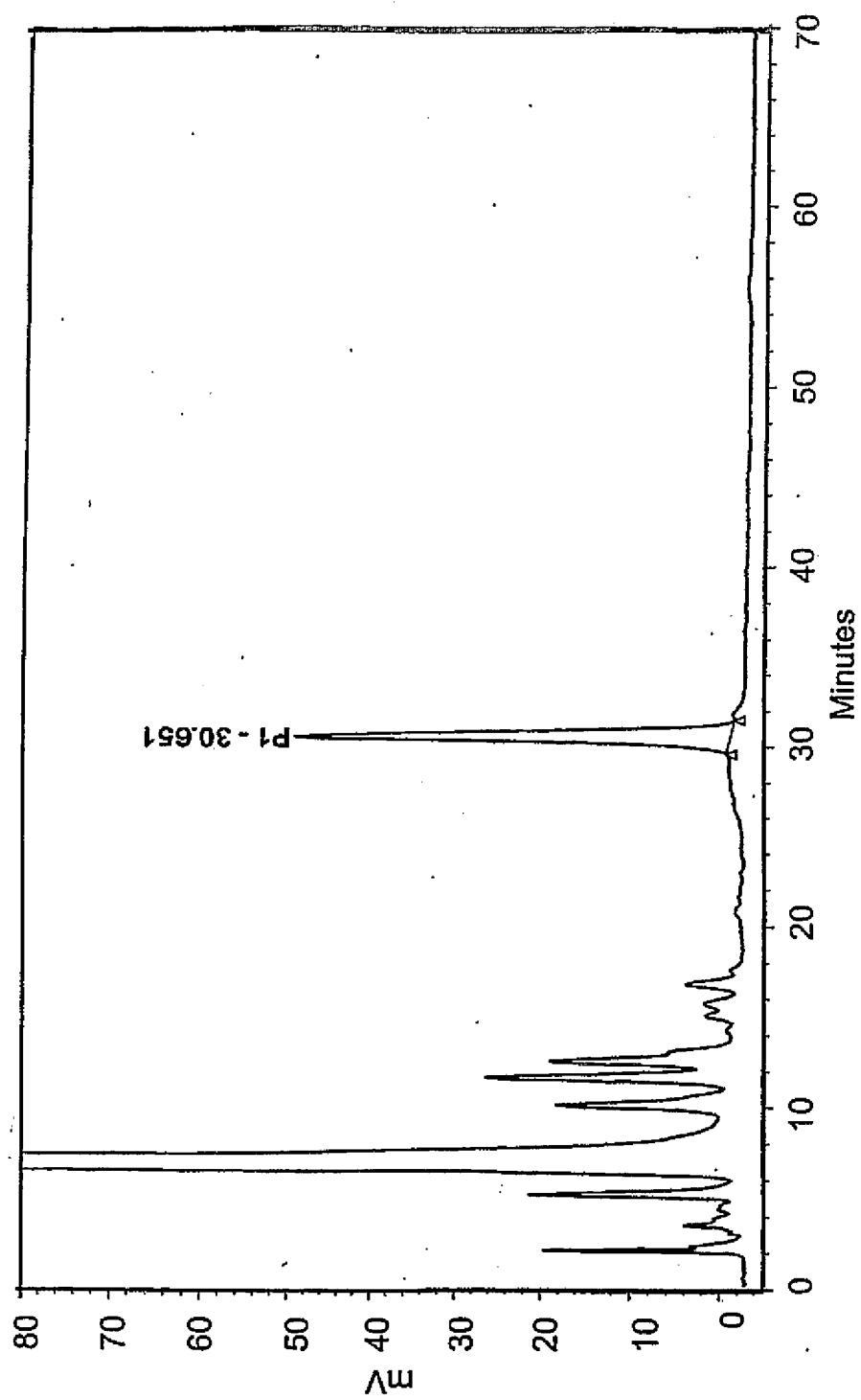


FIG. 124

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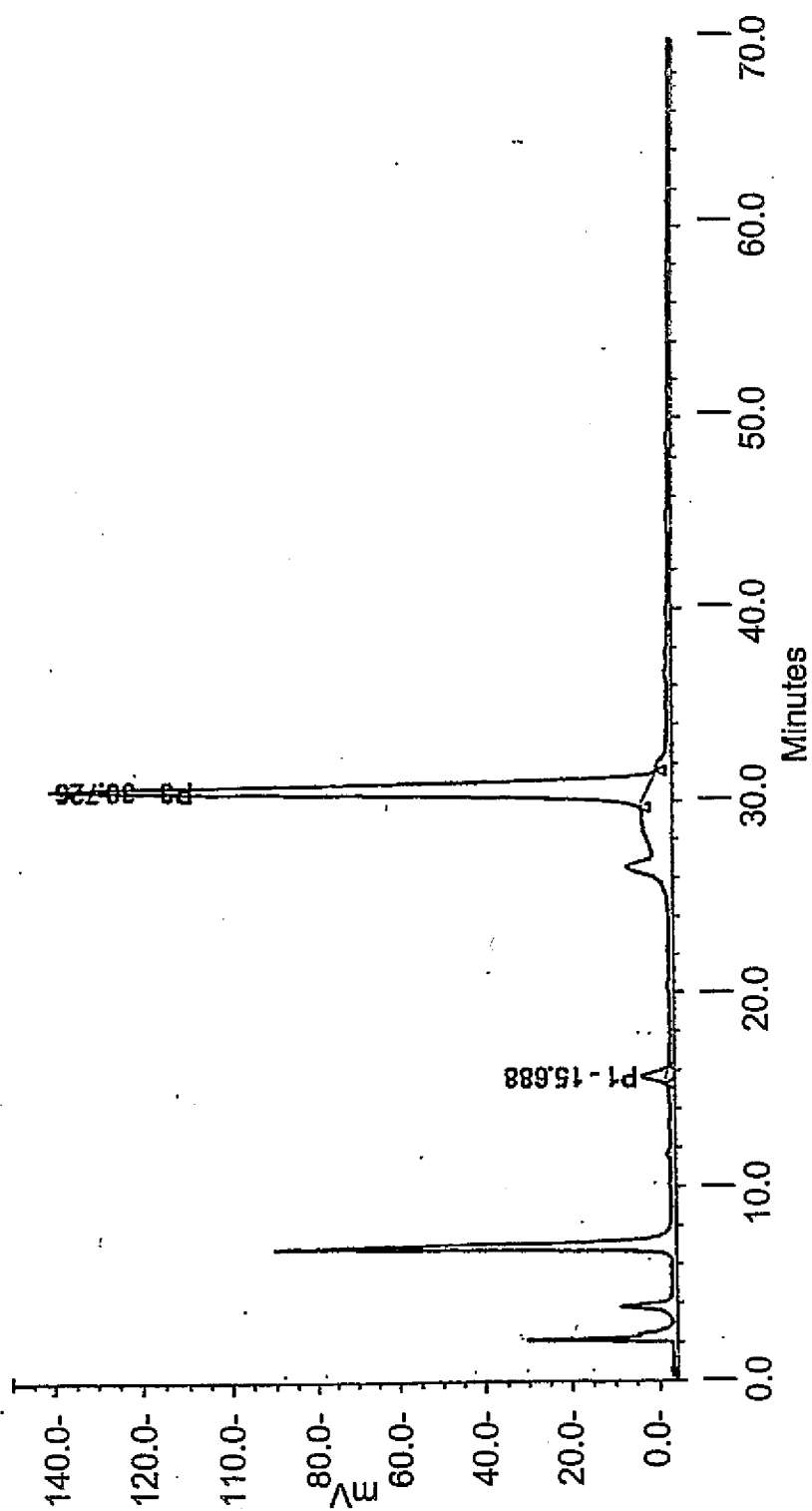


FIG. 125A

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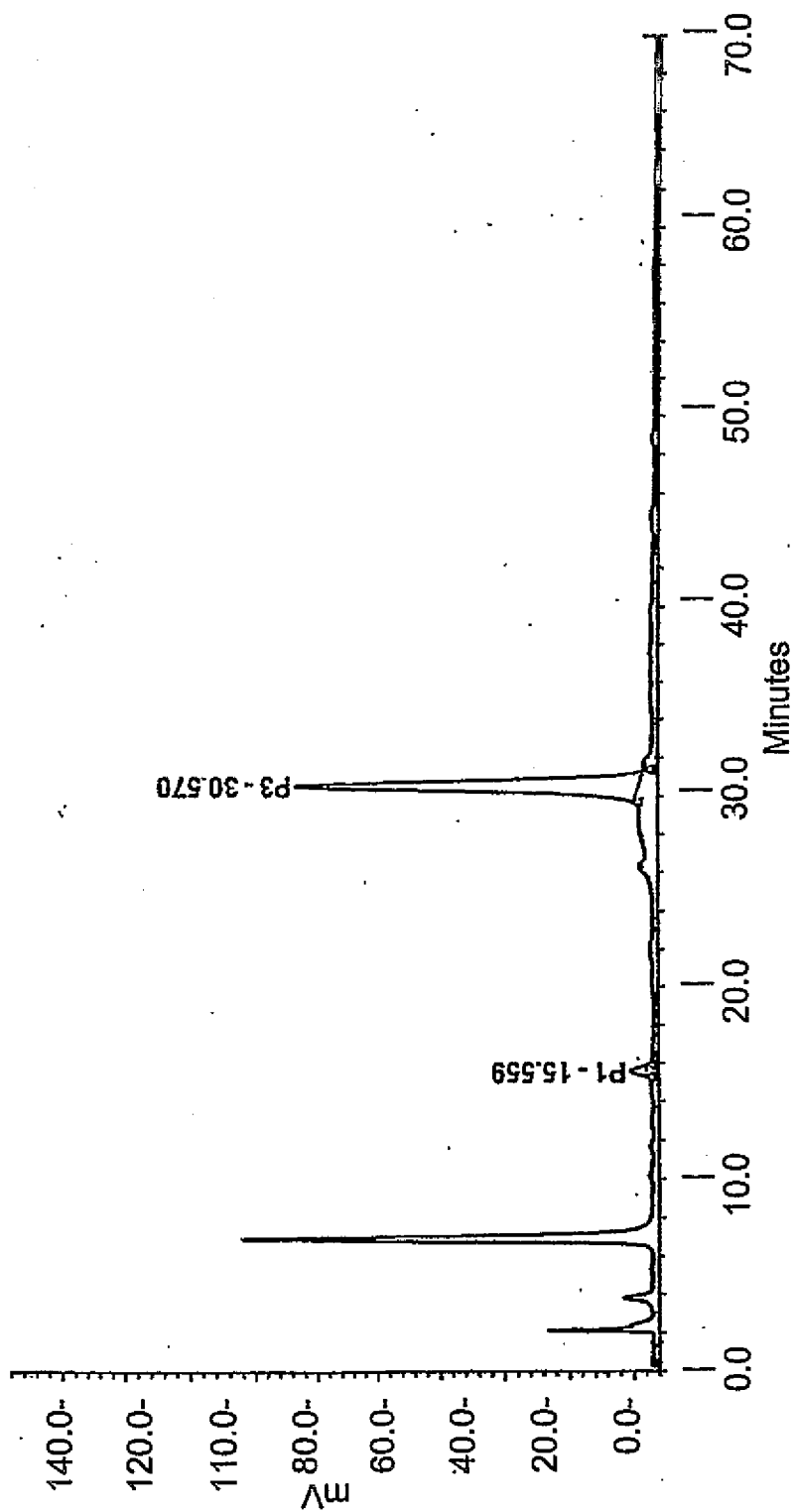


FIG. 125B

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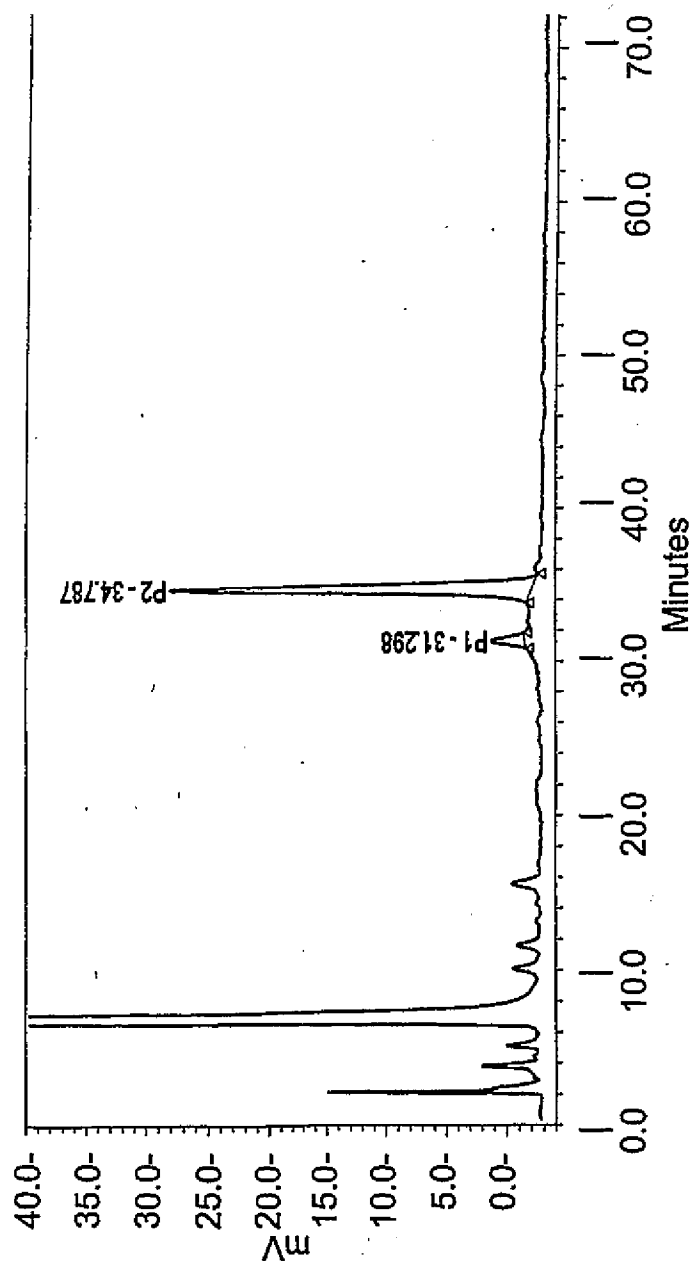
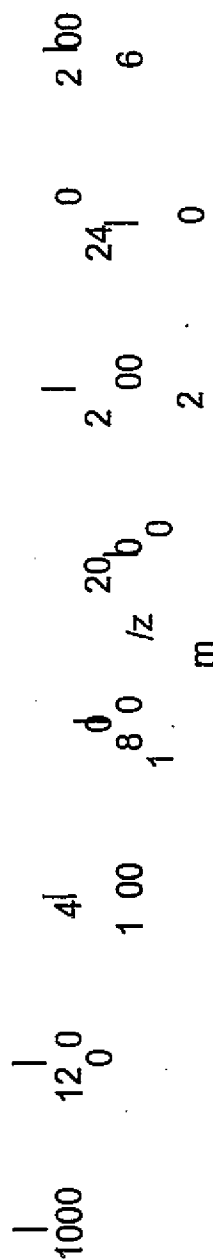
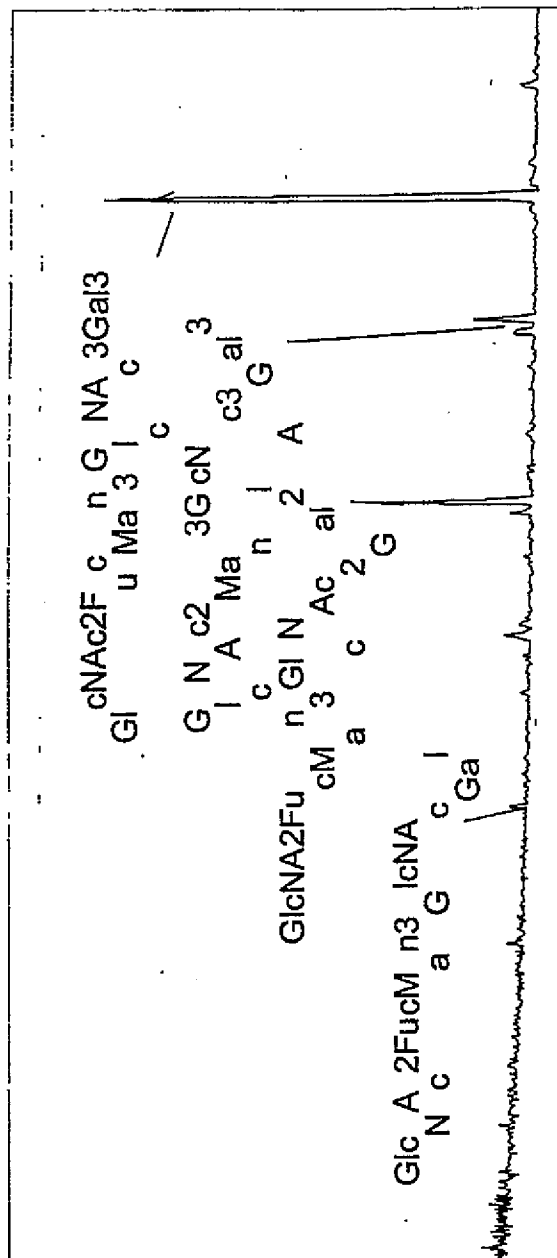


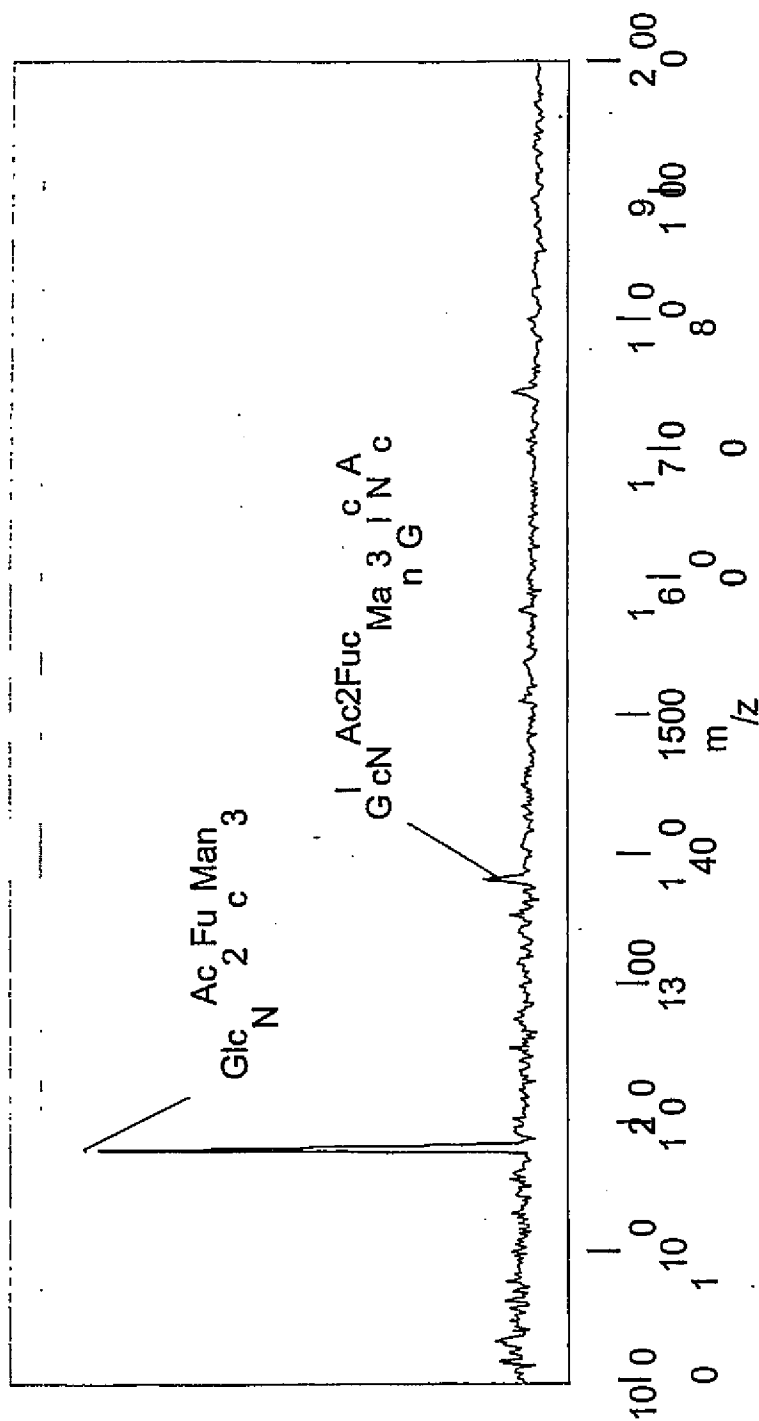
FIG. 126

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F₁₂₇G₁₂₇

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F₁G. 128

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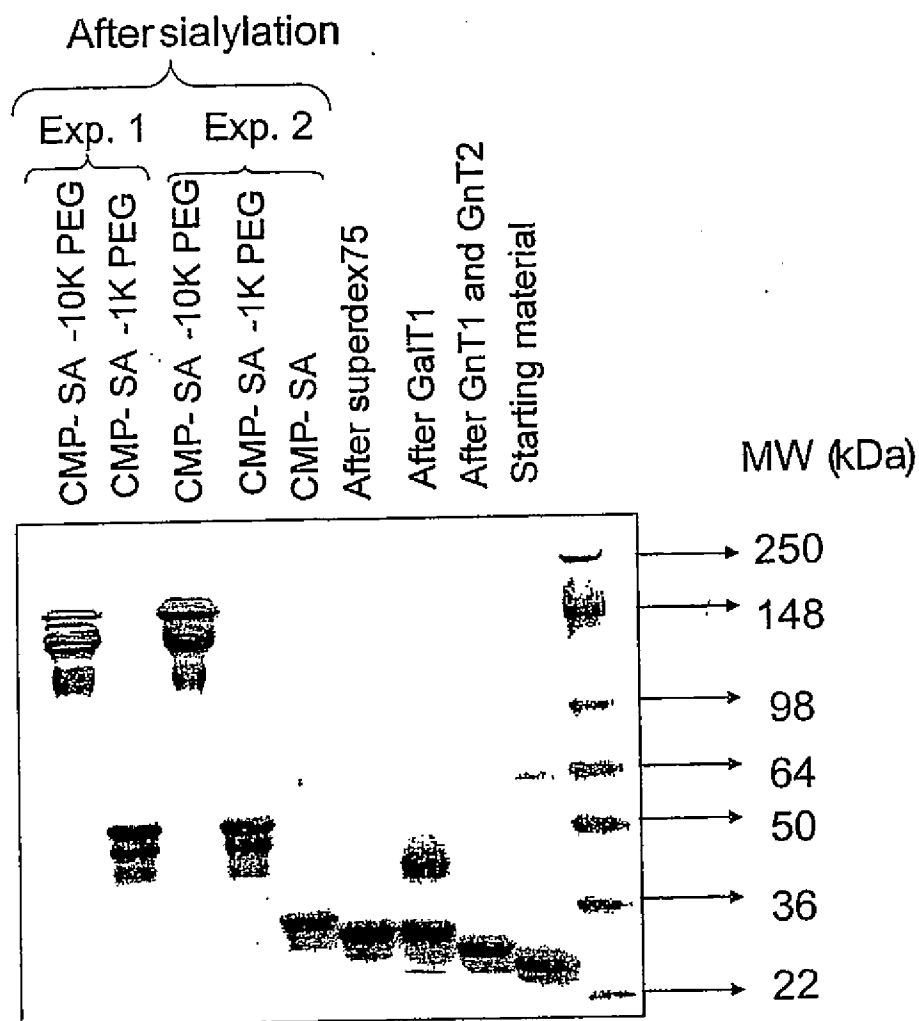
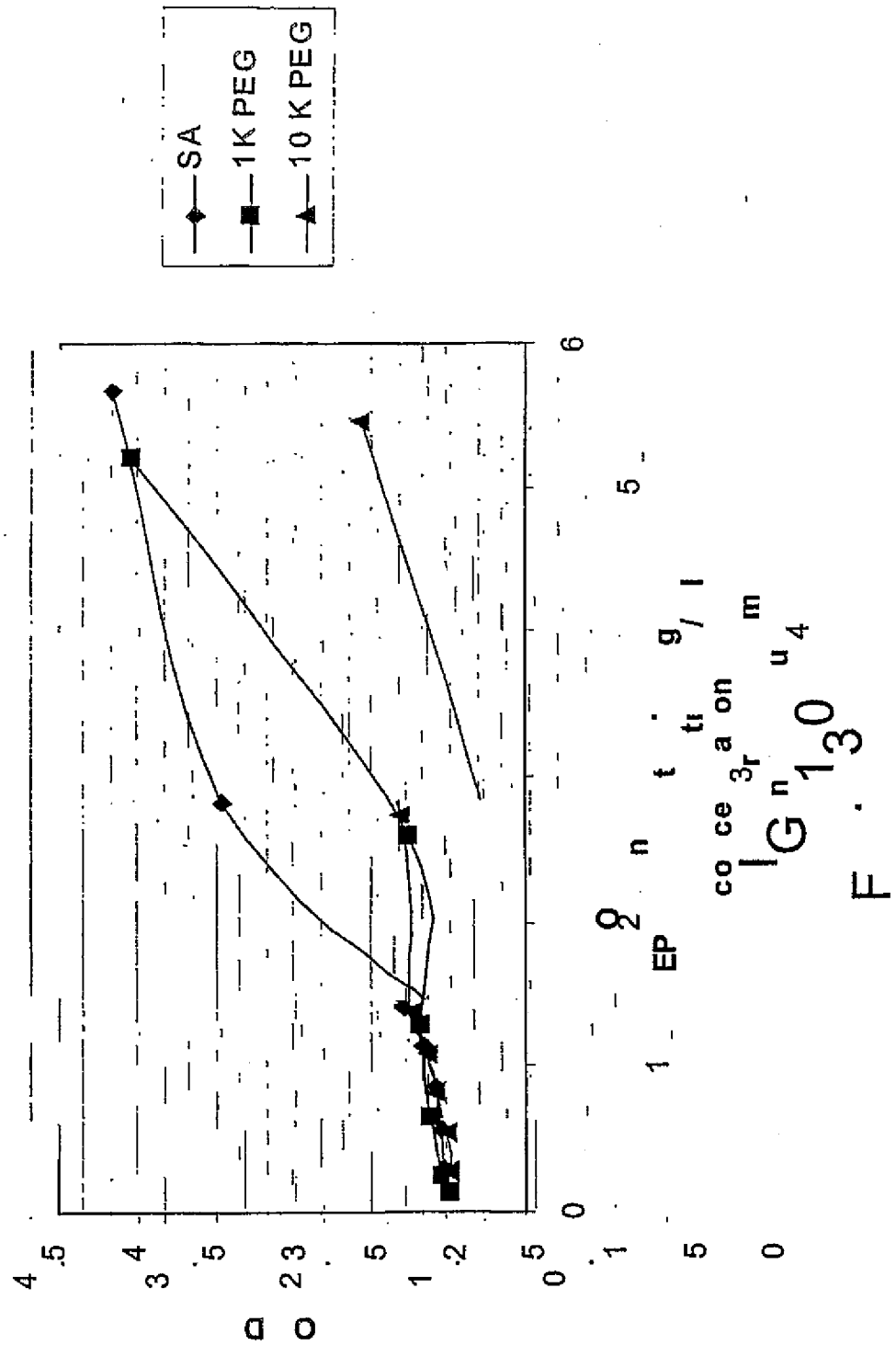
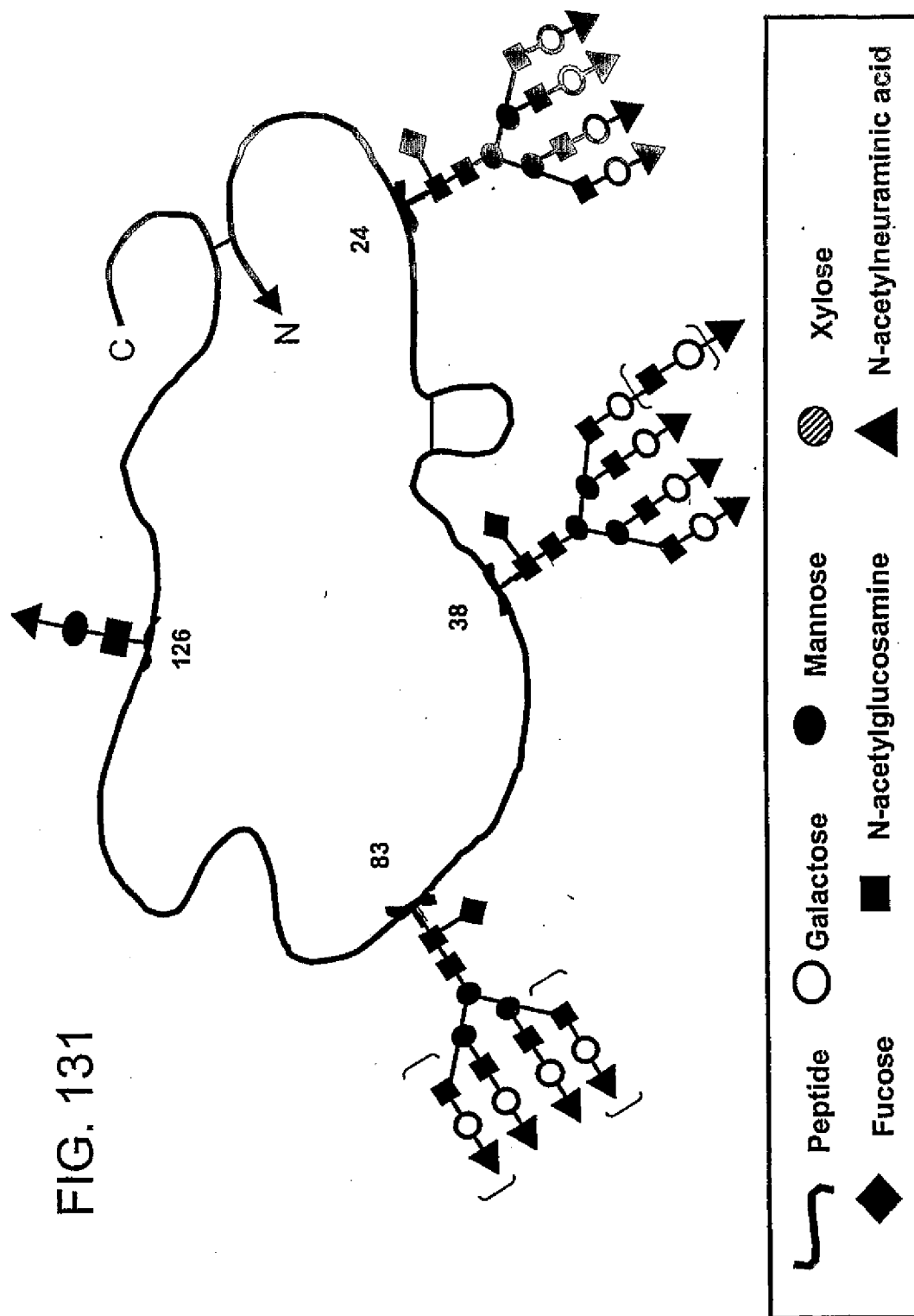


FIG. 129

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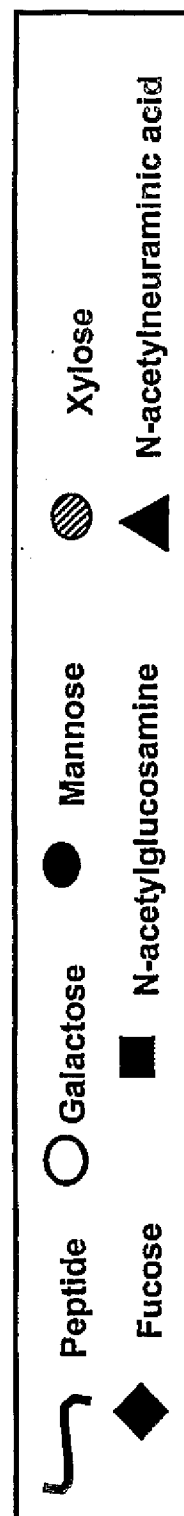
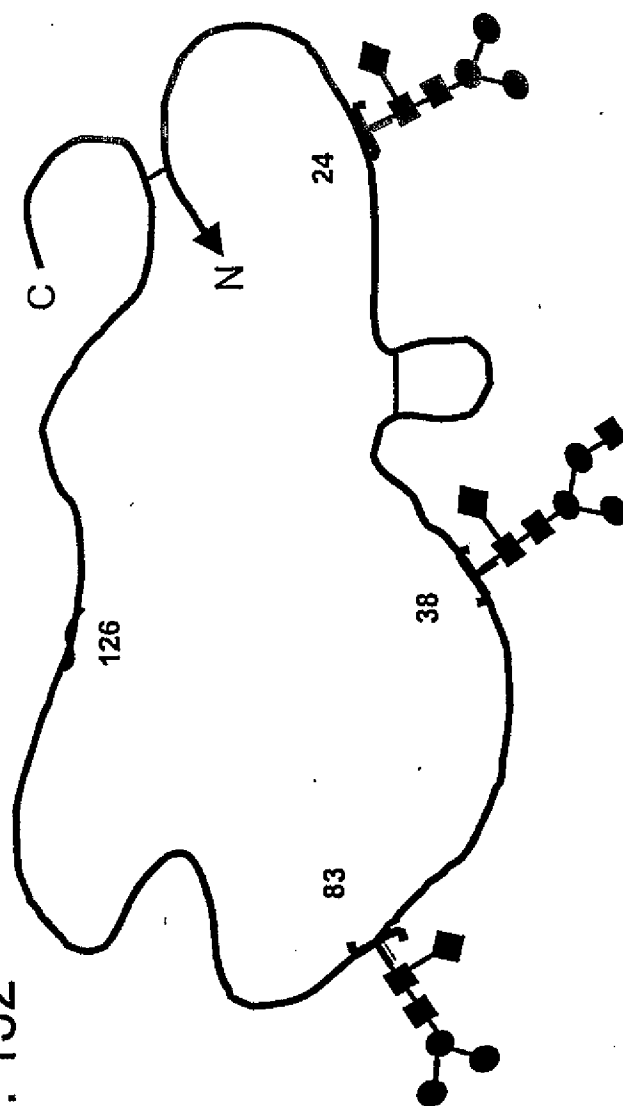


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FIG. 132



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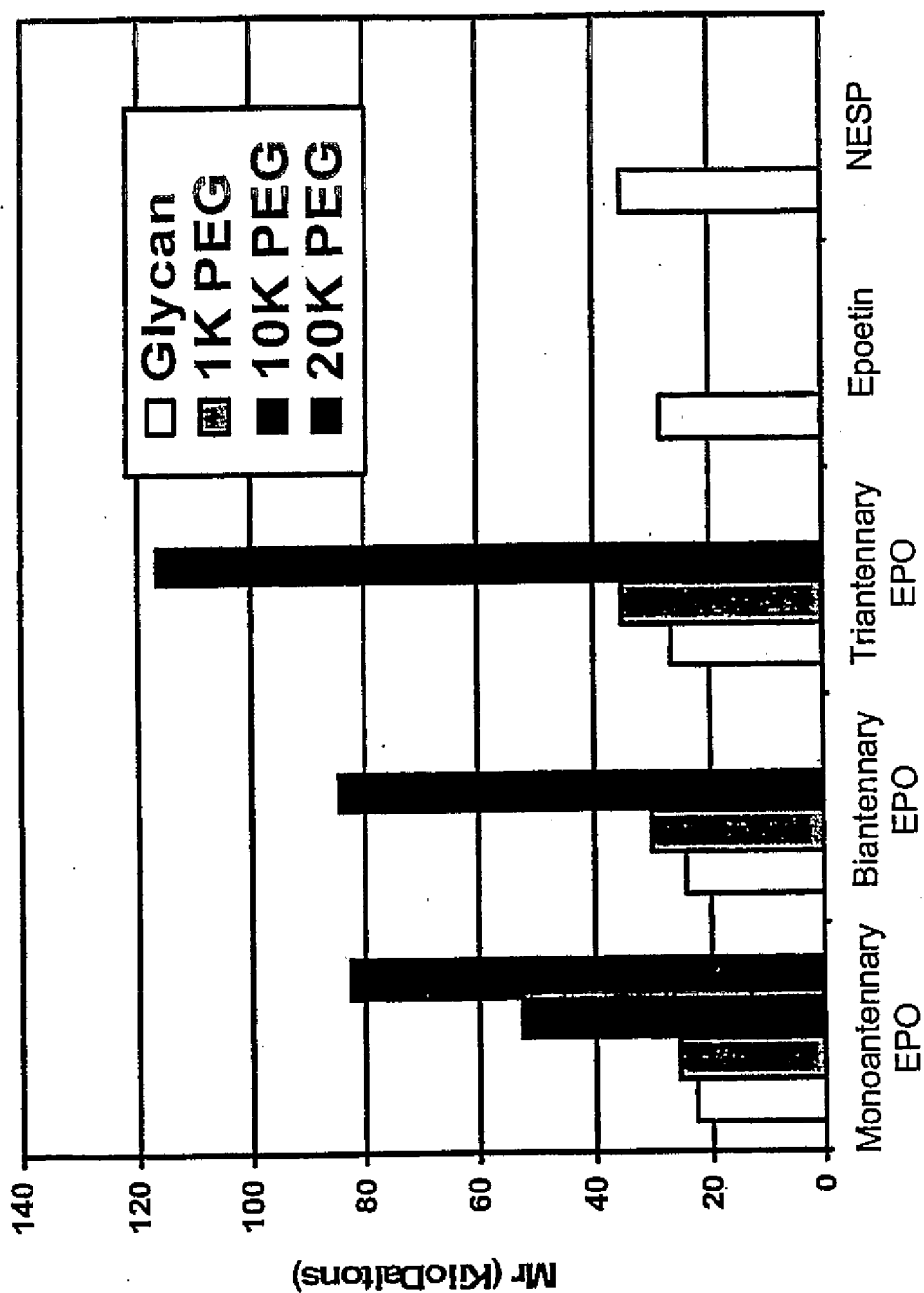
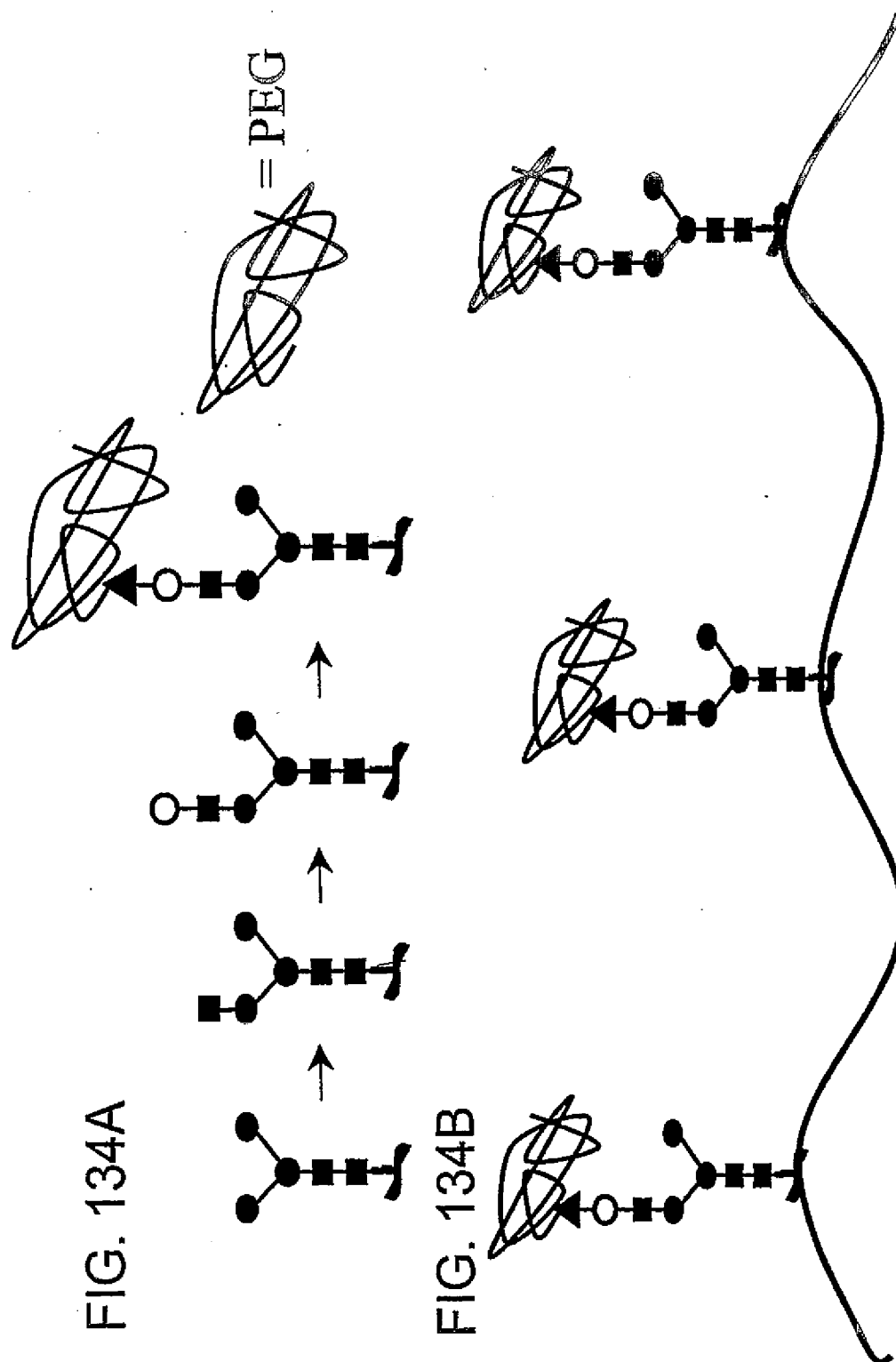


FIG. 133

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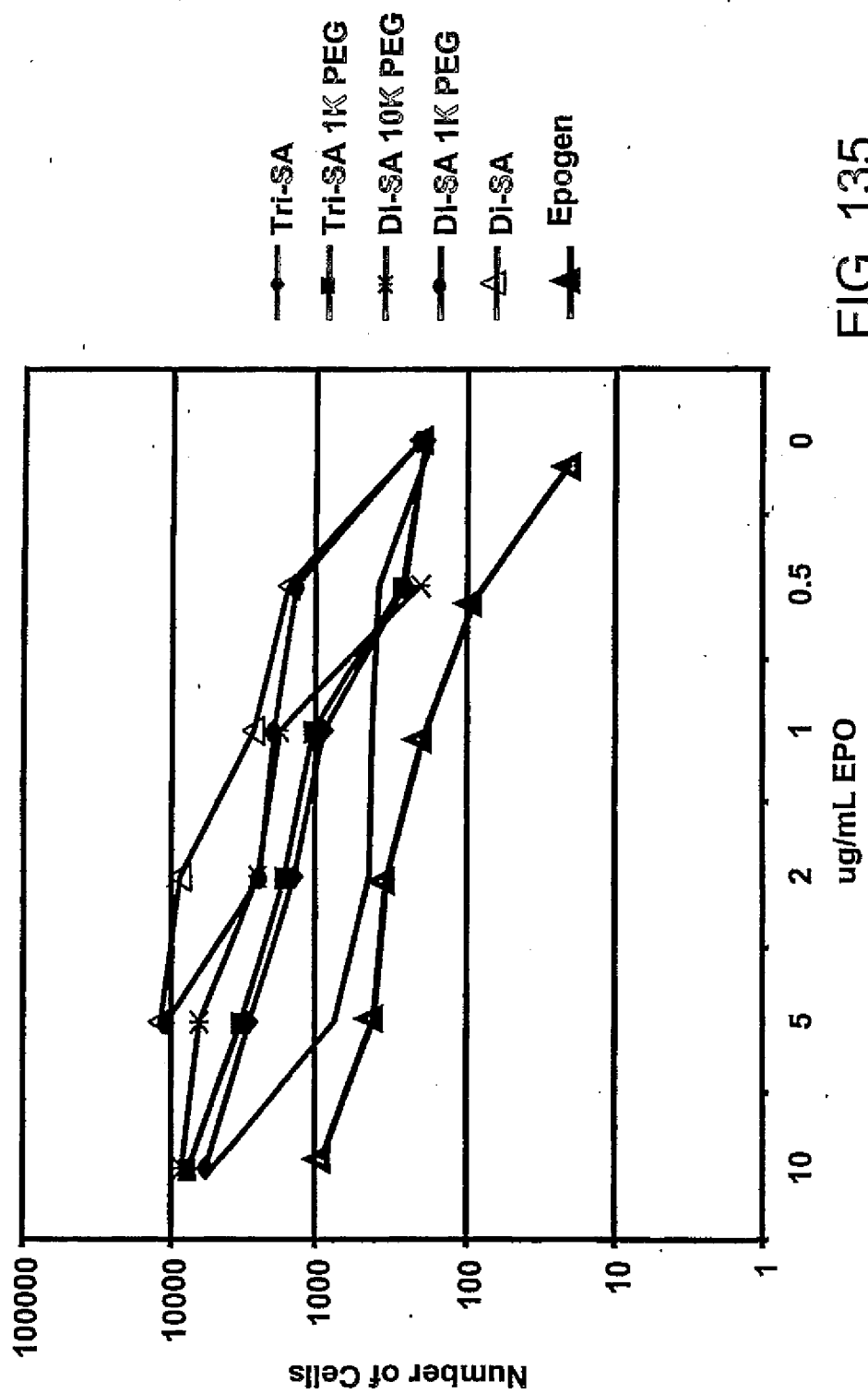


FIG. 135

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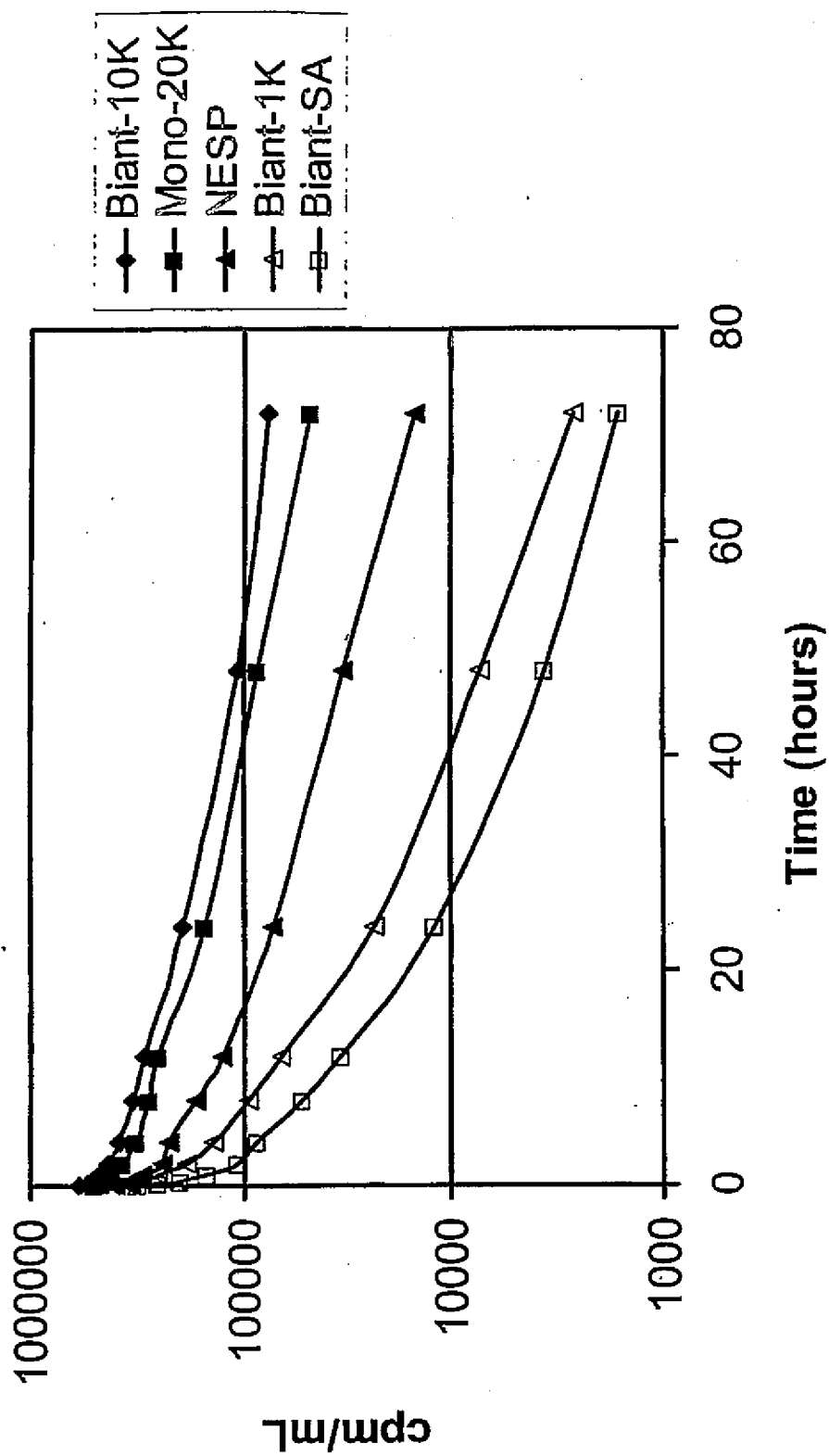


FIG. 136

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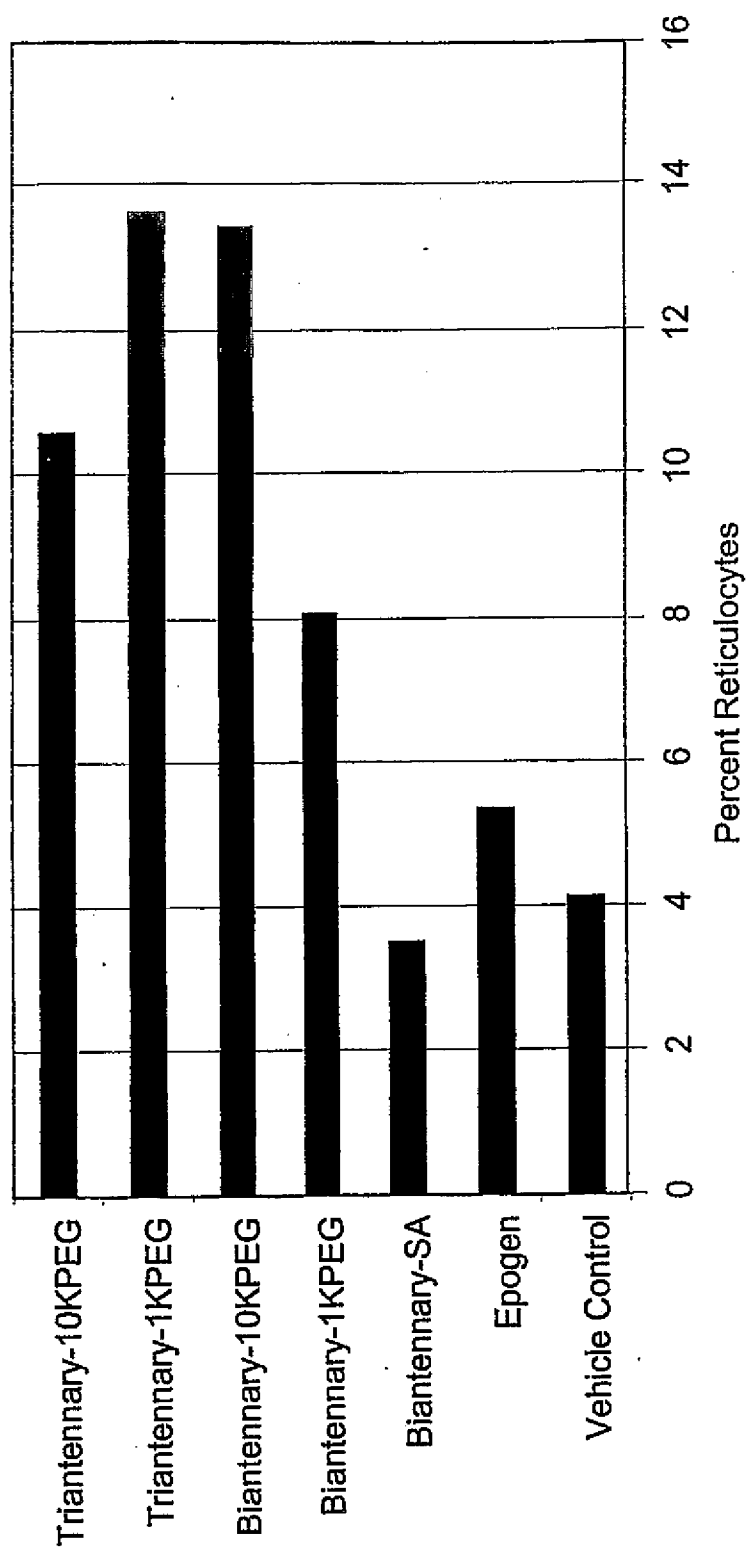


FIG. 137

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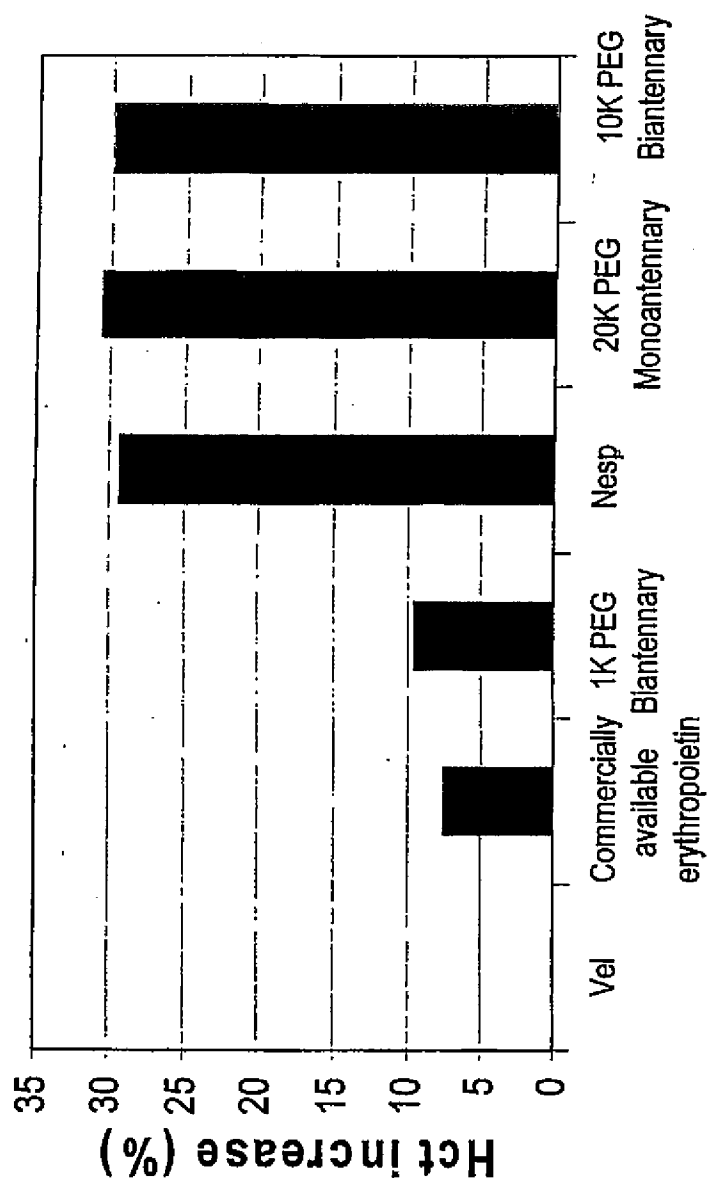


FIG. 138

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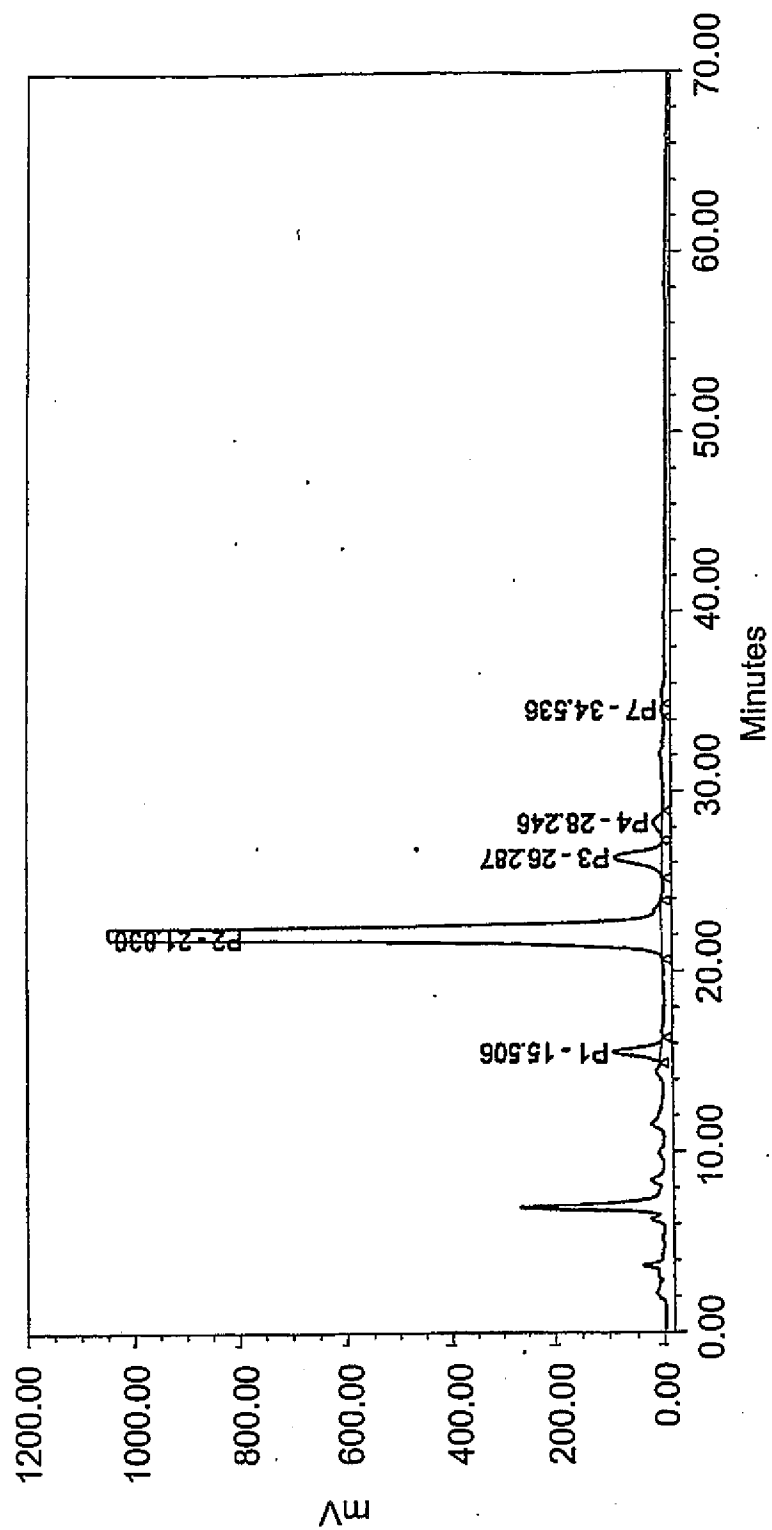


FIG. 139A

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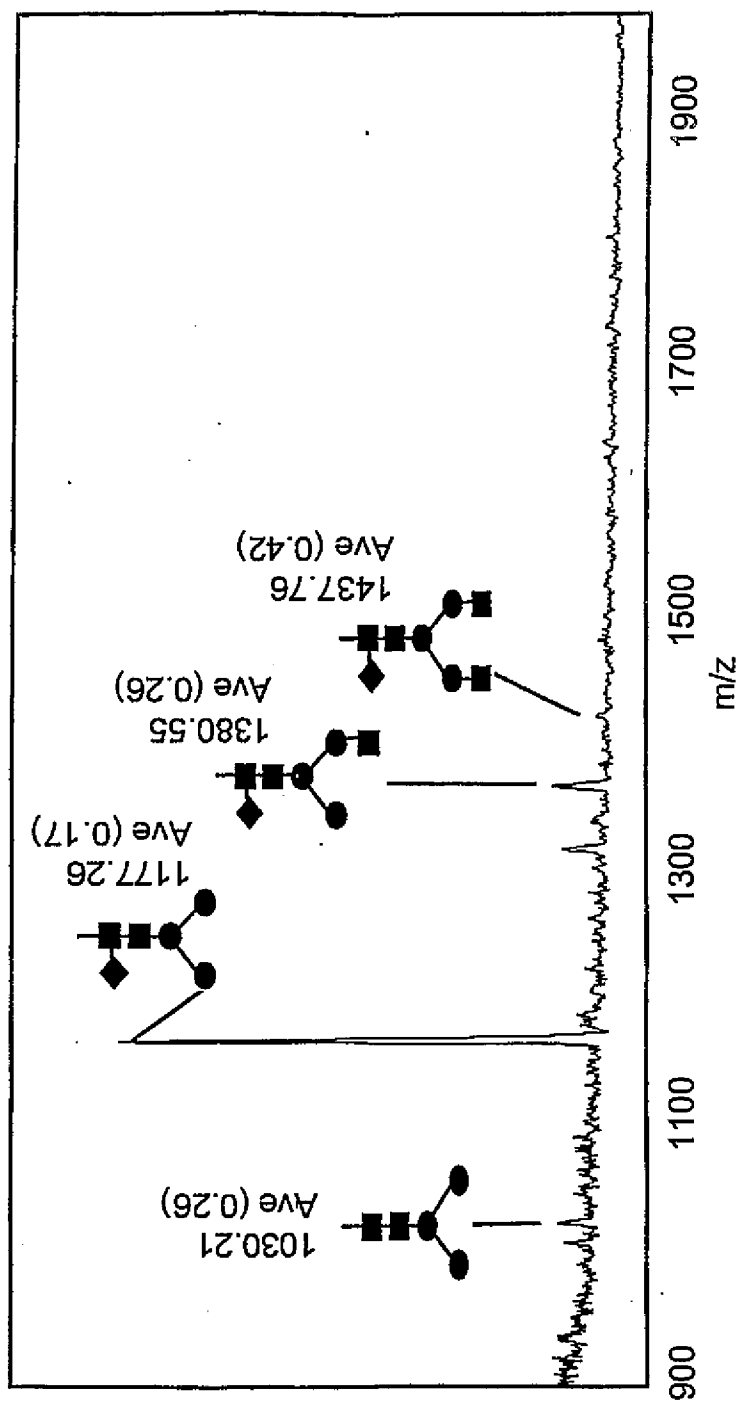


FIG. 139B

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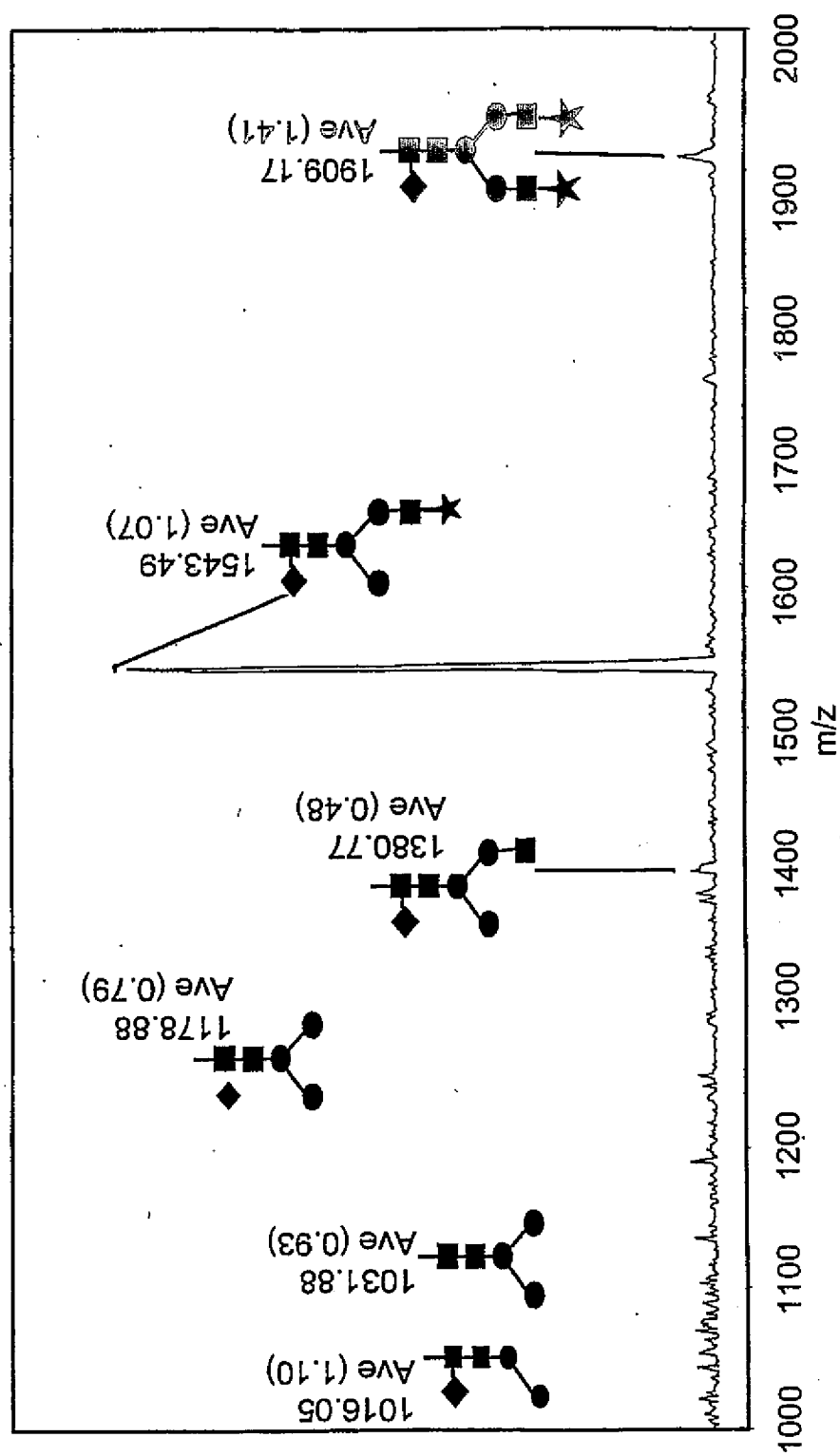


FIG. 140

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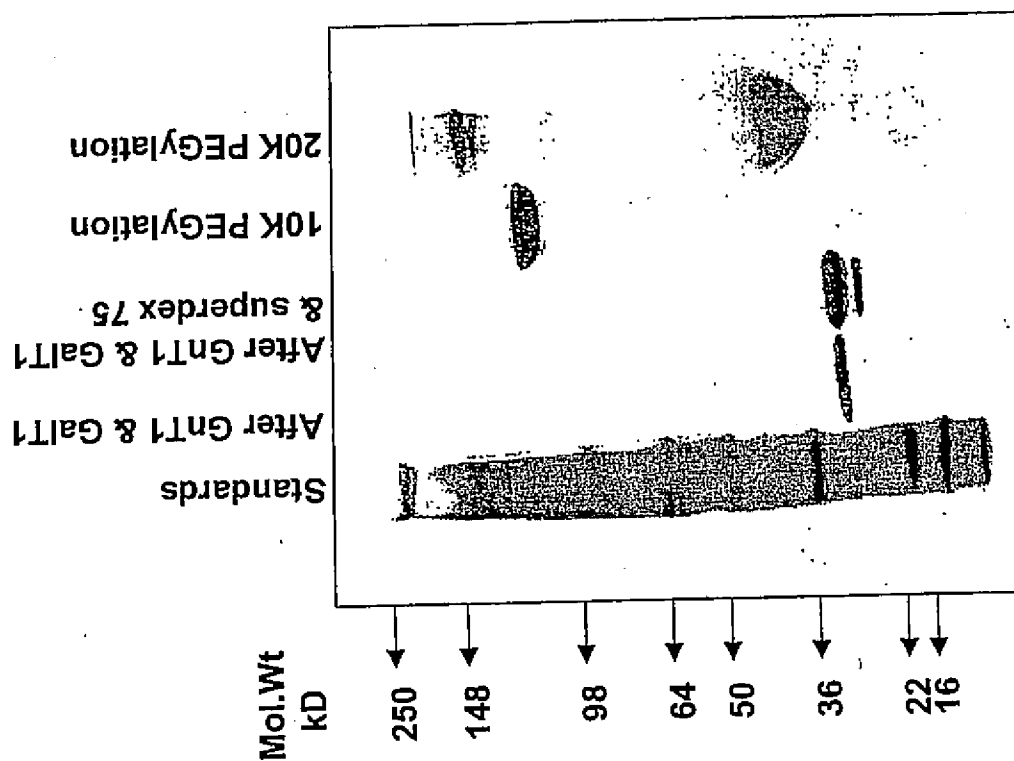


FIG. 141

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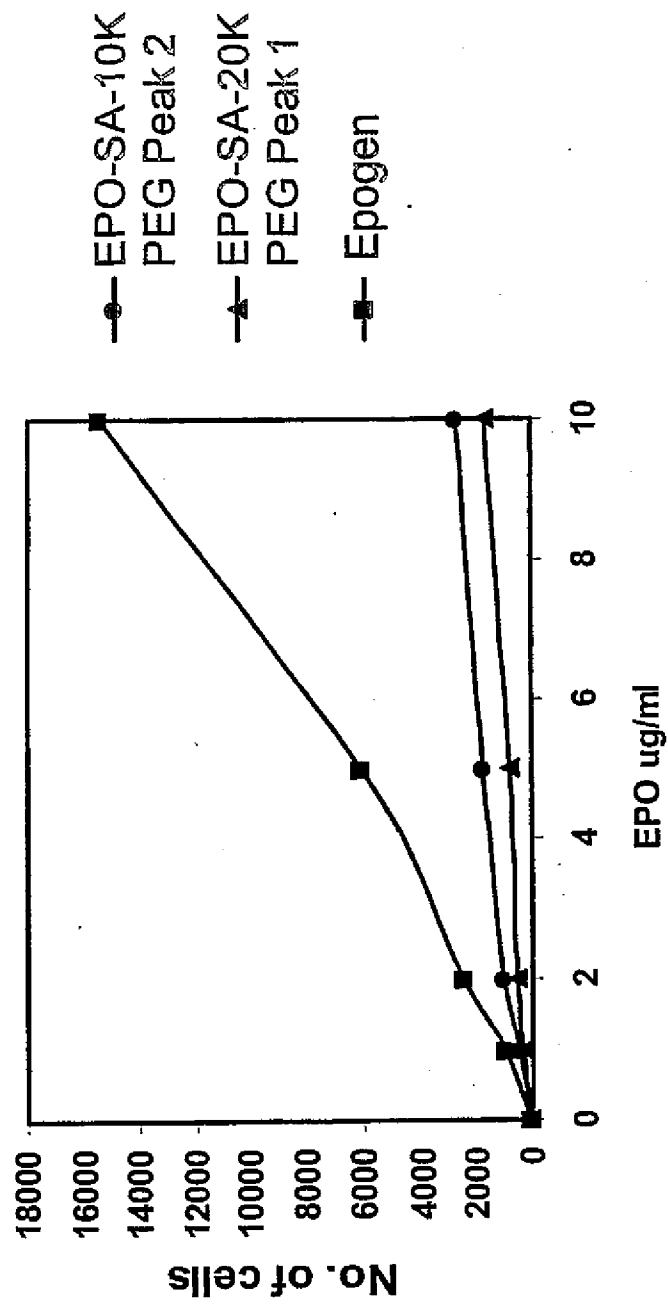


FIG. 142

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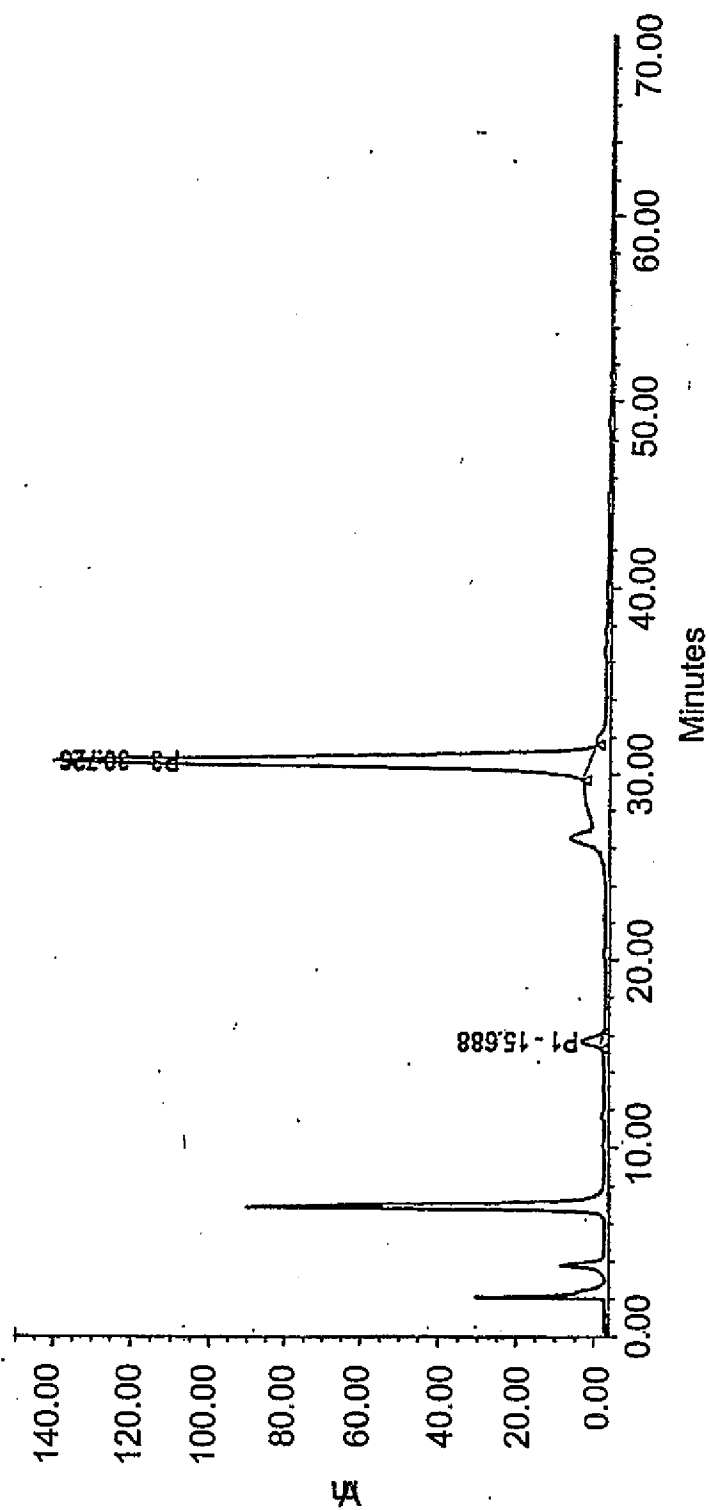


FIG. 143A

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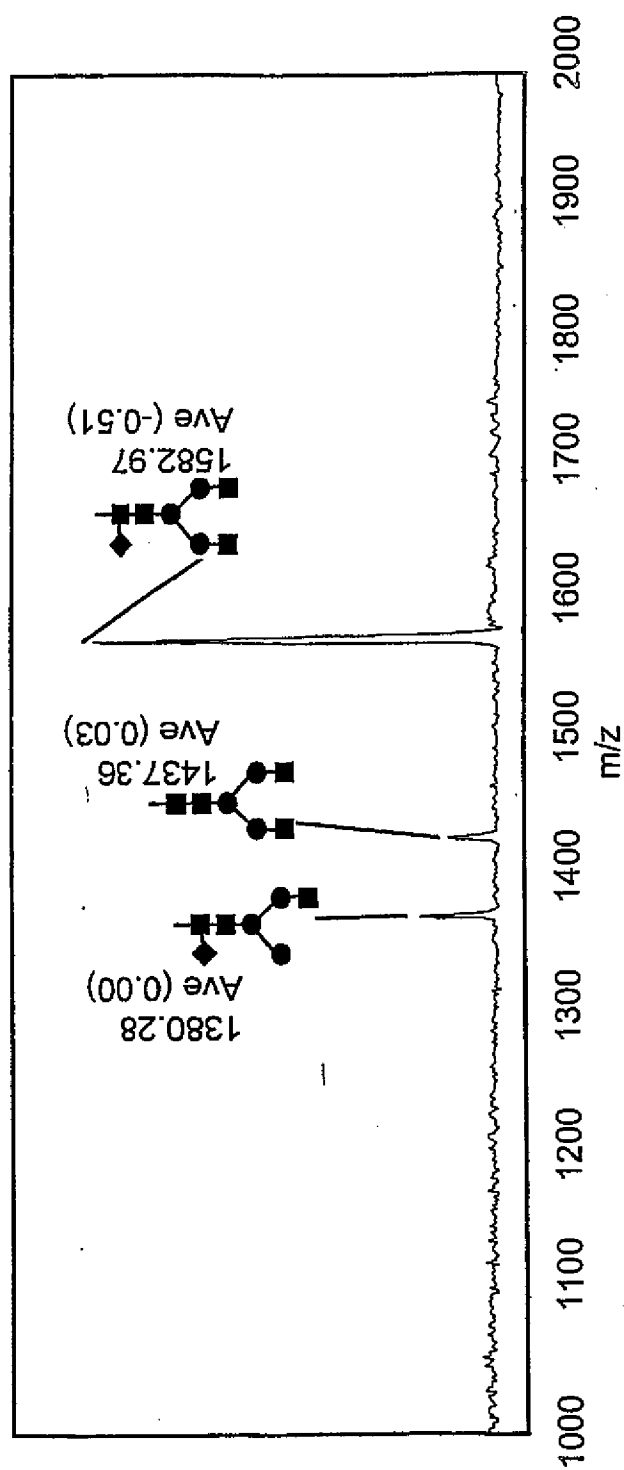


FIG. 143B

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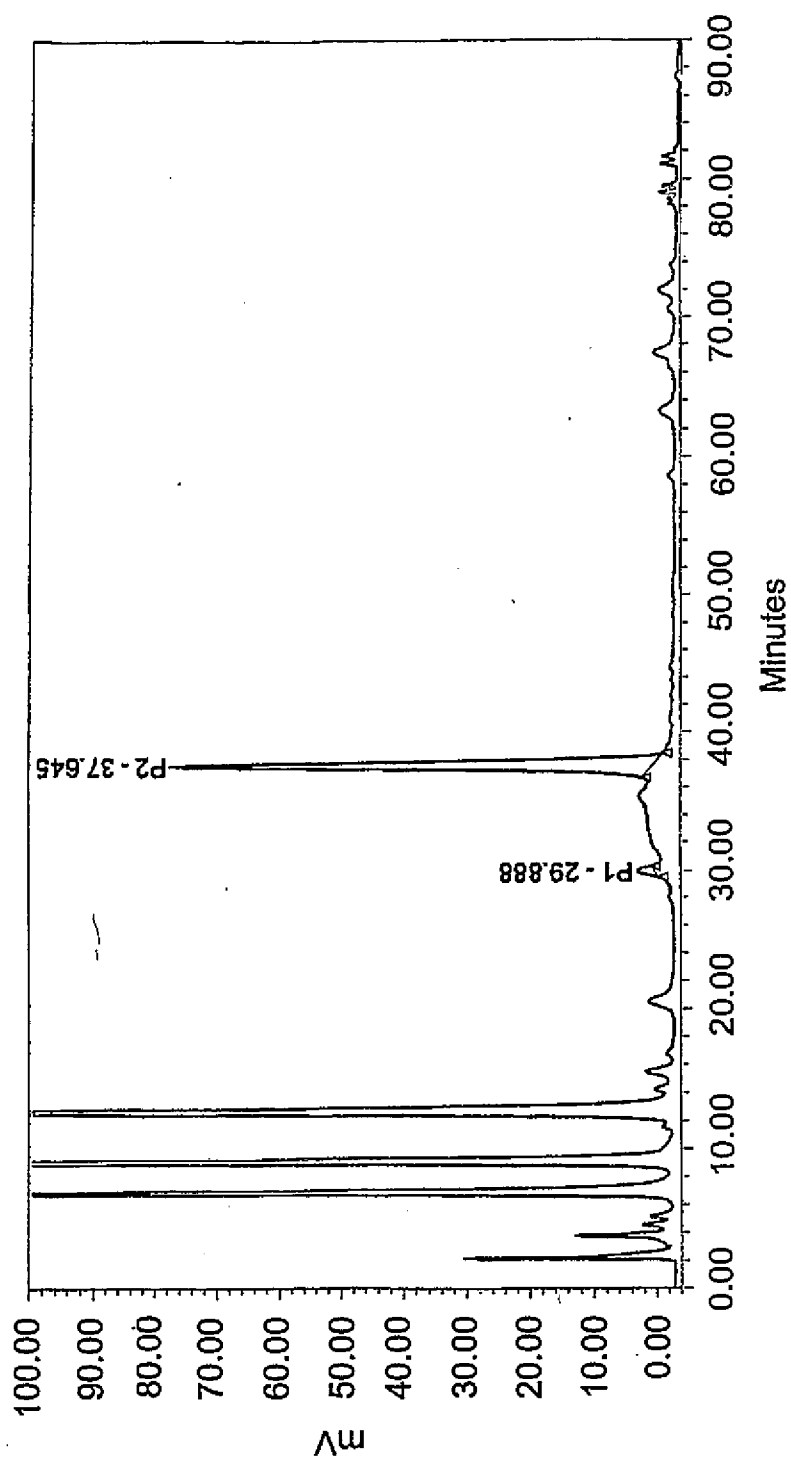


FIG. 144A

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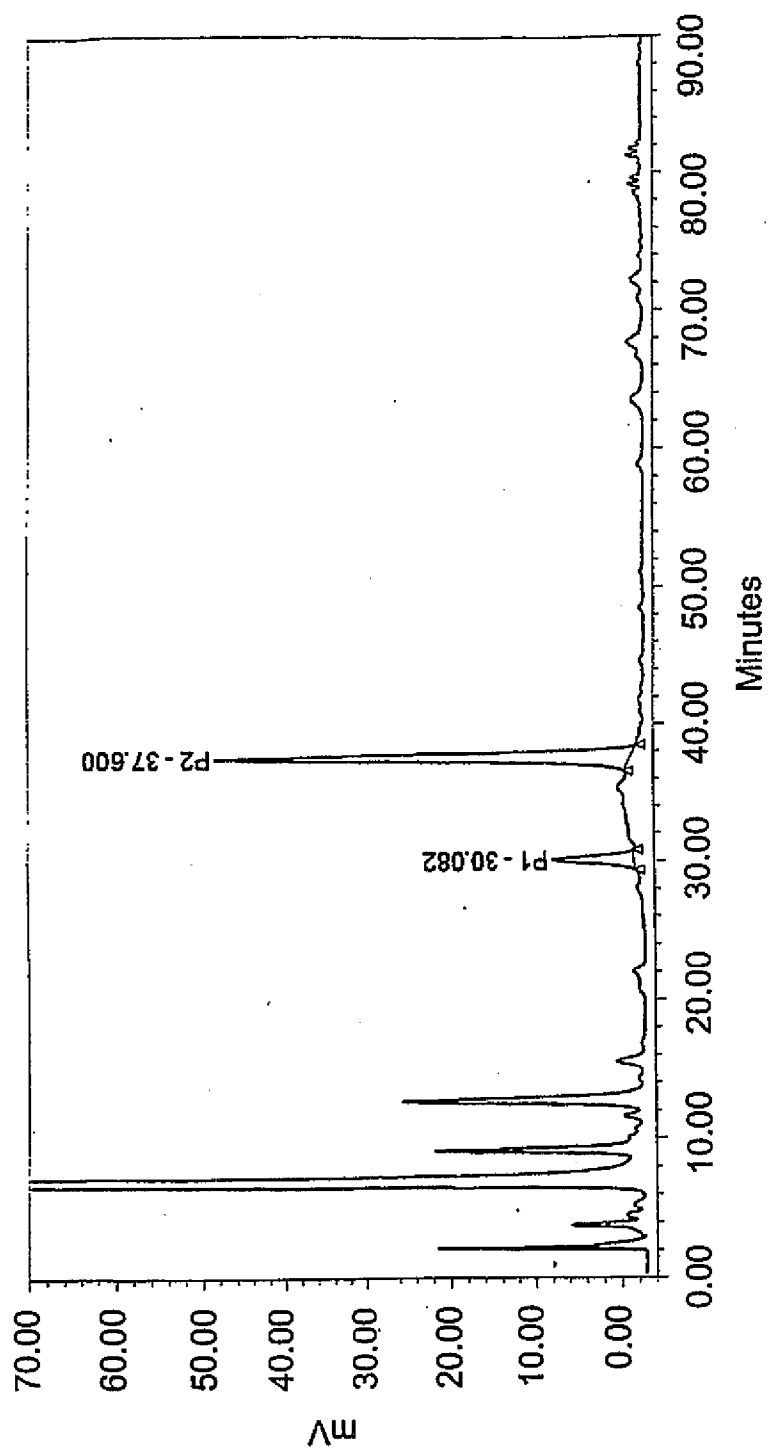


FIG. 144B

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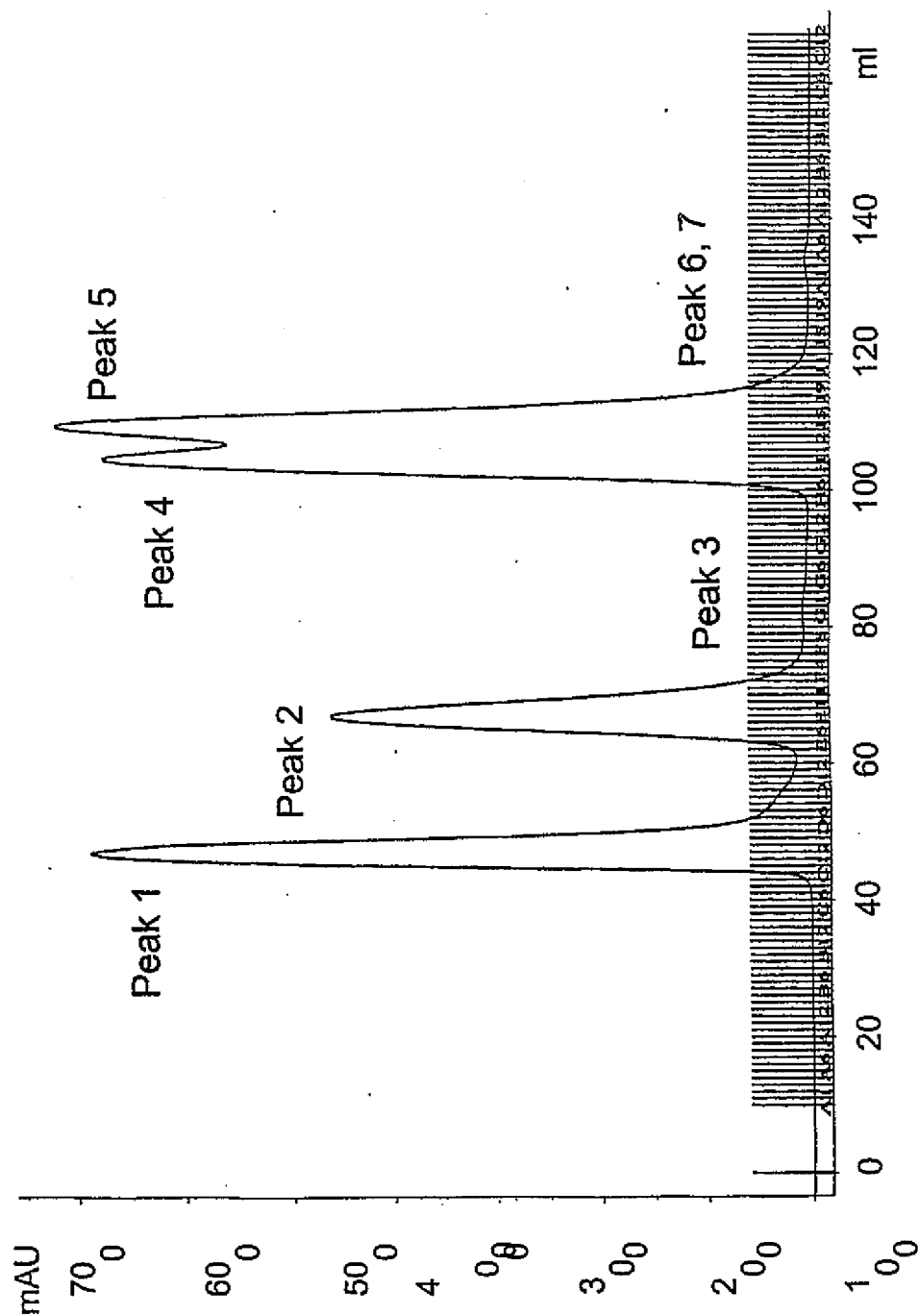


FIG. 145

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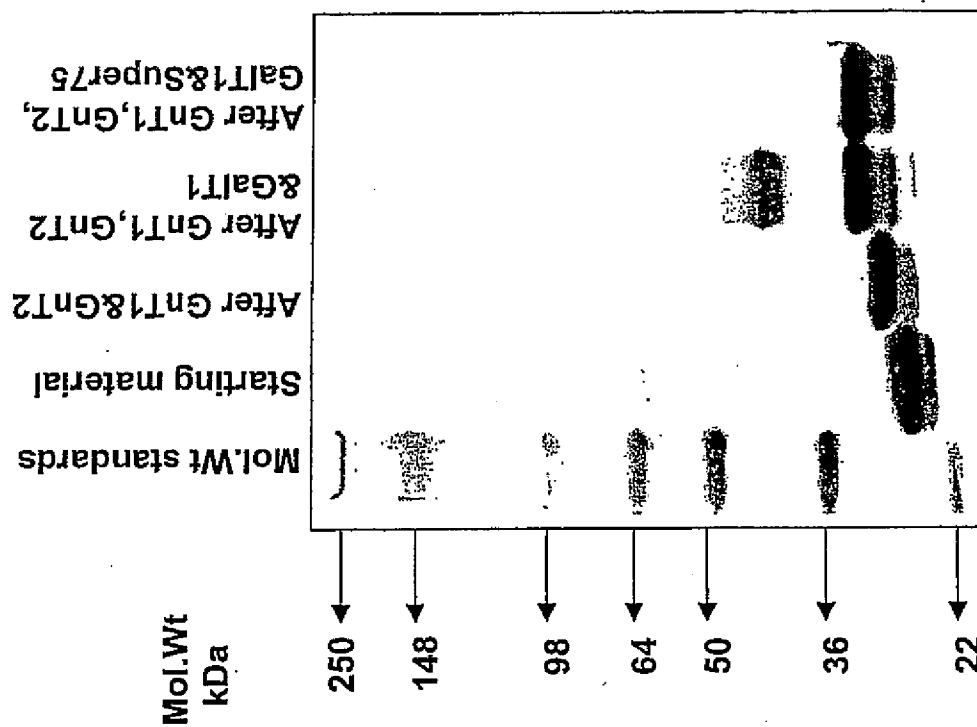


FIG. 146

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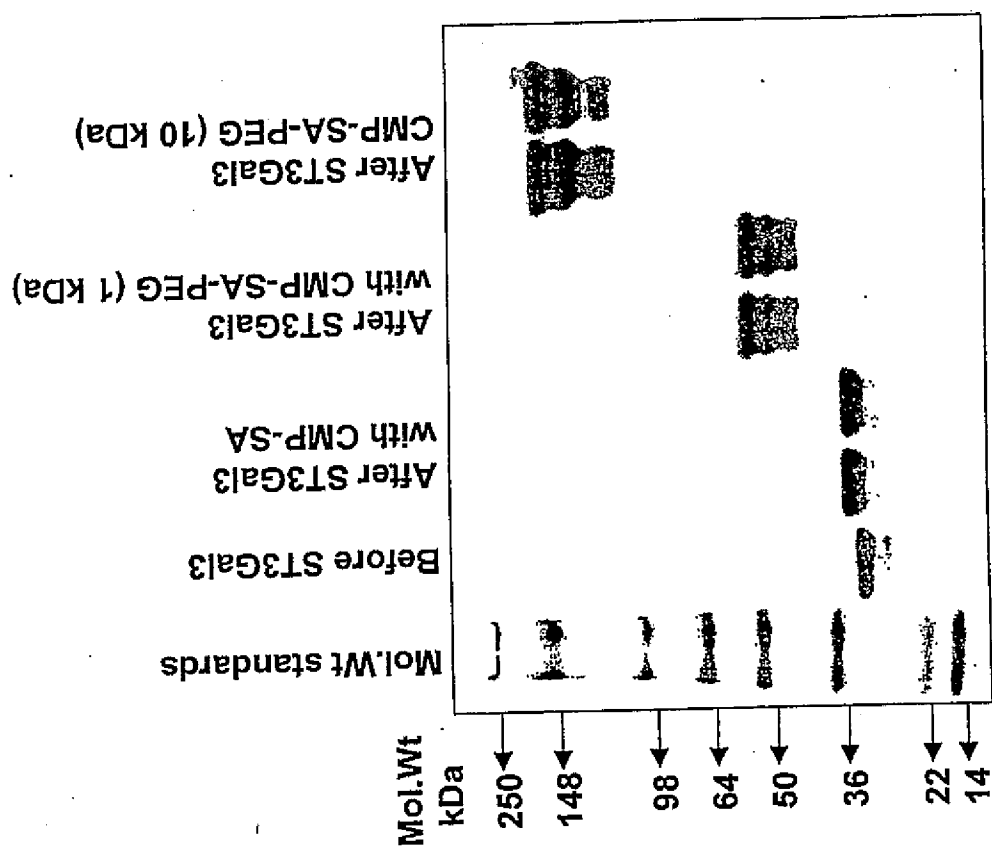


FIG. 147

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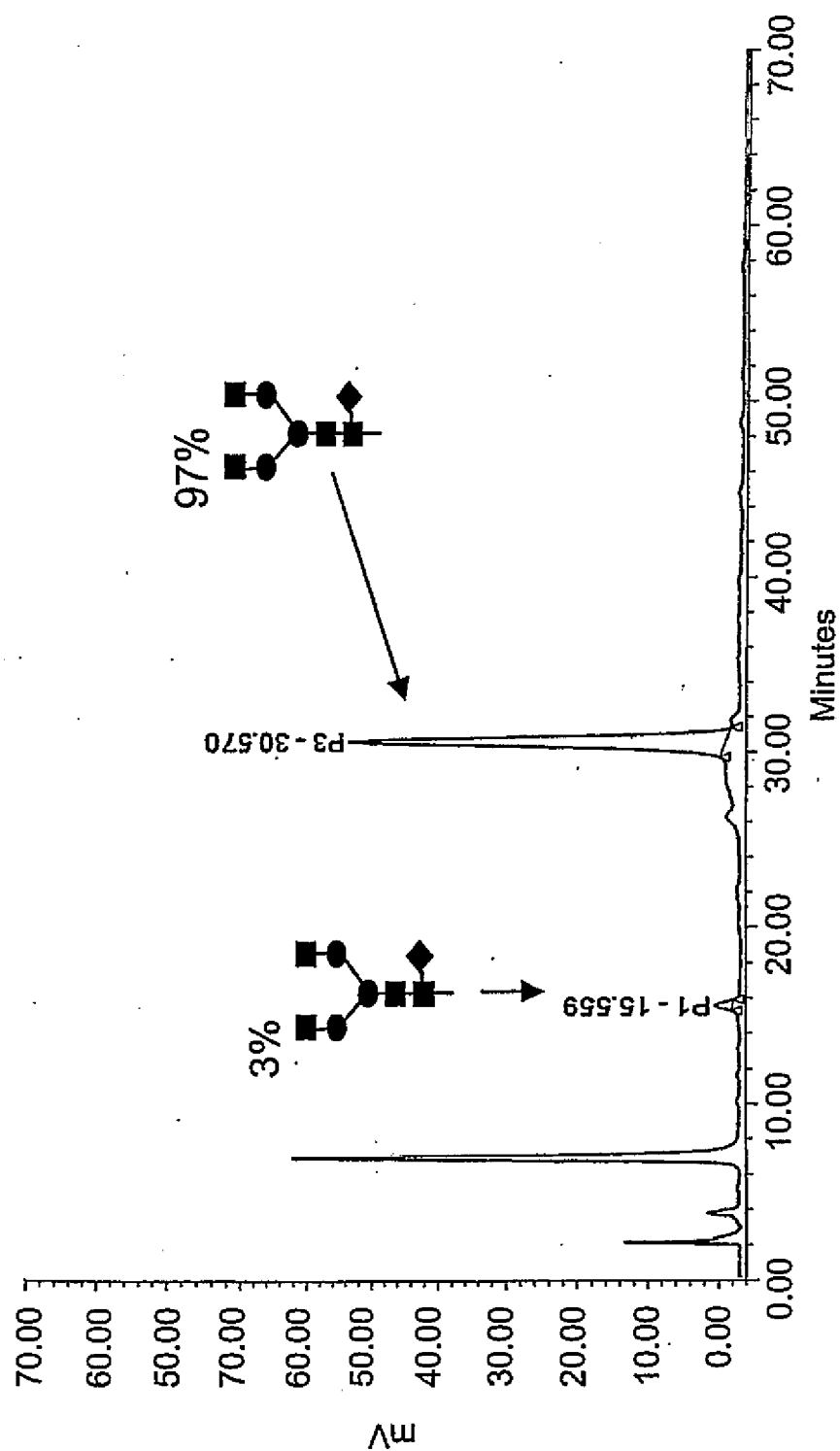


FIG. 148

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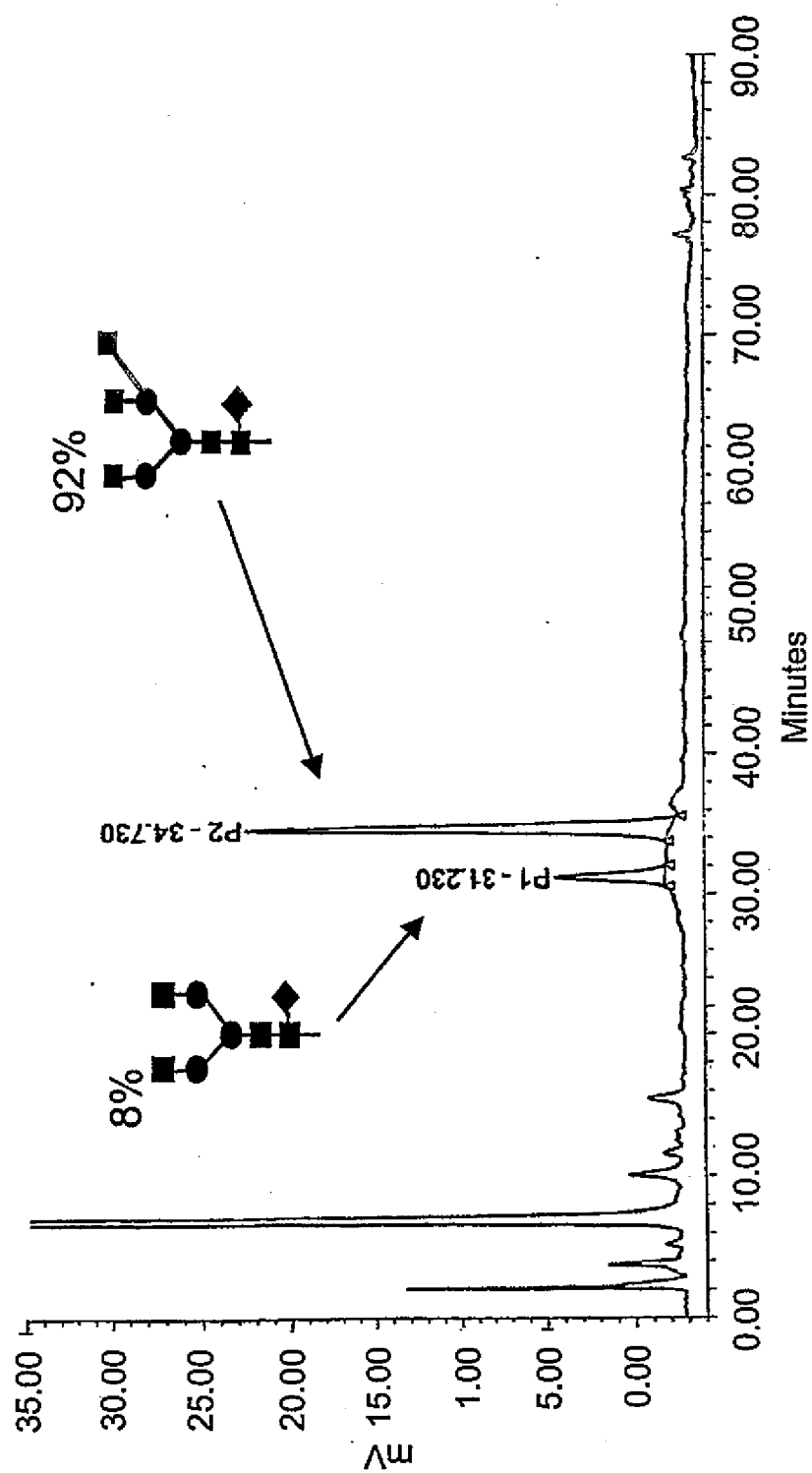


FIG. 149

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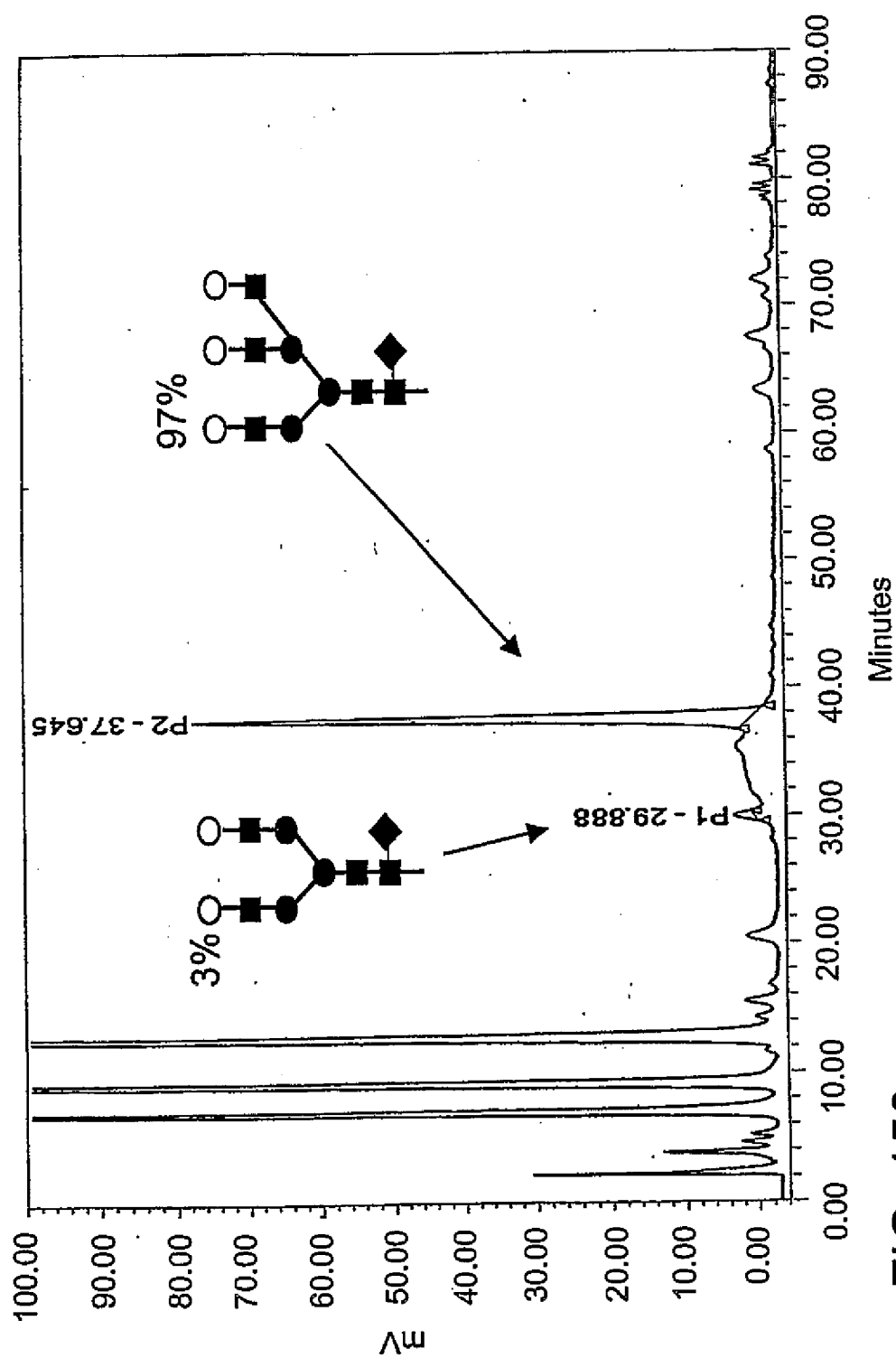


FIG. 150

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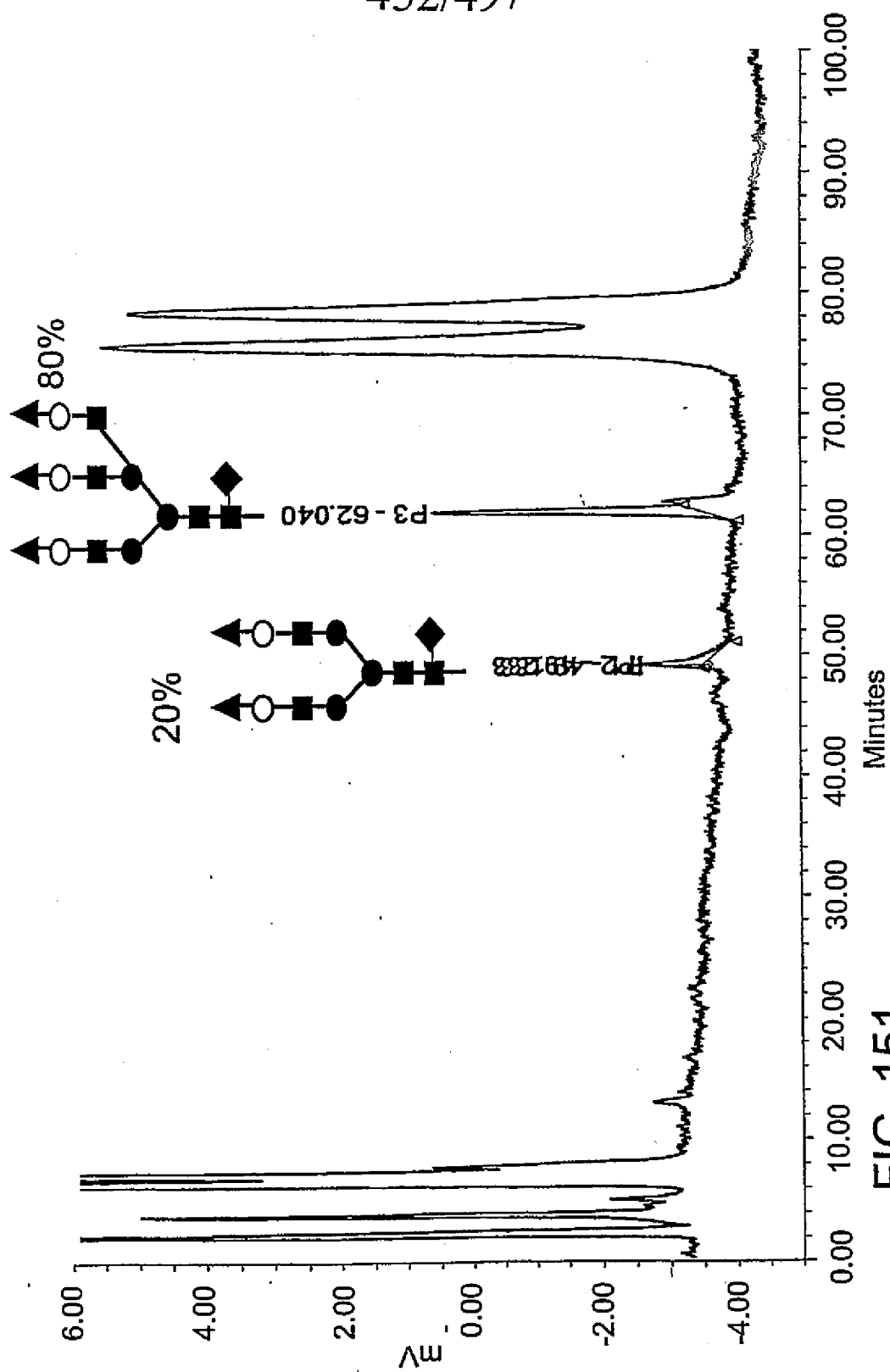


FIG. 151

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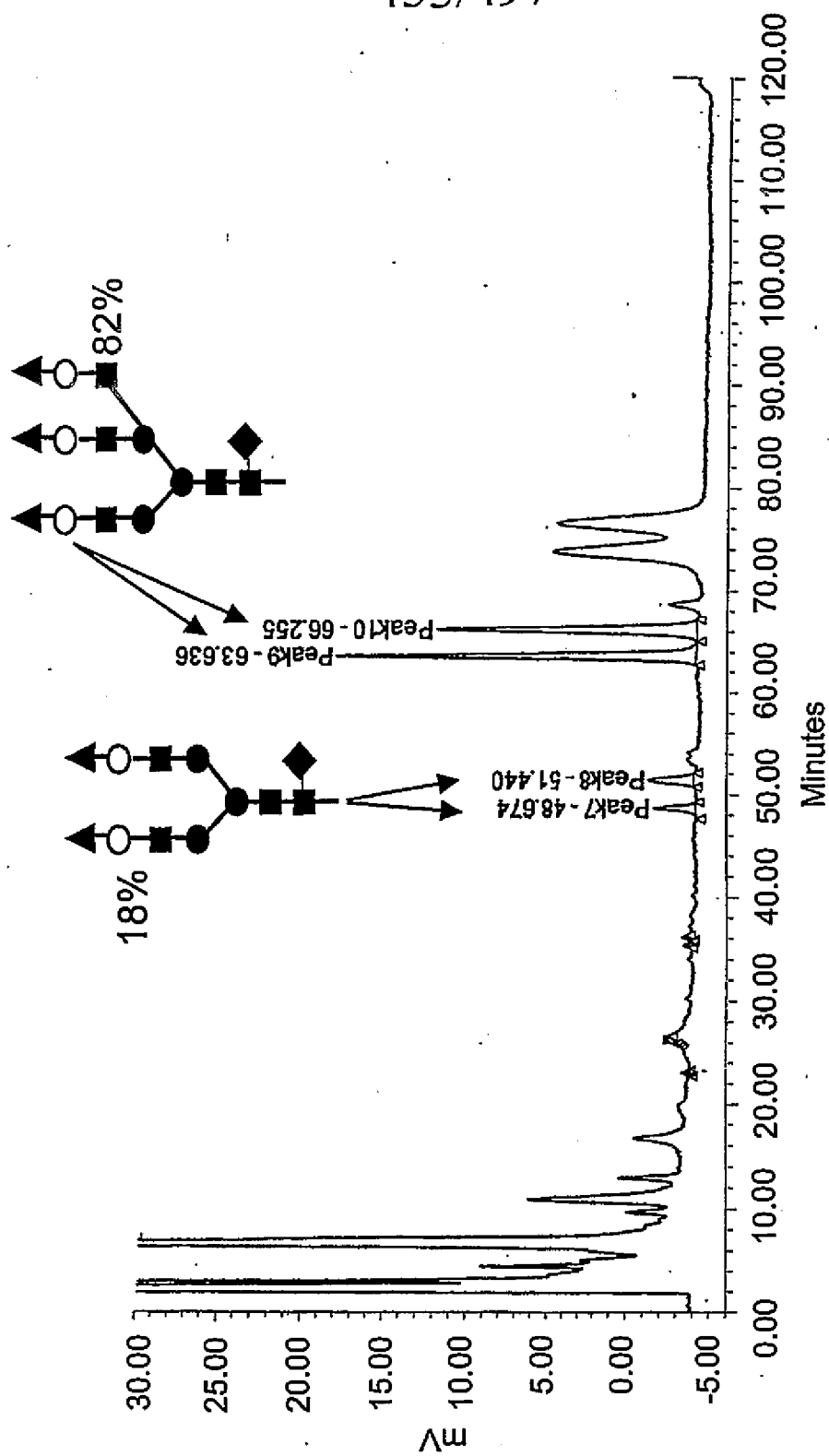


FIG. 152

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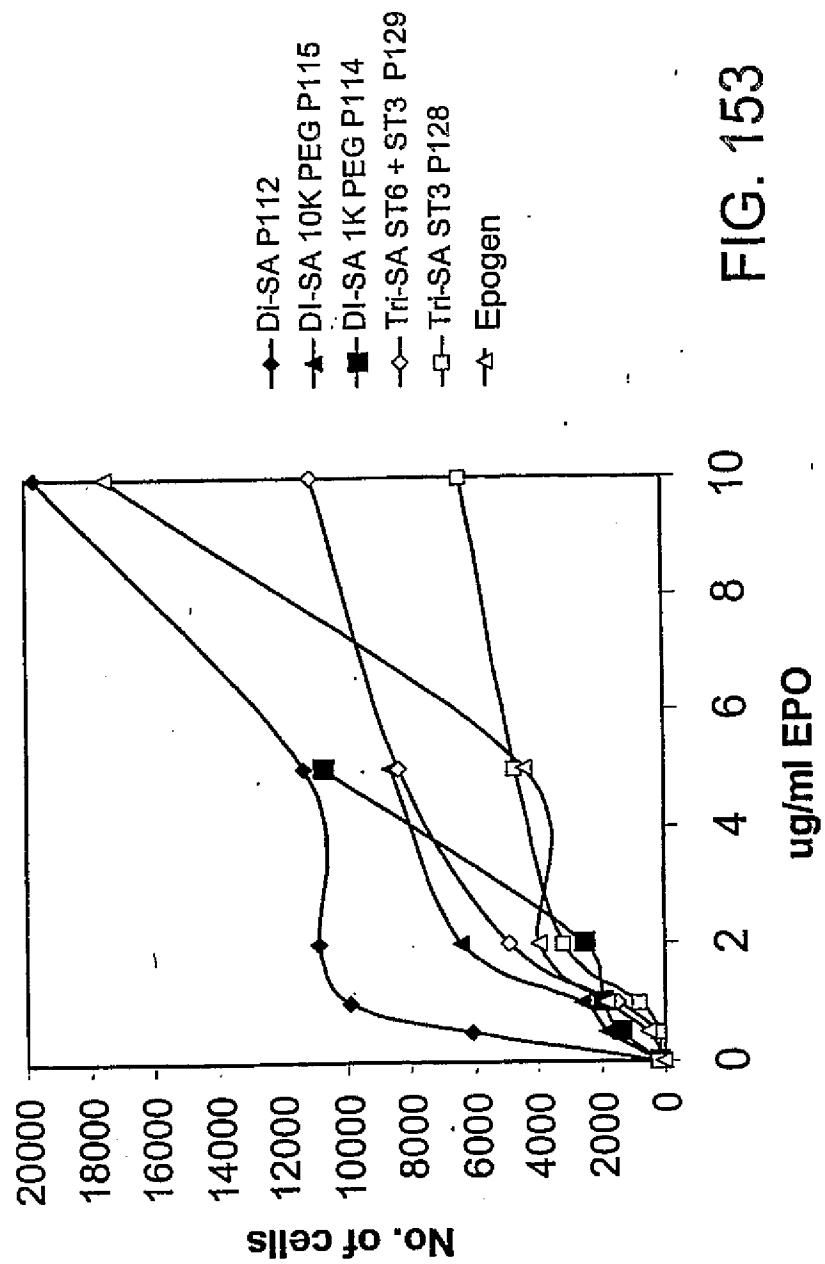


FIG. 153

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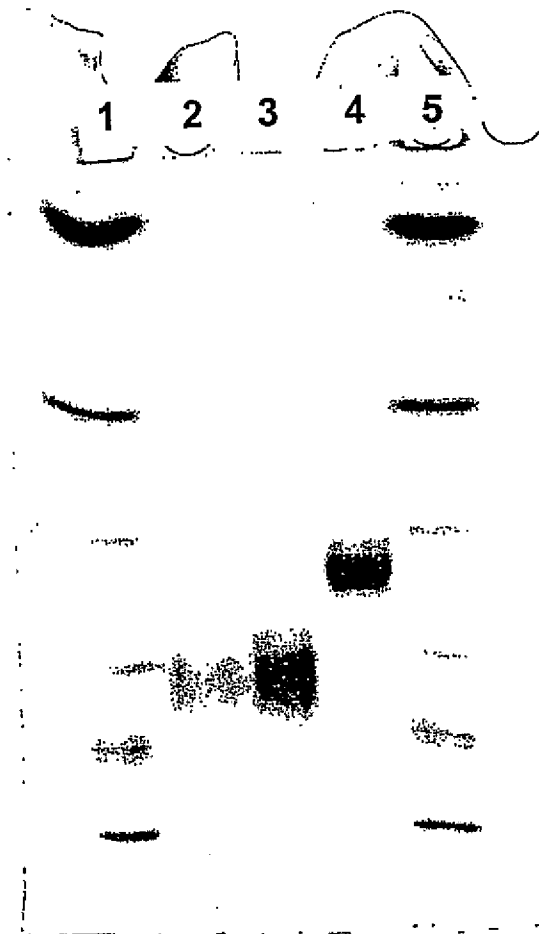


FIG. 154

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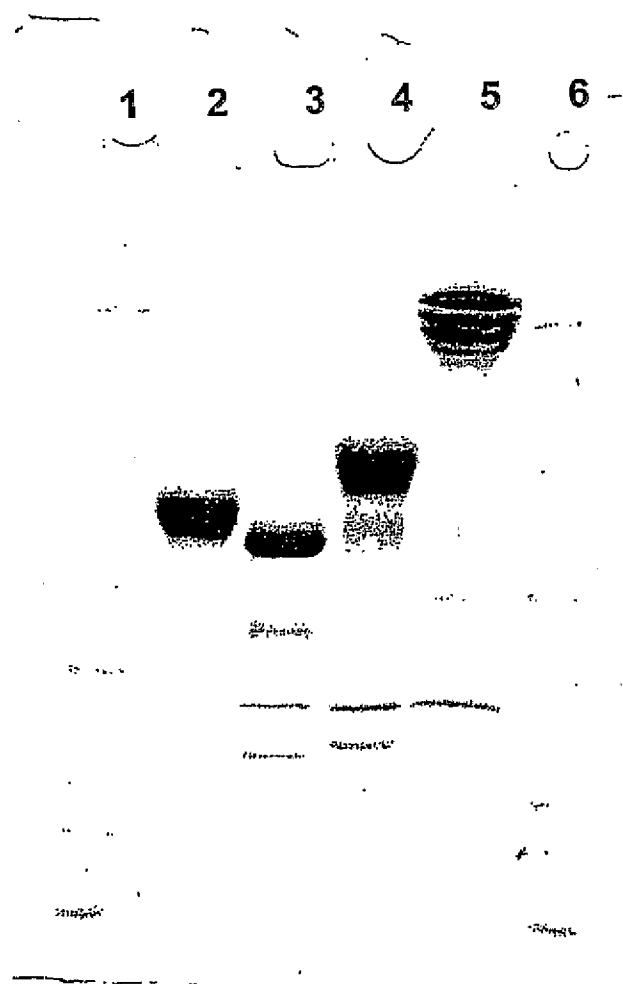


FIG. 155

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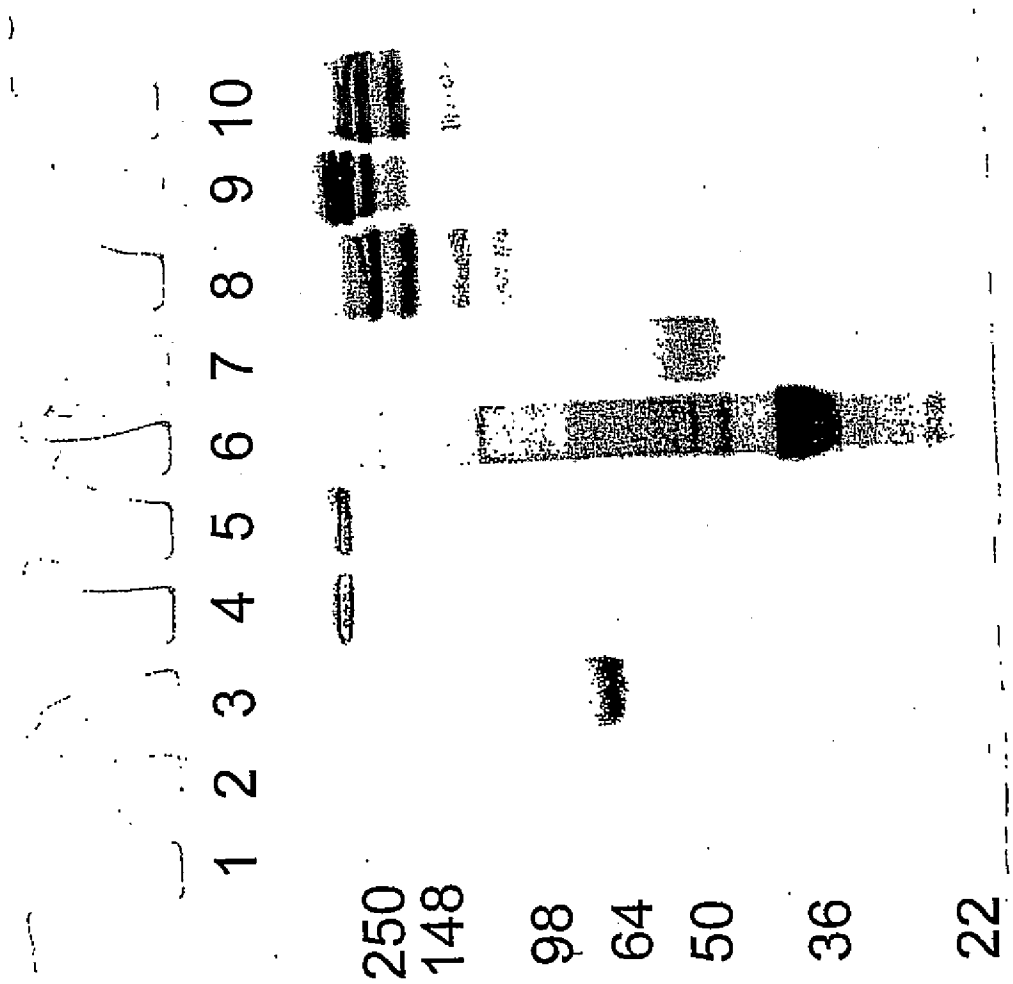


FIG 15₆

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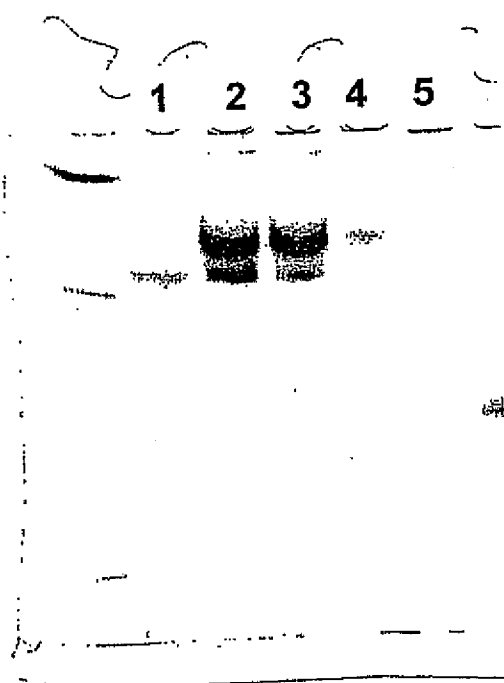


FIG. 157

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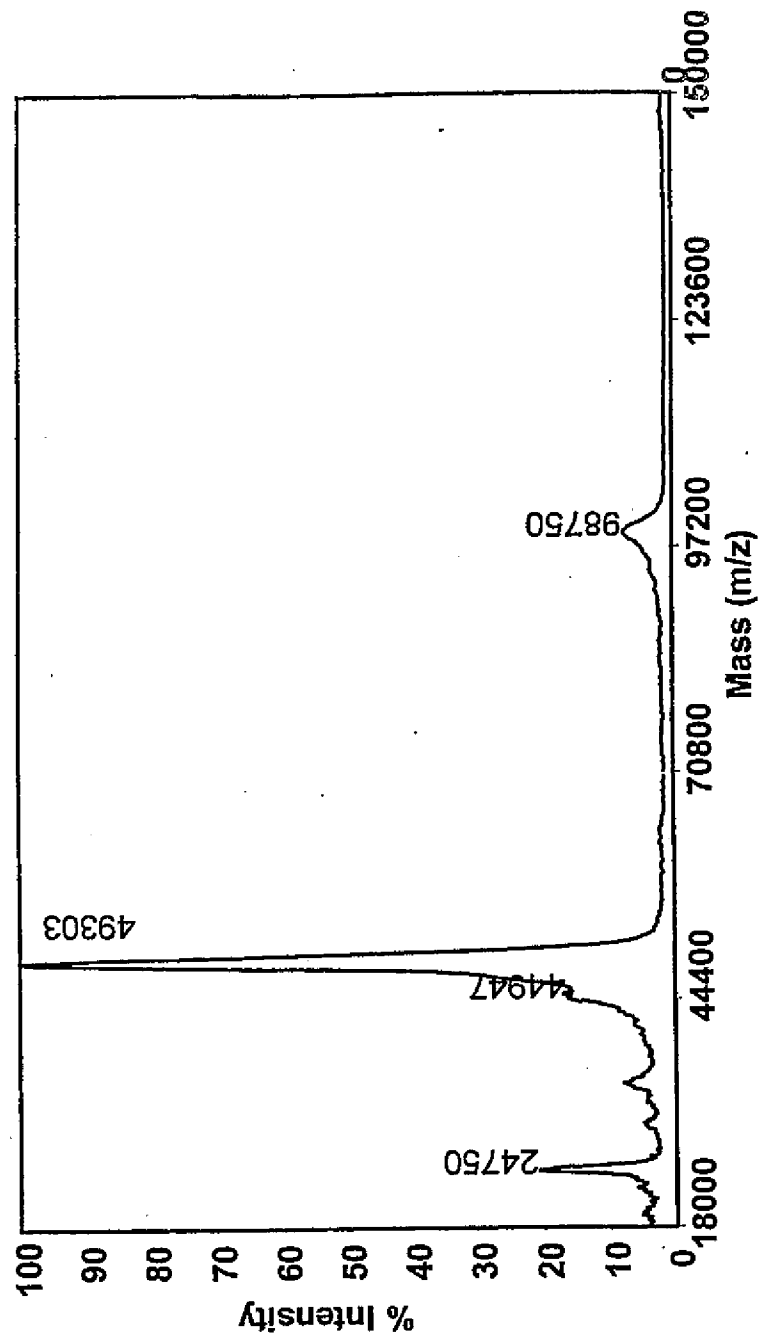


FIG. 158

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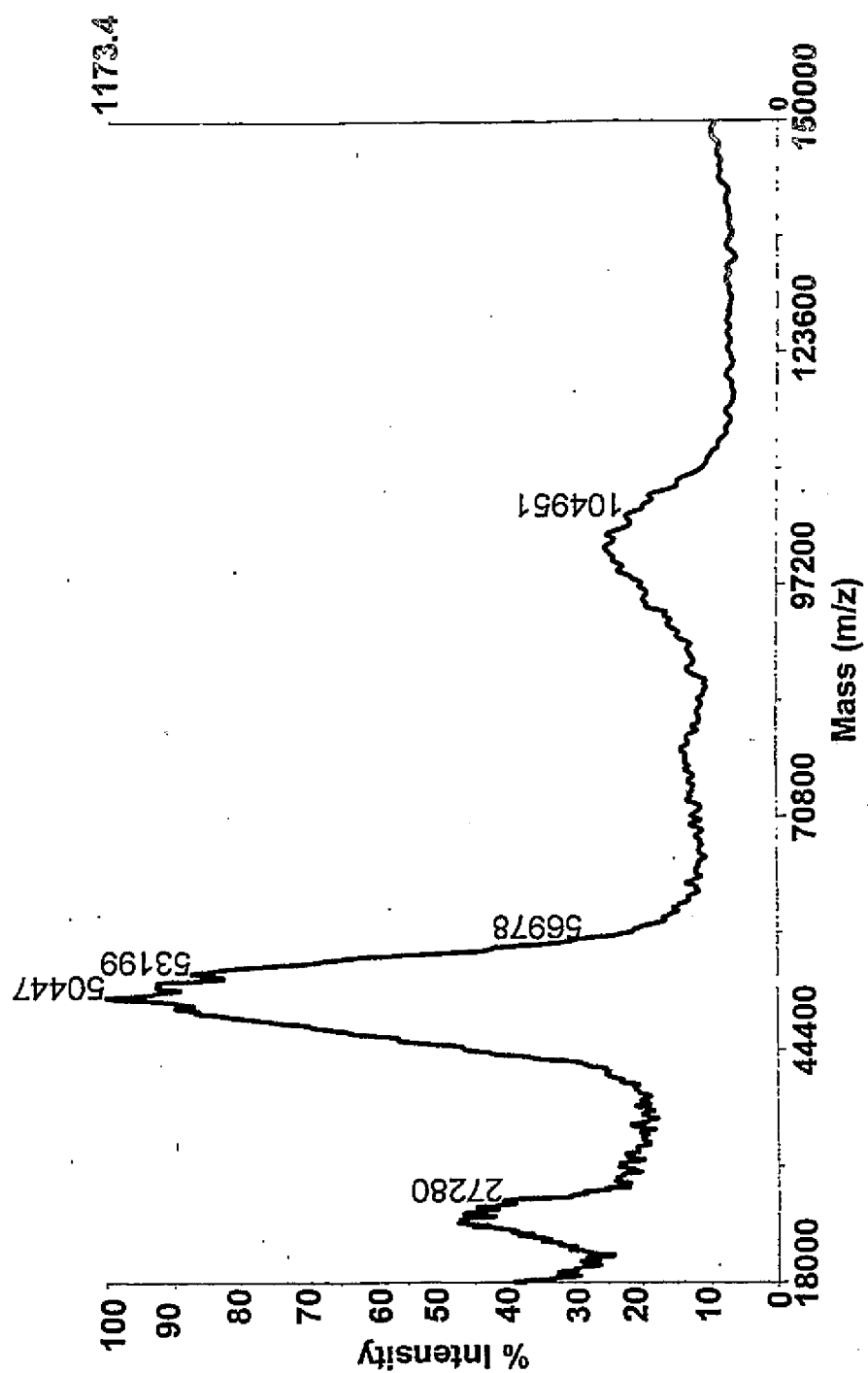


FIG. 159

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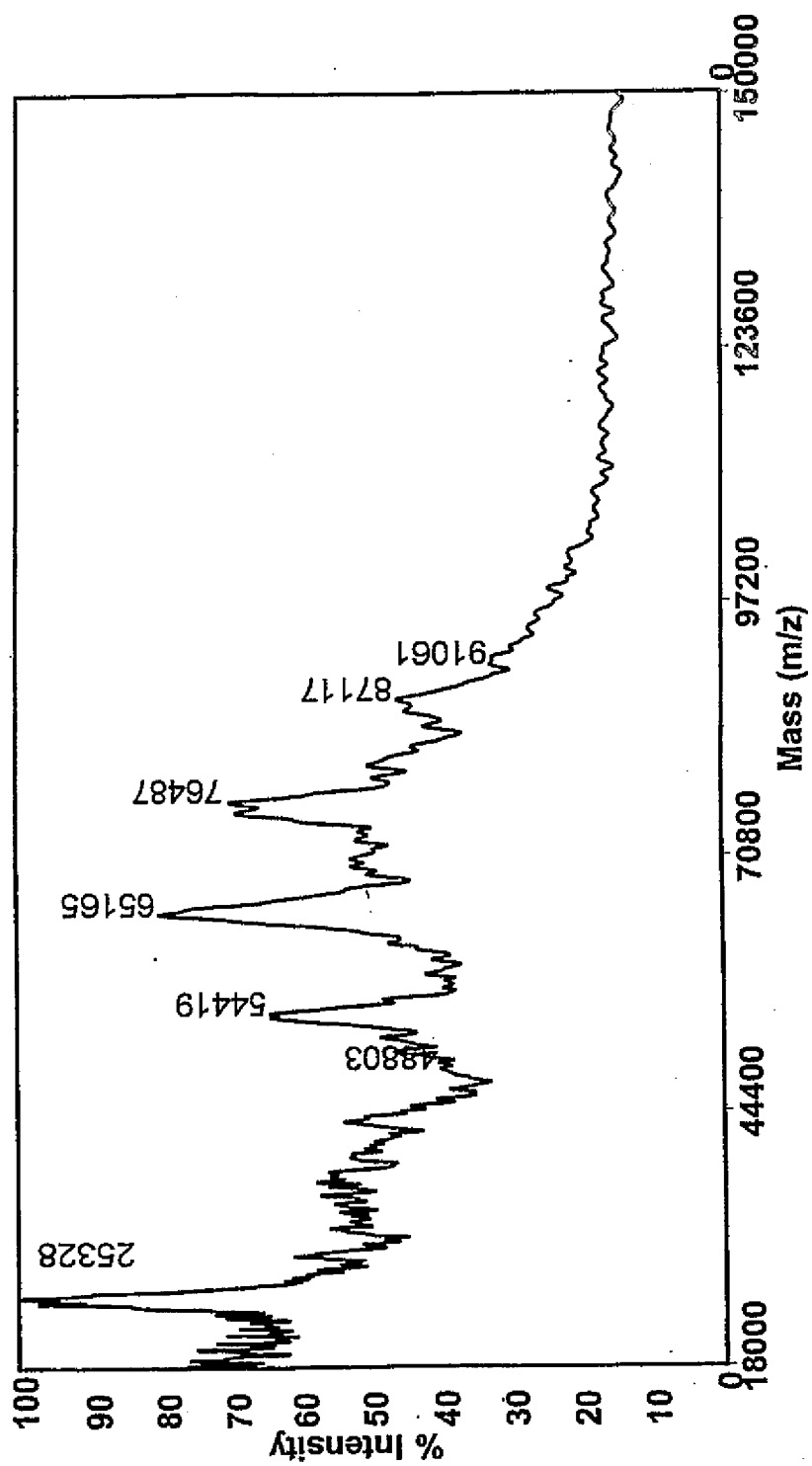


FIG. 160

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FIG. 161

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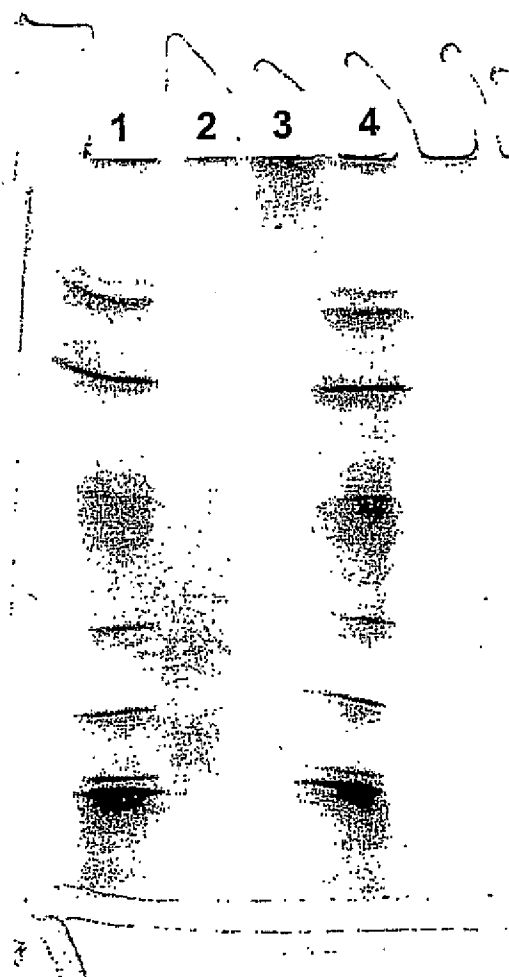


FIG. 162

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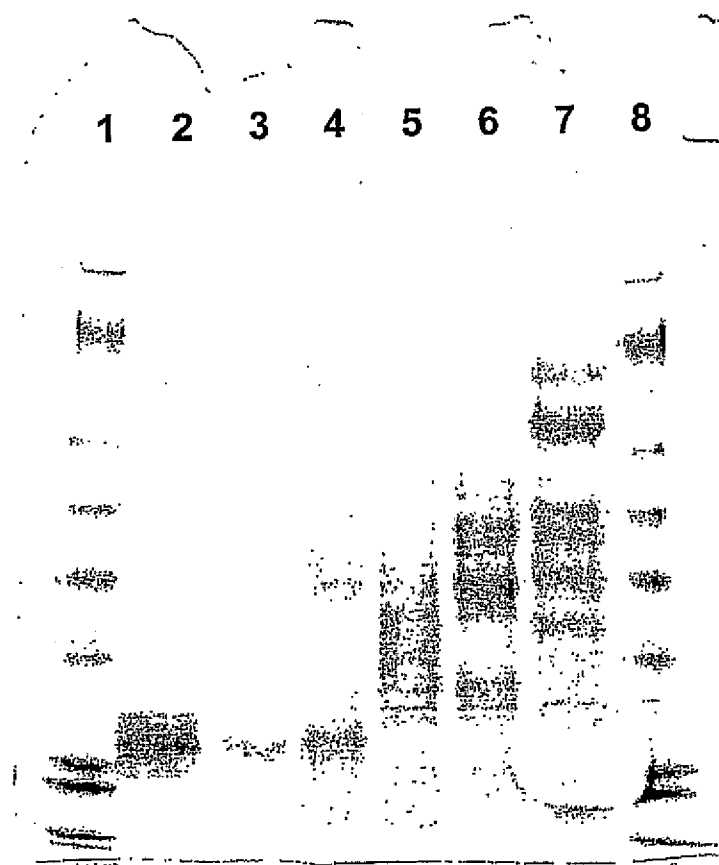


FIG. 163

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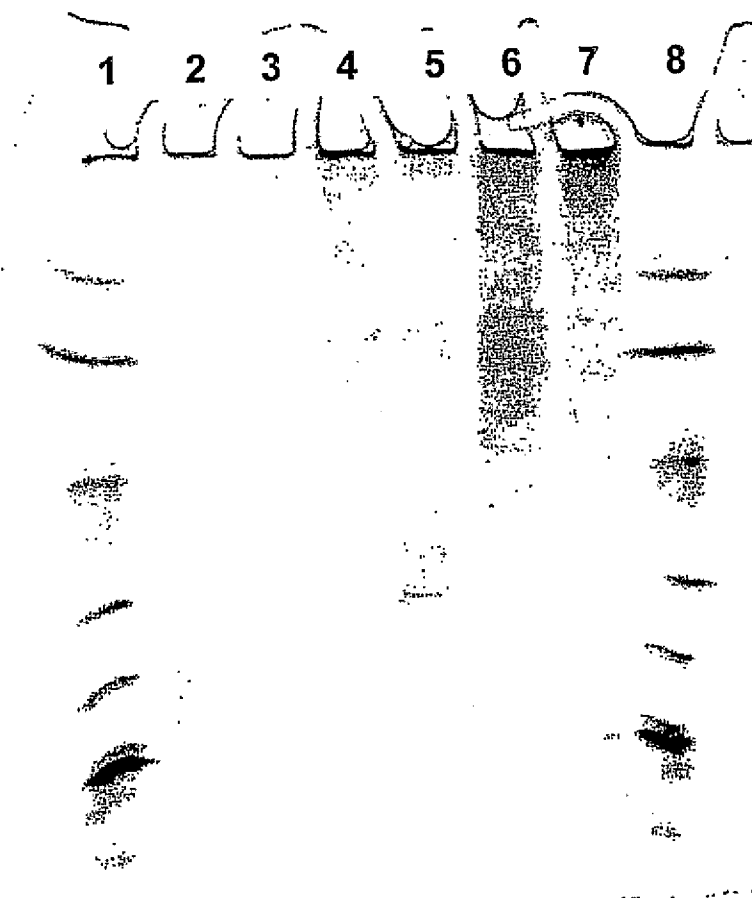


FIG. 164

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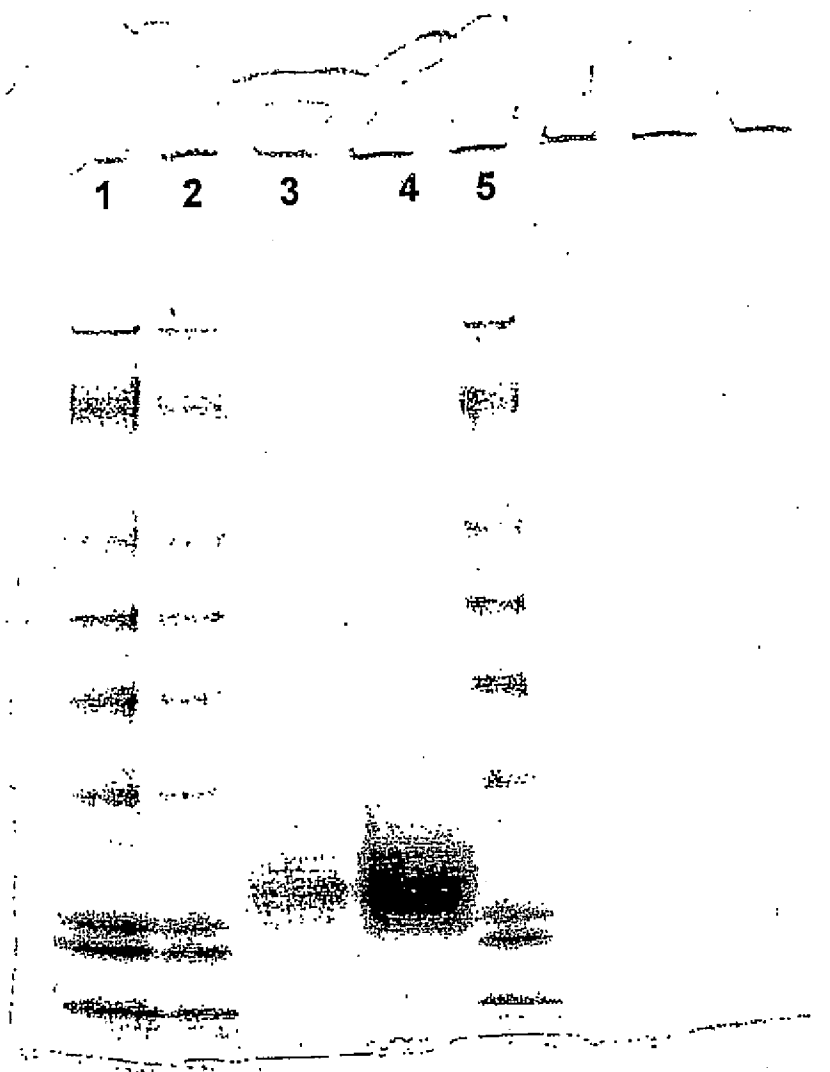


FIG. 165

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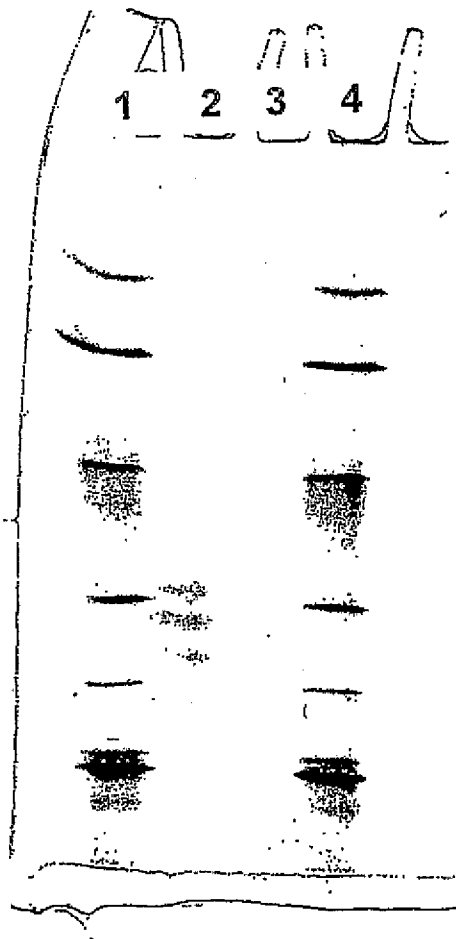


FIG. 166

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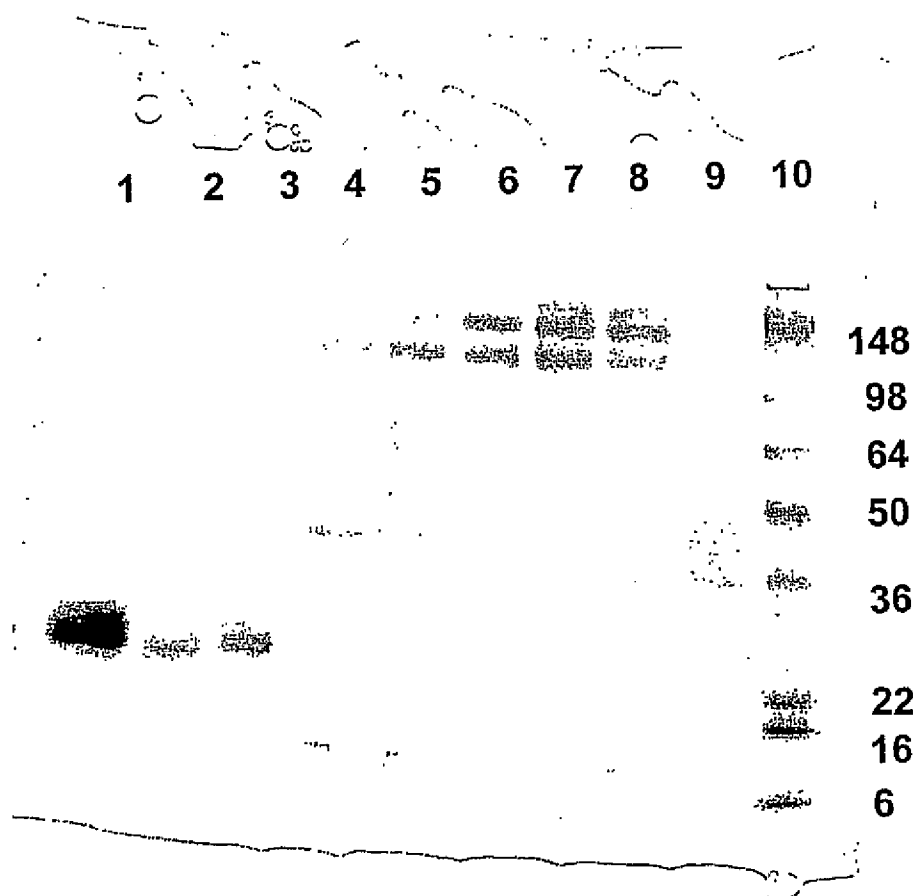


FIG. 167

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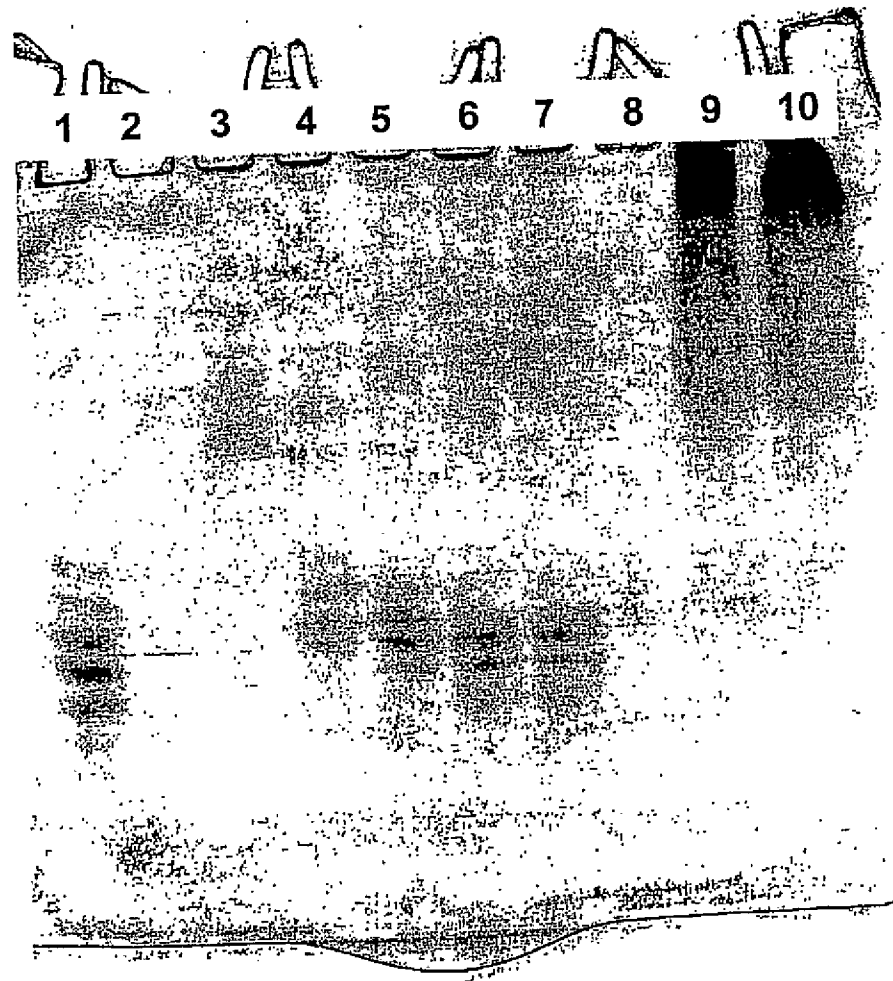


FIG. 168

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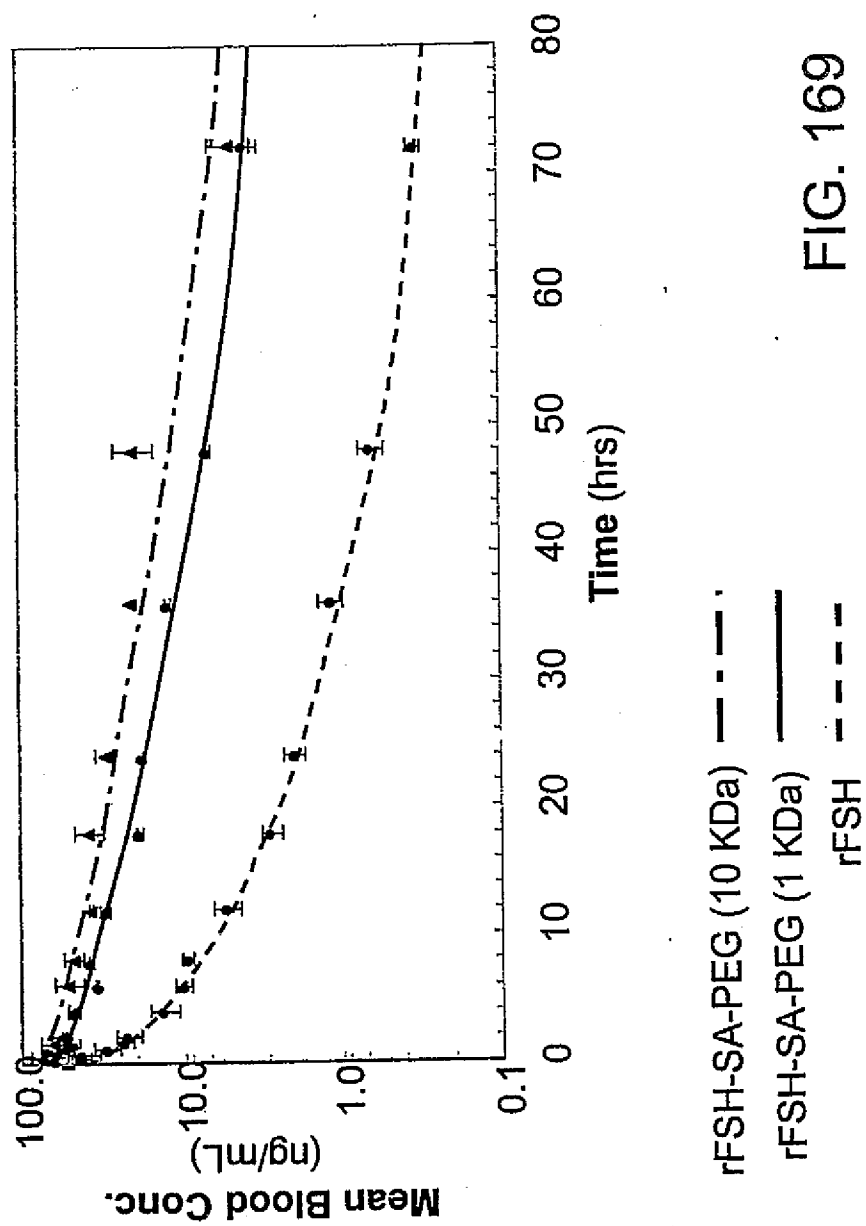


FIG. 169

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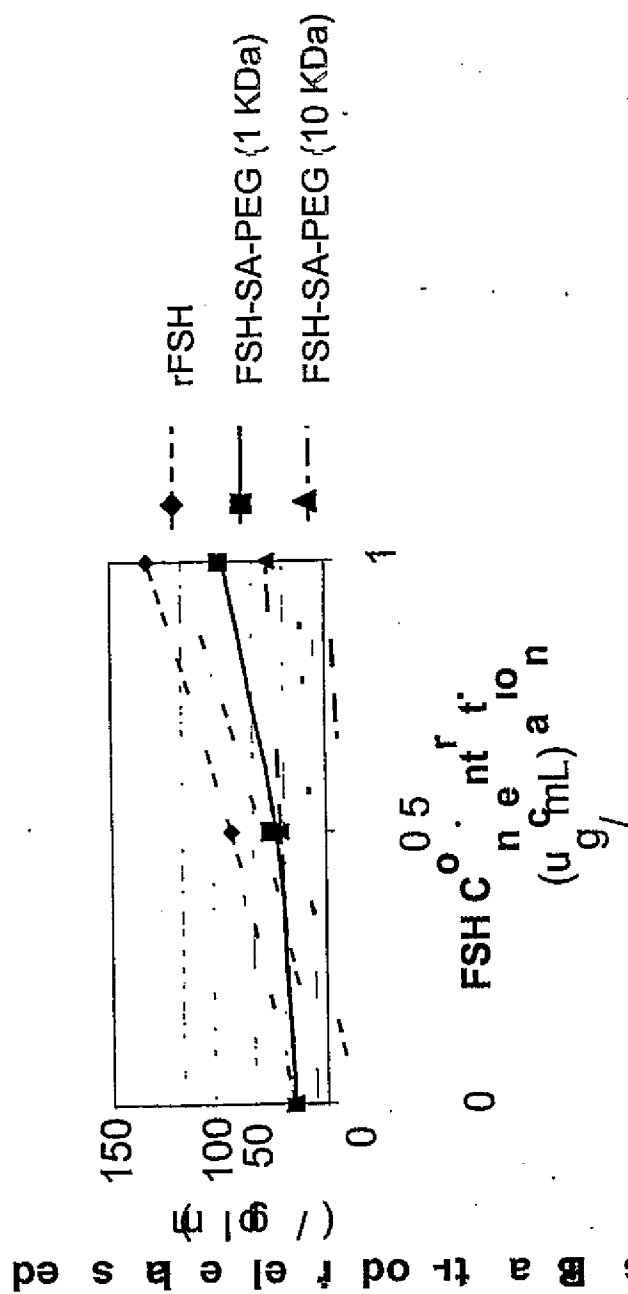


FIG 17

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FIG. 171

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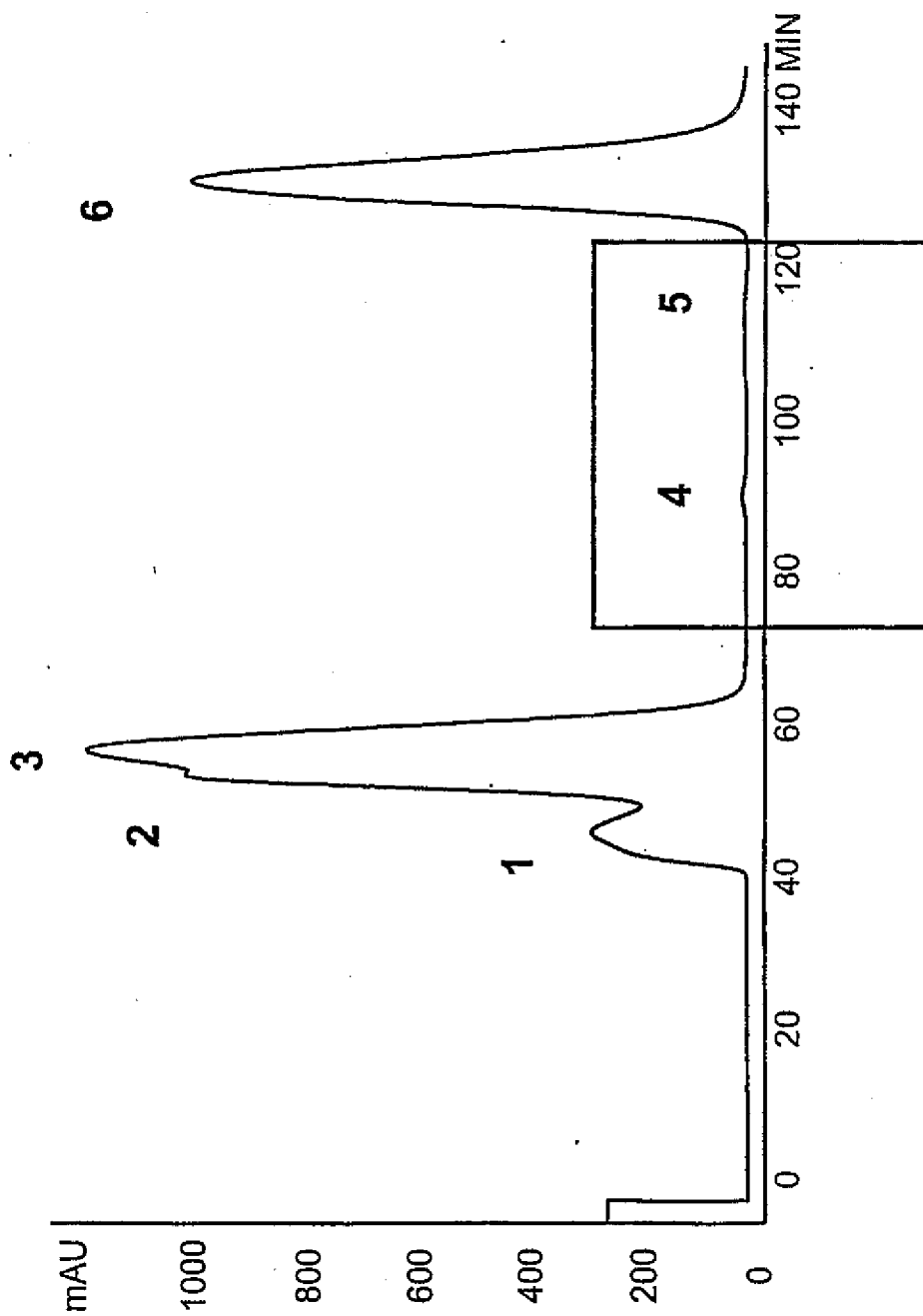


FIG. 172A

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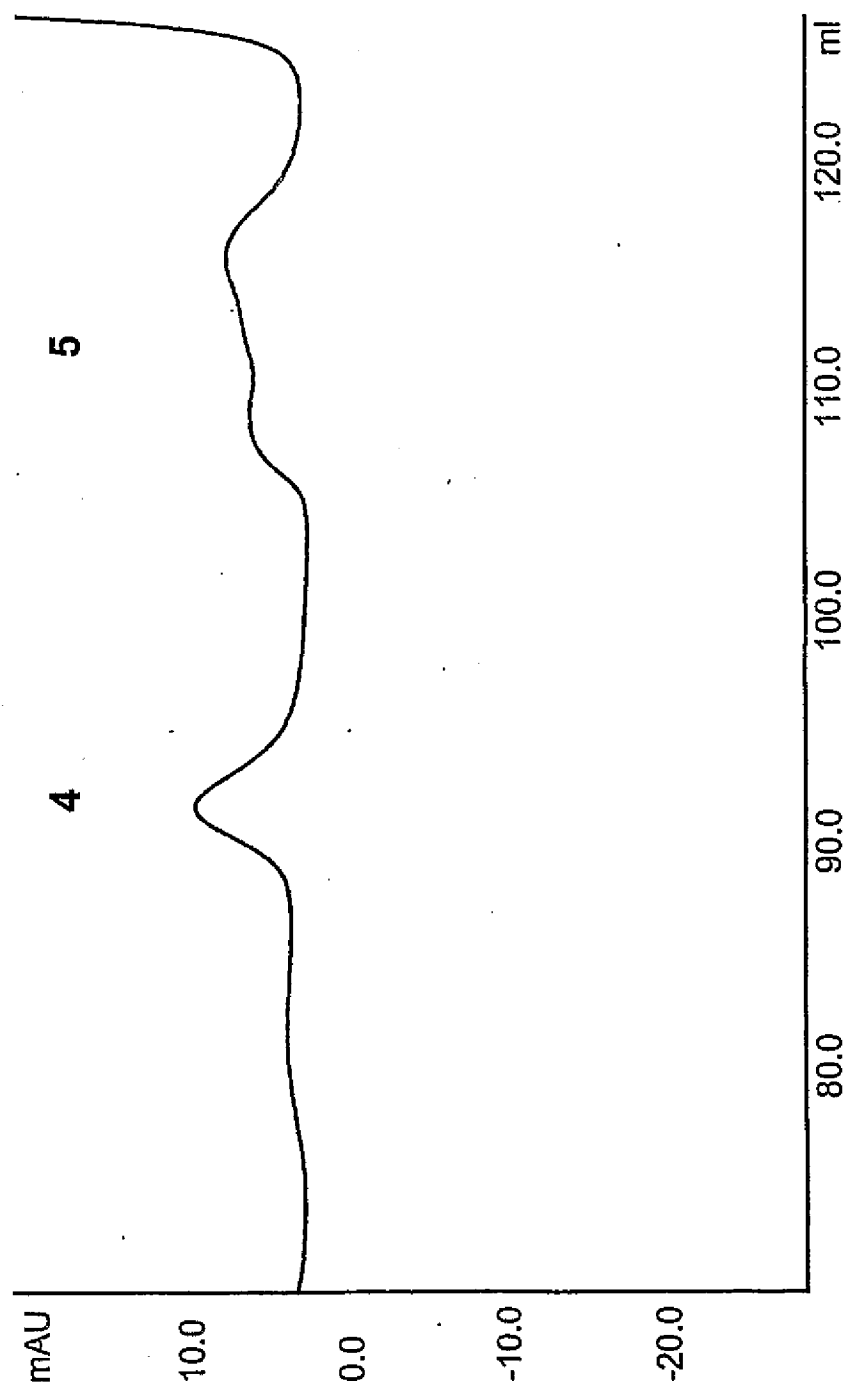


FIG. 172B

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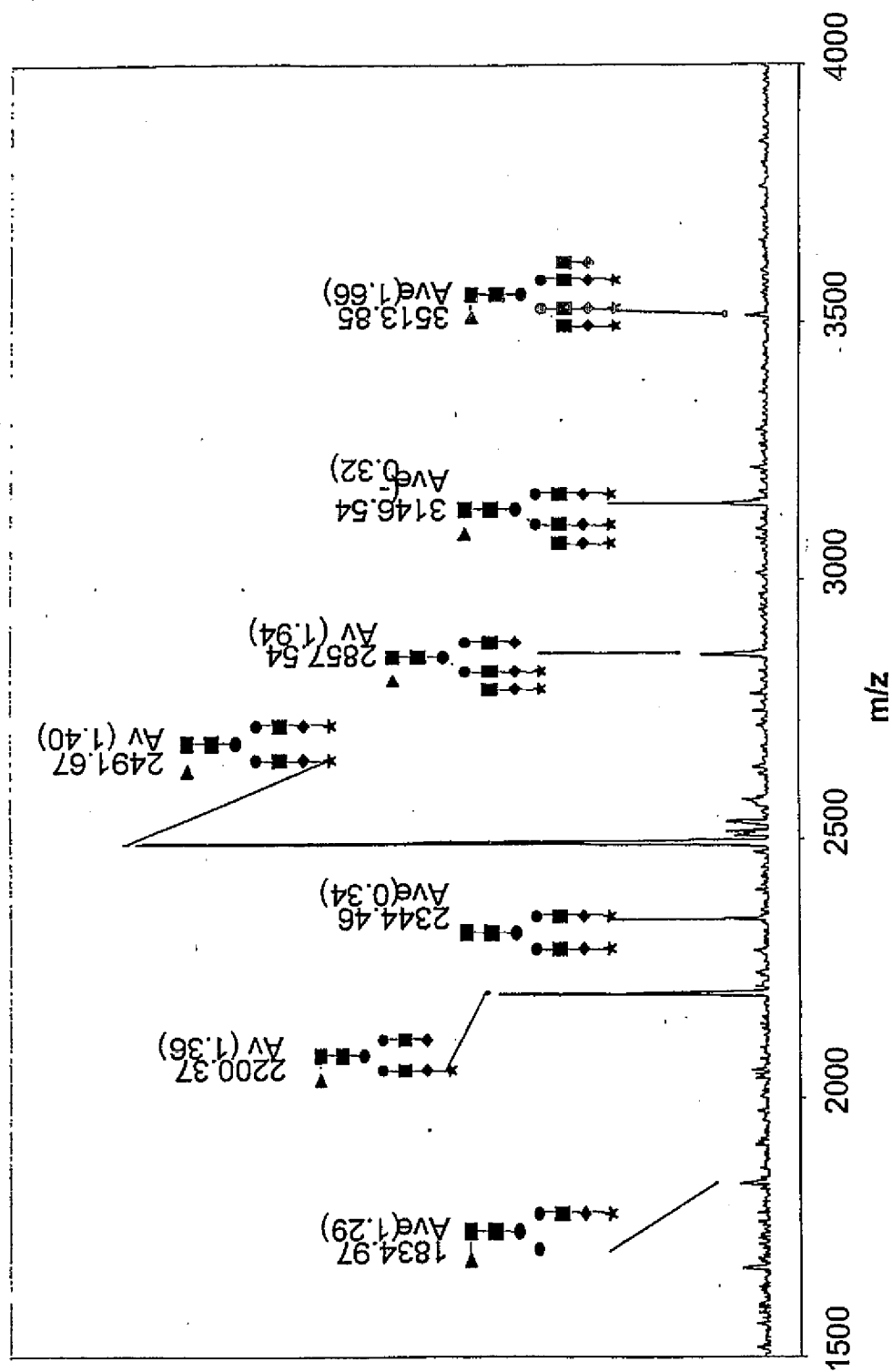


FIG. 173A

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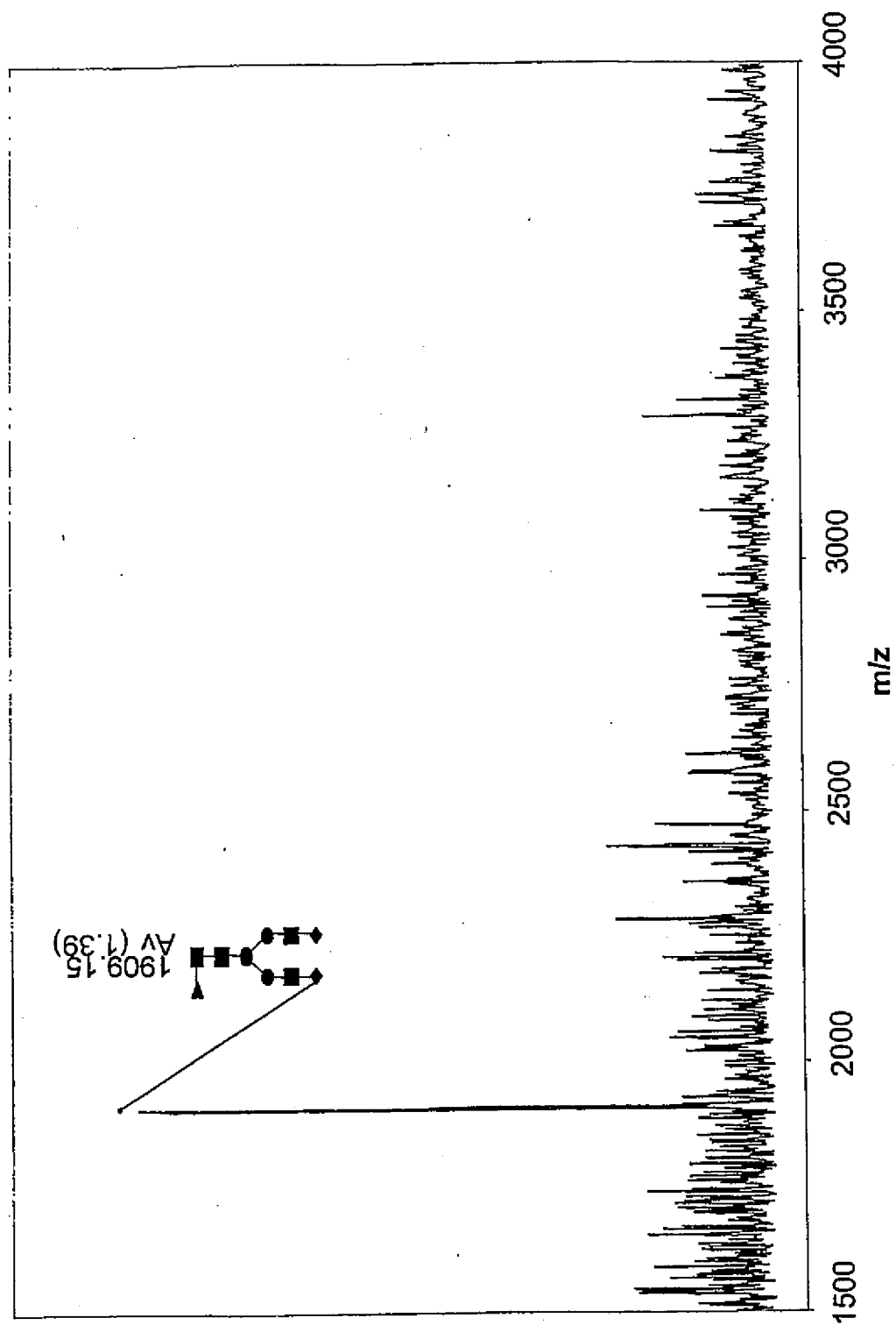


FIG. 173B

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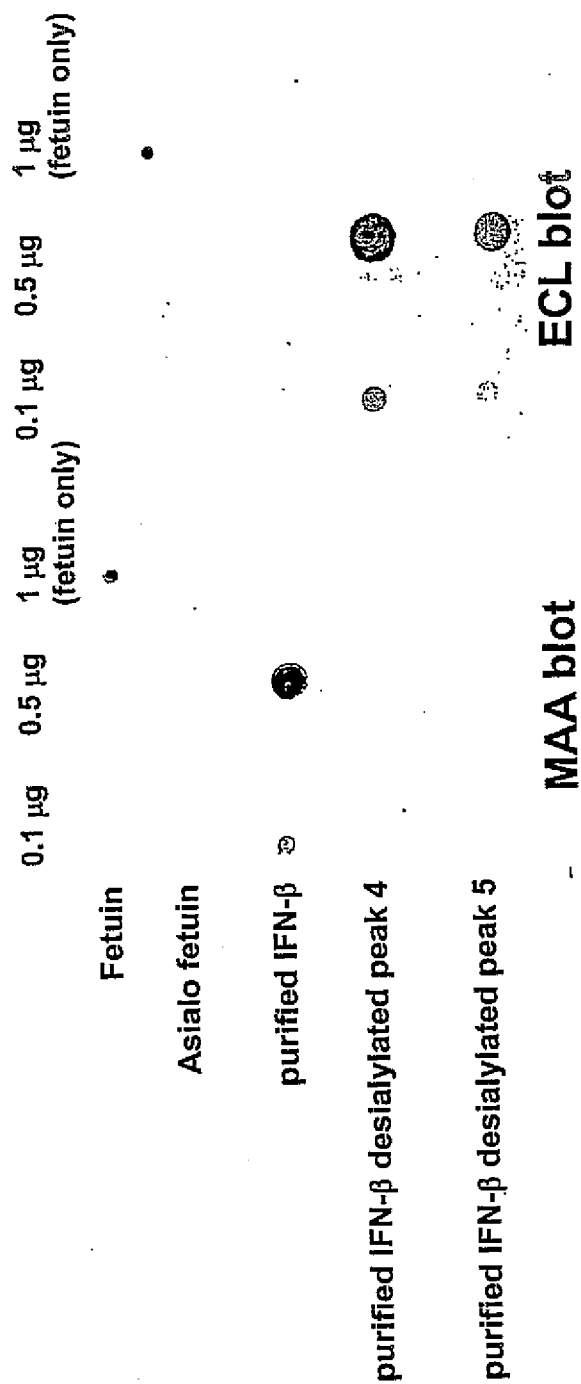


FIG. 174

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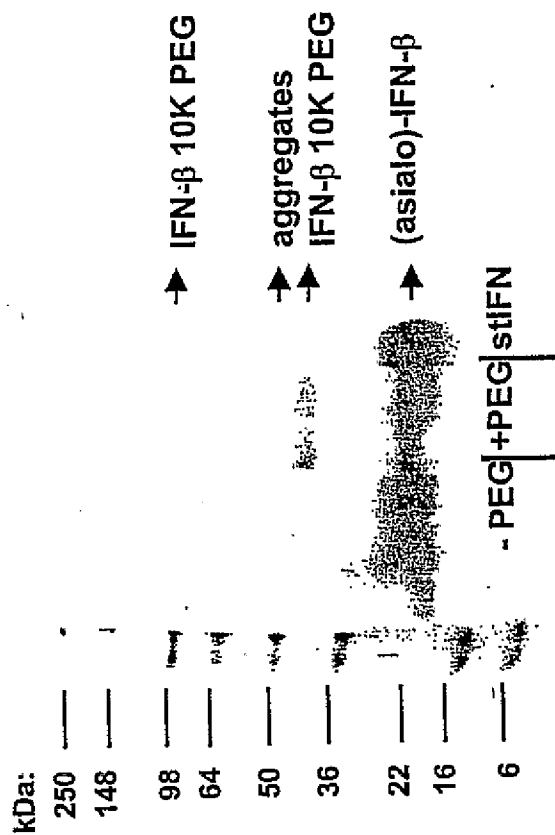
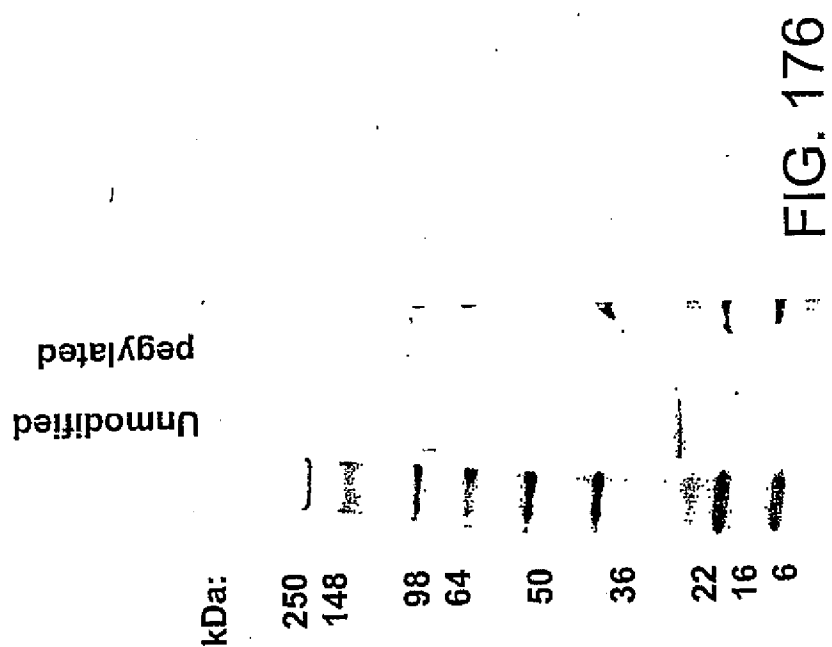


FIG. 175

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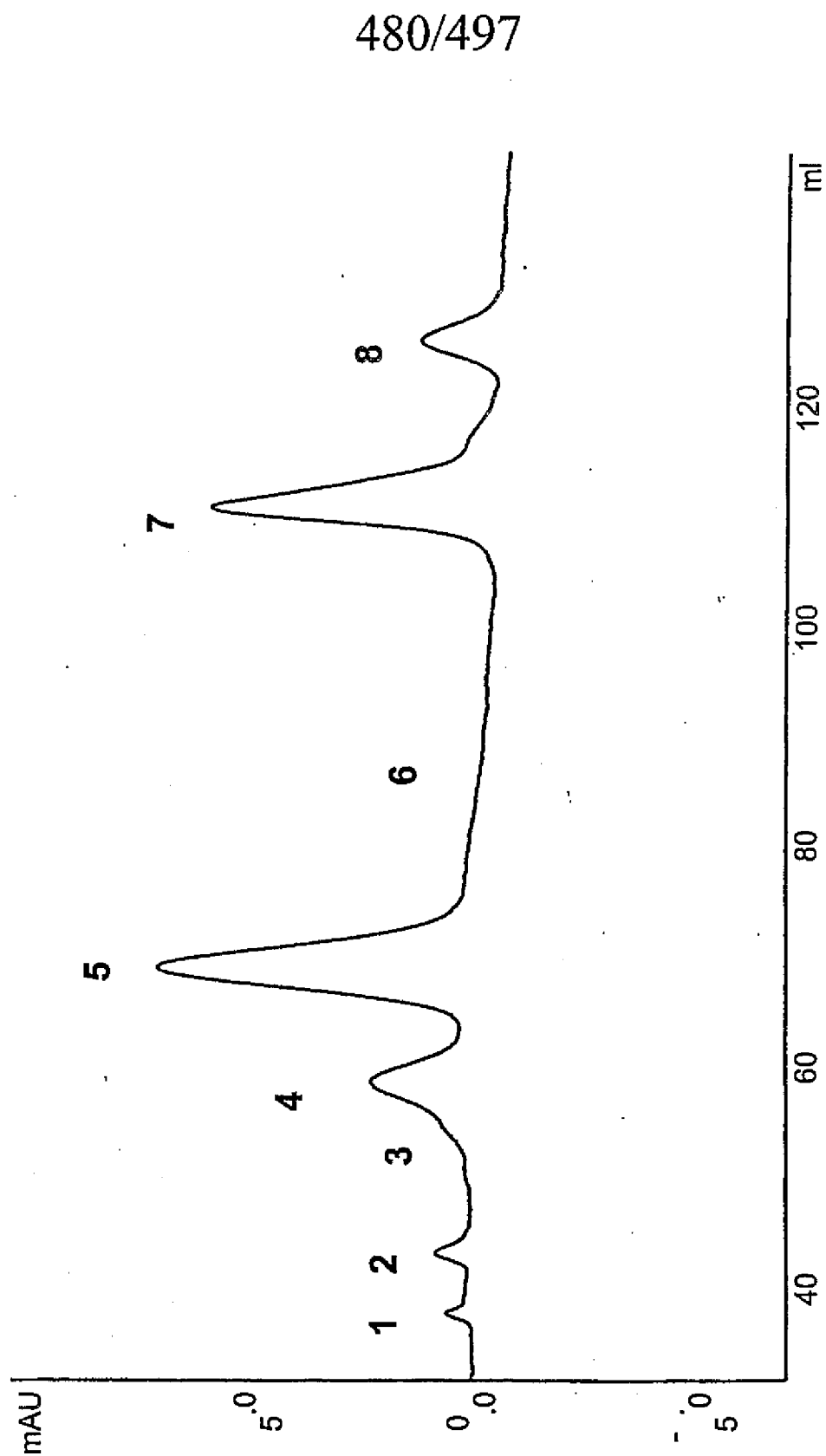
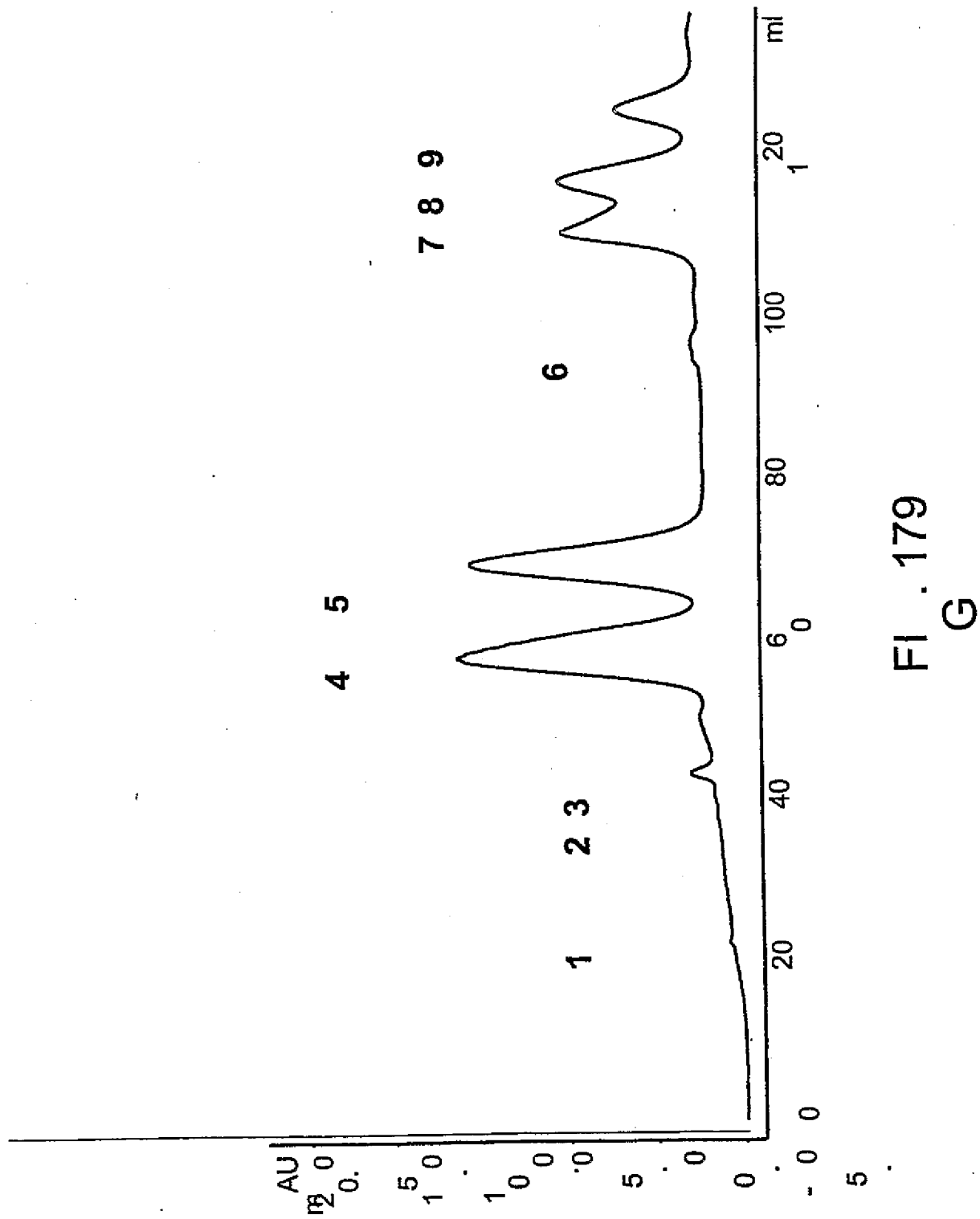
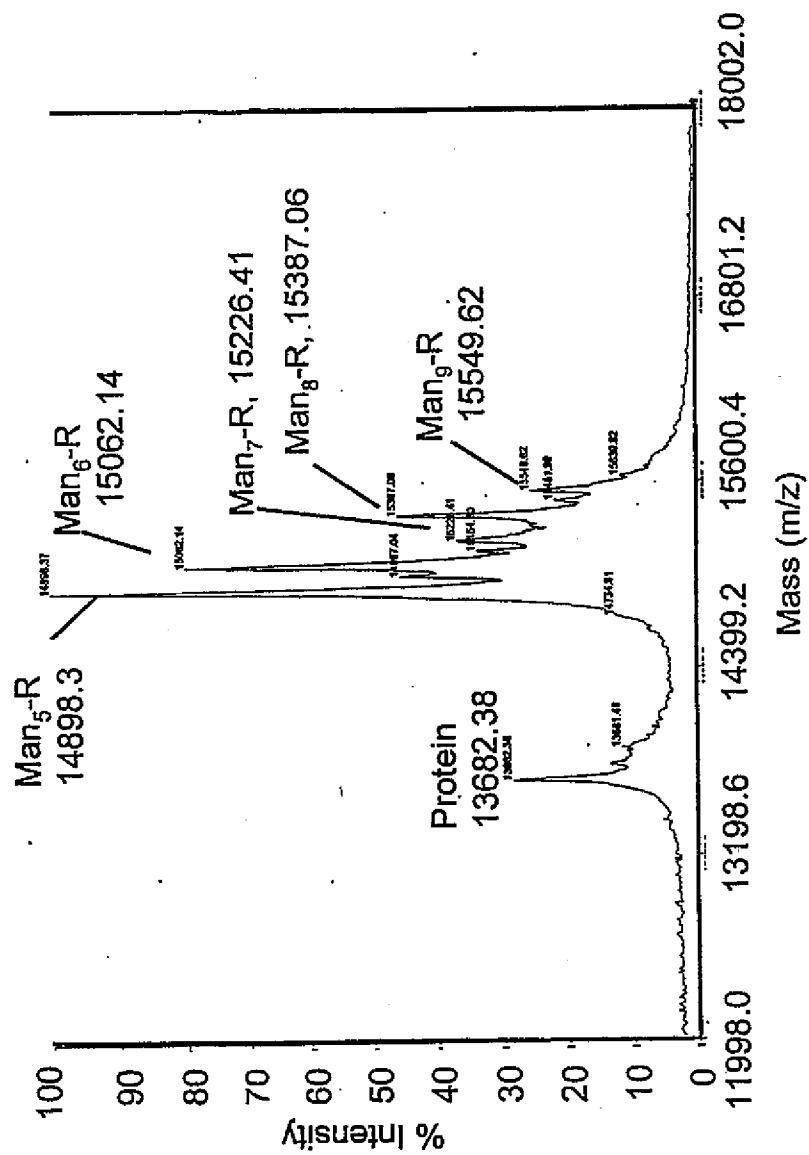


FIG. 177

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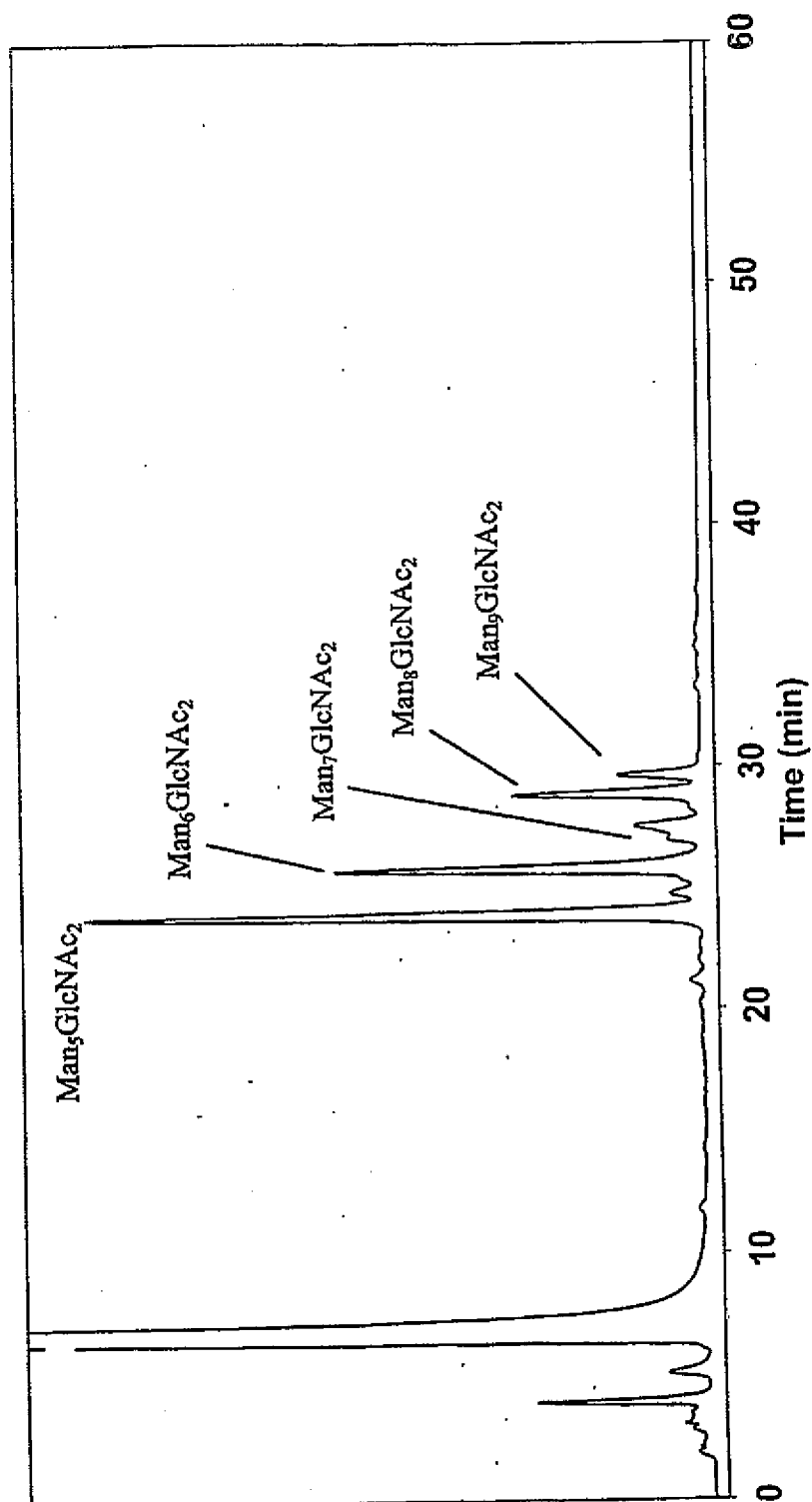
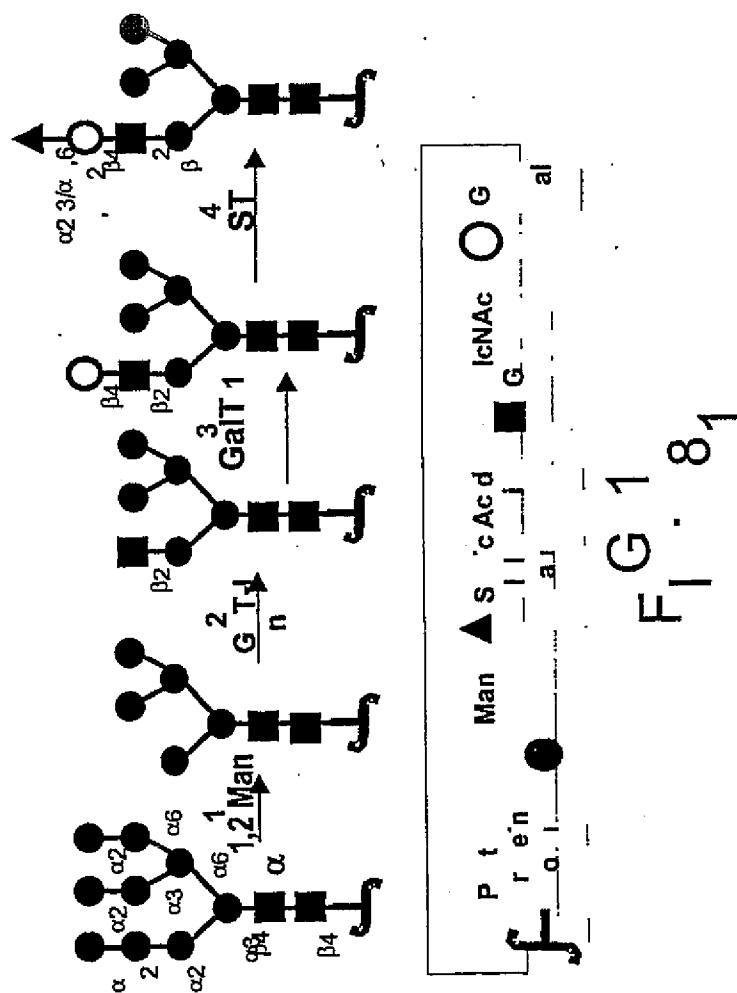


FIG. 180B

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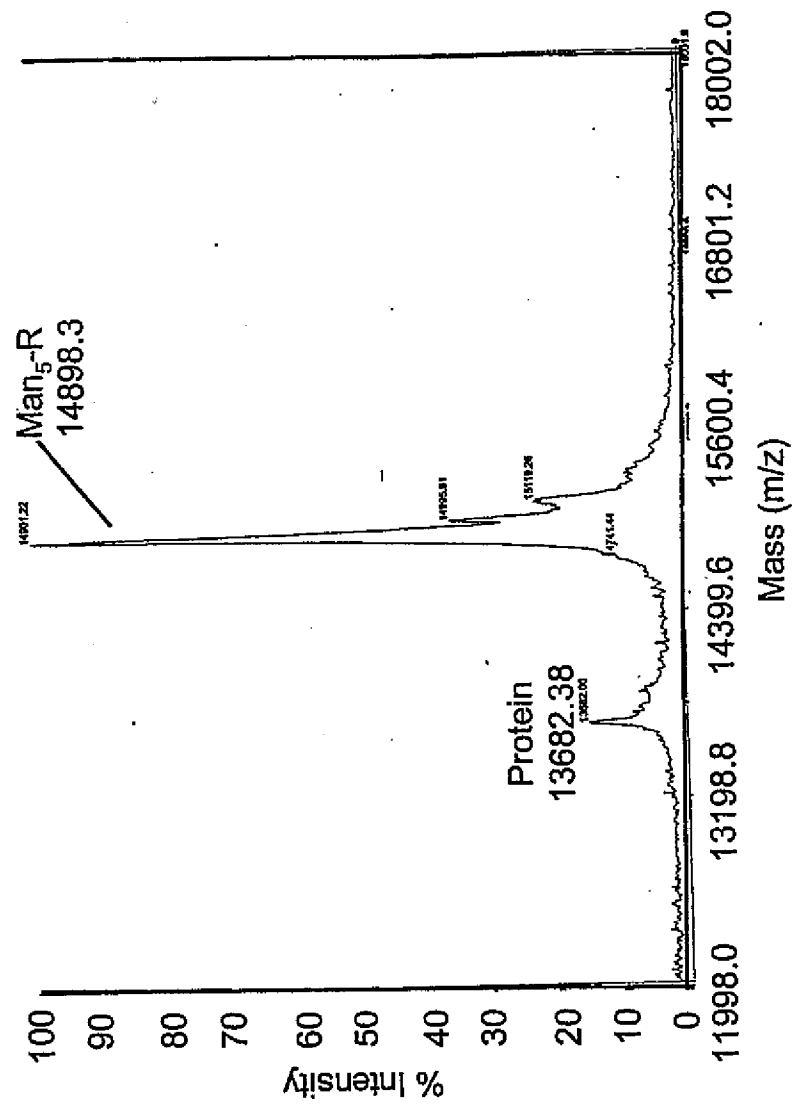


FIG. 182A

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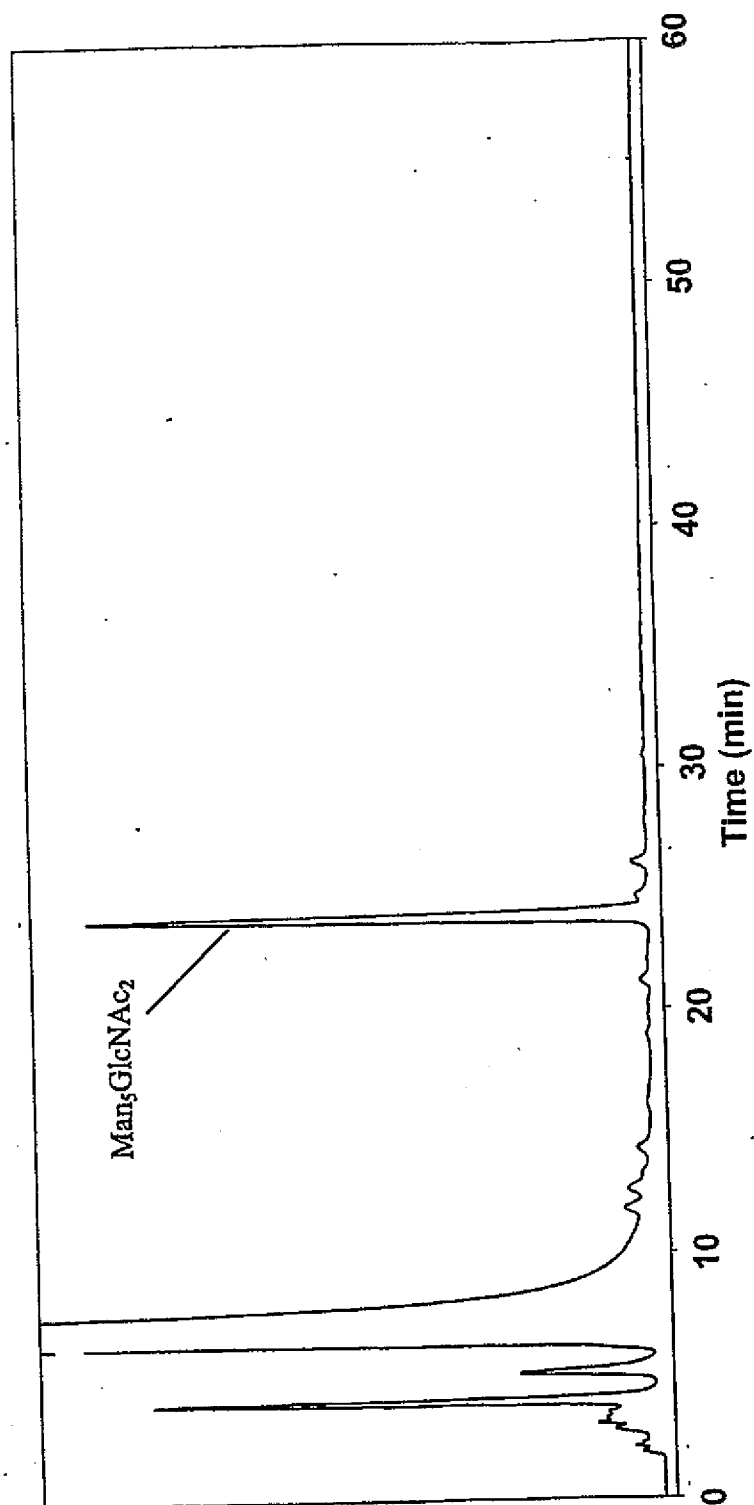
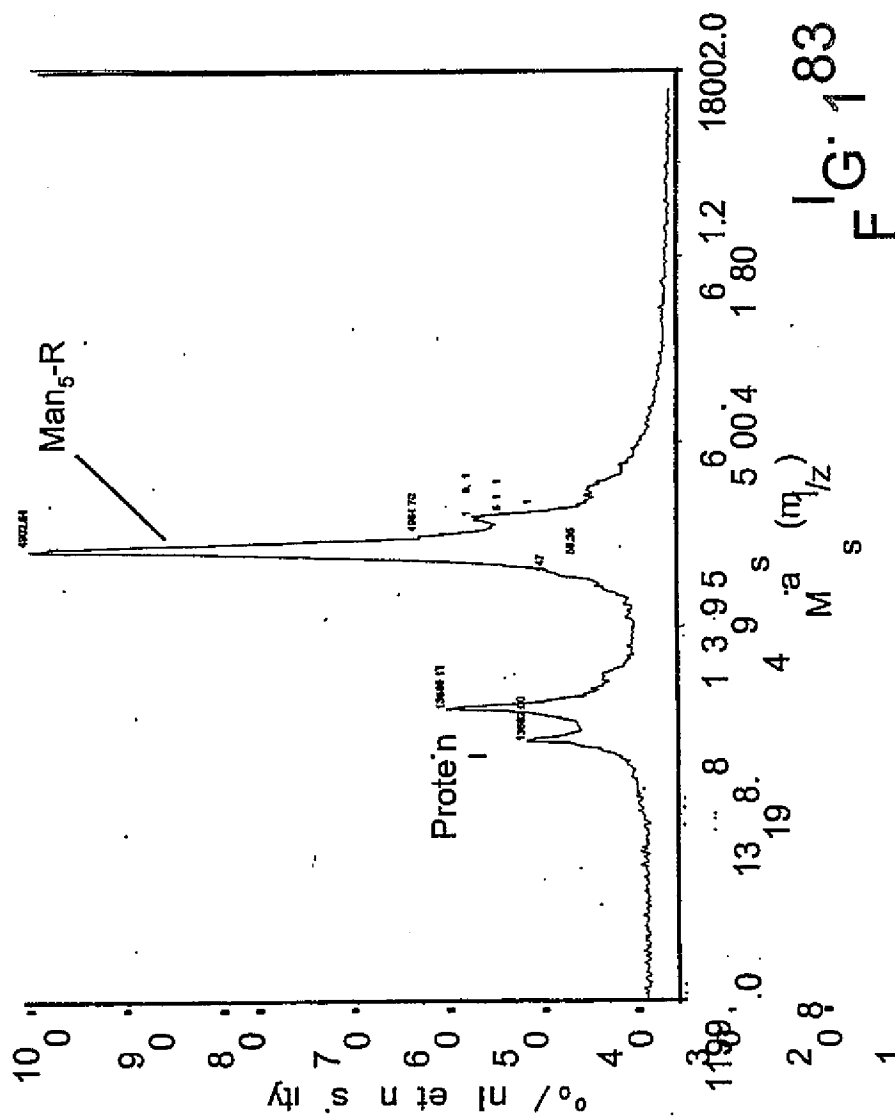


FIG. 182B

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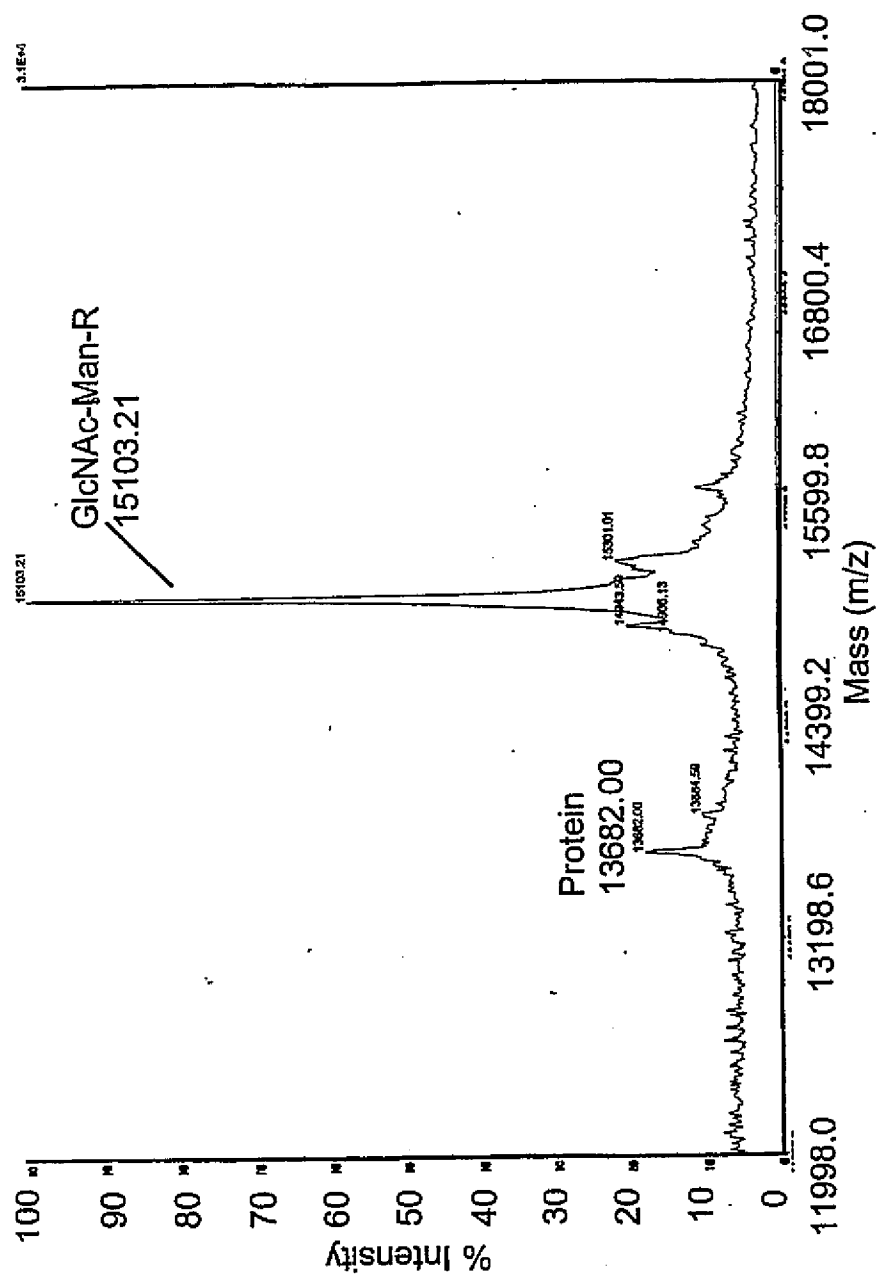


FIG. 184

Mass spectrum showing % Intensity versus Mass (m/z). The x-axis ranges from 6999.0 to 30002.0, and the y-axis ranges from 0 to 100. The spectrum displays a series of peaks, with the most intense peak at m/z 7540.71. Two arrows point to specific peaks: one to m/z 12373.34 labeled "CMP-SA-PEG (10K)" and another to m/z 25466.33 labeled "PEG-SA-Gal-GlcNAc-Man-R".

FIG. 187A

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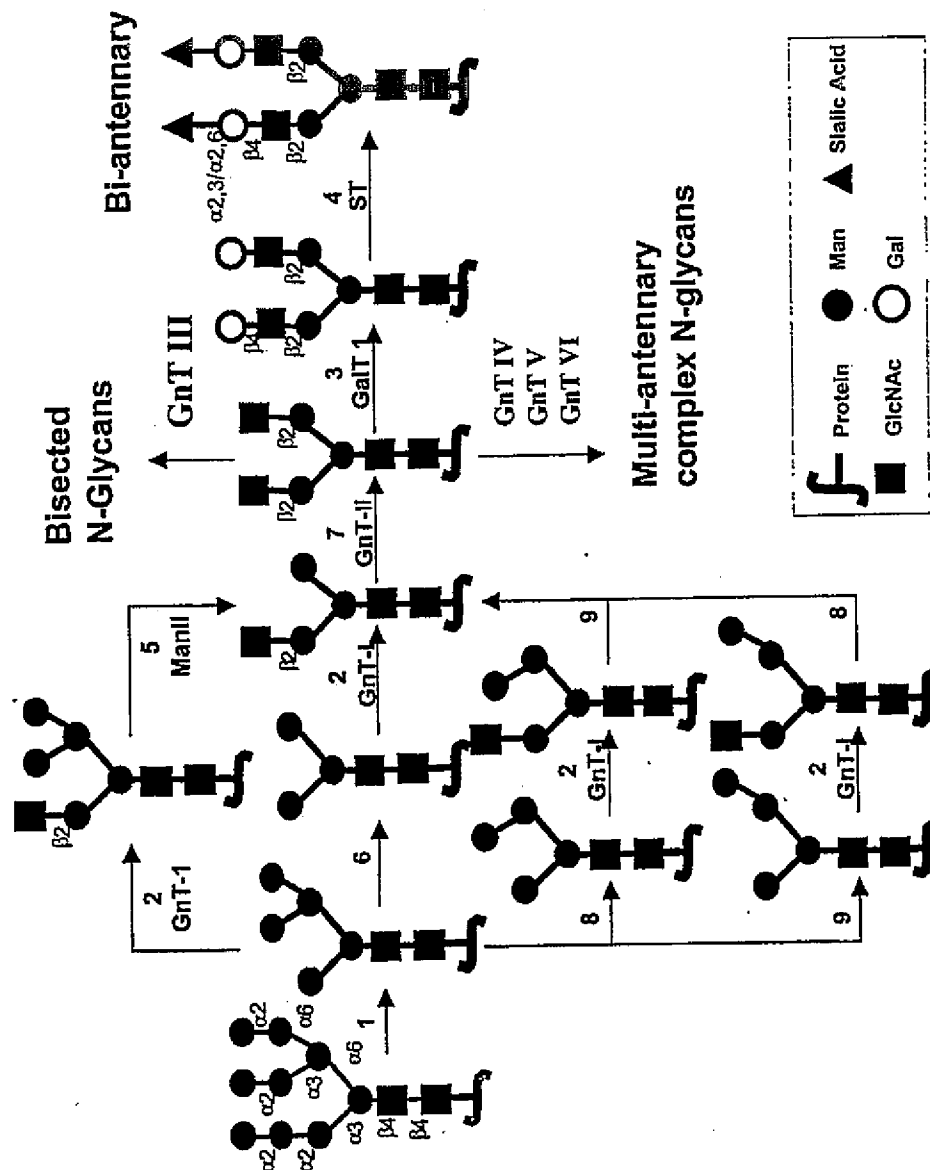


FIG. 188

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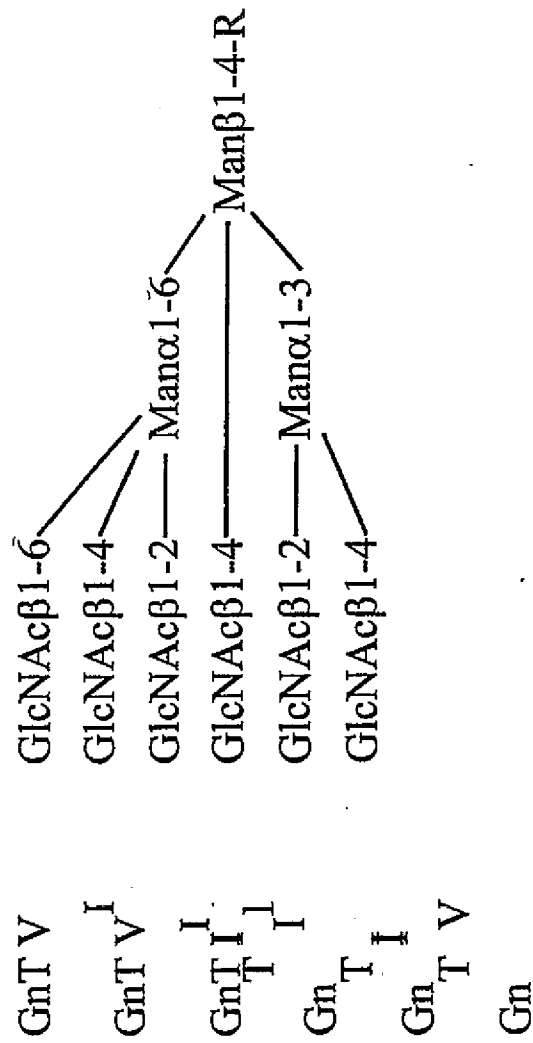


FIG. 189

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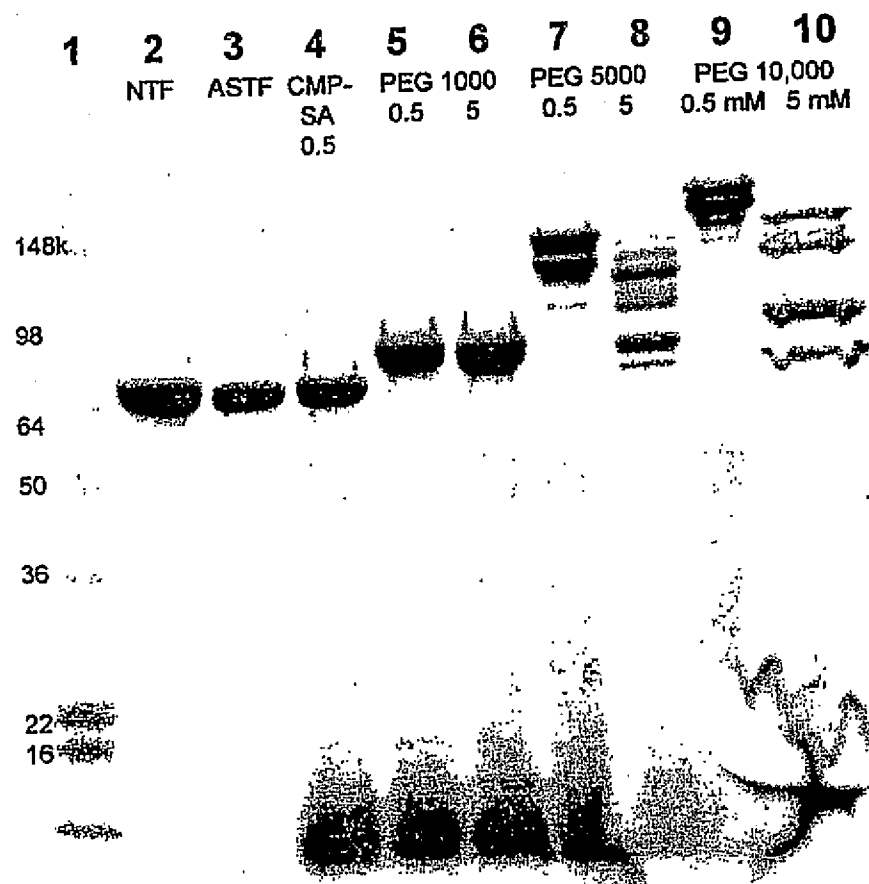


FIG. 190

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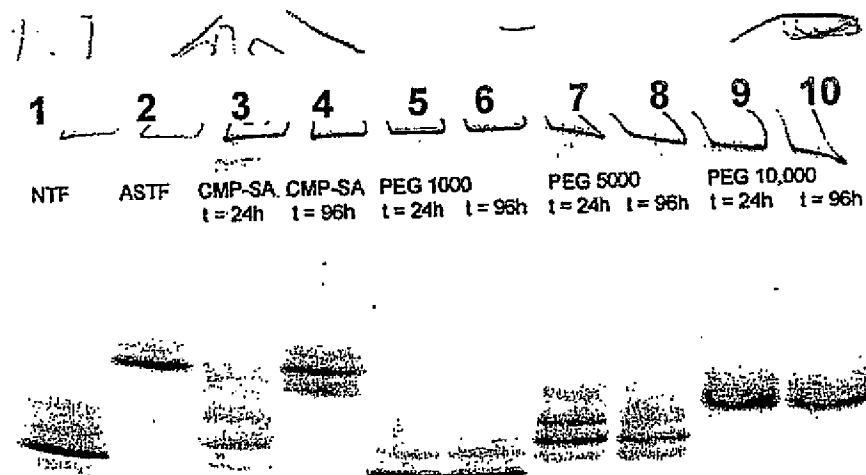


FIG. 191

SEQUENCE LISTING

<110> Neose Technologies, Inc.
DeFrees, Shawn
Zopf, David
Bayer, Robert
Hakes, David
Chen, Xi
Bowe, Caryne

<120> GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
METHODS

<130> 040853-01-5051WO

<150> US 60/328,523
<151> 2001-10-10

<150> US 60/334,233
<151> 2001-11-28

<150> US 60/334,301
<151> 2001-11-28

<150> US 60/344,692
<151> 2001-10-19

<150> US 60/387,292
<151> 2002-06-07

<150> US 60/391,777
<151> 2002-06-25

<150> US 60/396,594
<151> 2002-07-17

<150> US 60/404,249
<151> 2002-08-16

<150> US 60/407,527
<151> 2002-08-28

<150> PCT/US02/32263
<151> 2002-10-09

<150> US 10/360,779
<151> 2003-02-19

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120

ctgtgccacc ccgaggagct ggtgctgctc ggacactctc tgggcatccc ctgggctccc
180

ctgagcagct gccccagcca ggccctgcag ctggcaggct gcttgagcca actccatagc
240

ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc cgagttgggt
300

cccaccttgg acacactgca gctggacgtc gccgactttg ccaccacat ctggcagcag
360

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420

gcctctgctt tccagcgccg ggcaggaggg gtccctgggtg cctcccatct gcagagcttc
480

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<210> 2

<211> 174

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20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
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Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
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 120
 tgcaataata aaacattaac ttatatacttt ttaatttaat gtatagaata gagatataca
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 taggatatgt aaatagatac acagtgtata tgtgattaaa atataatggg agattcaatc
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 360
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 720
 caaaaggctg aaaccatccc tgtcctocat gagatgatcc agcagatctt caatctcttc
 780
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 840
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 900
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 960

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1020

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1080

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1500

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1620

aacaaatata attctgctct cttgtgtatt tgatttttgt atgaaaaaaaa ctaaaaatgg
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1733

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Lys Ser Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu
20 25 30
Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
35 40 45
Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
50 55 60
Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
65 70 75 80

Glu⁸⁵ Met⁸⁵ Ile⁸⁵ Gln⁸⁵ Gln⁸⁵ Ile⁸⁵ Phe⁸⁵ Asn⁸⁵ Leu⁸⁵ Phe⁸⁵ Ser⁸⁵ Thr⁸⁵ Lys⁸⁵ Asp⁸⁵ Ser⁹⁰ Ser⁹⁰

Ala¹⁰⁰ Ala¹⁰⁰ Trp¹⁰⁰ Asp¹⁰⁰ Glu¹⁰⁰ Thr¹⁰⁰ Leu¹⁰⁰ Leu¹⁰⁰ Asp¹⁰⁰ Lys¹⁰⁵ Phe¹⁰⁵ Tyr¹⁰⁵ Thr¹⁰⁵ Glu¹¹⁰ Leu¹¹⁰ Tyr¹¹⁰

Gln¹¹⁵ Gln¹¹⁵ Leu¹¹⁵ Asn¹¹⁵ Asp¹¹⁵ Leu¹¹⁵ Glu¹¹⁵ Ala¹¹⁵ Cys¹¹⁵ Val¹¹⁵ Ile¹¹⁵ Gln¹²⁰ Gly¹²⁰ Val¹²⁰ Gly¹²⁵ Val¹²⁵

Thr¹³⁰ Glu¹³⁰ Thr¹³⁰ Pro¹³⁰ Leu¹³⁰ Met¹³⁰ Lys¹³⁵ Glu¹³⁵ Asp¹³⁵ Ser¹³⁵ Ile¹³⁵ Leu¹⁴⁰ Ala¹⁴⁰ Val¹⁴⁰ Arg¹⁴⁰ Lys¹⁴⁰

Tyr¹⁴⁵ Phe¹⁴⁵ Gln¹⁴⁵ Arg¹⁴⁵ Ile¹⁴⁵ Thr¹⁵⁰ Leu¹⁵⁰ Tyr¹⁵⁰ Leu¹⁵⁰ Lys¹⁵⁰ Glu¹⁵⁵ Lys¹⁵⁵ Lys¹⁵⁵ Tyr¹⁵⁵ Ser¹⁶⁰ Pro¹⁶⁰

Cys¹⁶⁵ Ala¹⁶⁵ Trp¹⁶⁵ Glu¹⁶⁵ Val¹⁶⁵ Val¹⁶⁵ Arg¹⁶⁵ Ala¹⁶⁵ Glu¹⁶⁵ Ile¹⁷⁰ Met¹⁷⁰ Arg¹⁷⁰ Ser¹⁷⁰ Phe¹⁷⁰ Ser¹⁷⁵ Leu¹⁷⁵

Ser¹⁸⁰ Thr¹⁸⁰ Asn¹⁸⁰ Leu¹⁸⁰ Gln¹⁸⁰ Glu¹⁸⁰ Ser¹⁸⁰ Leu¹⁸⁰ Arg¹⁸⁵ Ser¹⁸⁵ Lys¹⁸⁵ Glu¹⁸⁵

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120

ctctgtggc aattgaatgg gaggcttgaa tattgcctca aggacaggat gaactttgac
180

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240

tatgagatgc tccagaacat ctttgctatt ttccagacaag attcatctag cactggctgg
300

aatgagacta ttgttgagaa cctcctggct aatgtctatc atcagataaa ccatctgaag
360

acagtcttg aagaaaaact ggagaaagaa gattttacca ggggaaaact catgagcagt
420

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480

cactgtgcct ggaccatagt cagagtggaa atoctaagga acttttactt cattaacaga
540

cttacagggt acctccgaaa ctgaagatct cctagcctgt ccctctggga ctggacaatt
600

gcttcaagca ttcttcaacc agcagatgct gtttaagtga ctgatggcta atgtactgca
660

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Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
35 40 45
Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
50 55 60
Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
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85 90 95
Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
100 105 110
Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
115 120 125
Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
130 135 140
Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
145 150 155 160
His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
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180 185

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120

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180

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240

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300

gaccagctcc agtctatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag
360

acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc
420

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480

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540

aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaagggtgtg ccccaaaggg
600

gagtgtccat ggcaggctct gttgttggtg aatggagctc agttgtgtgg ggggaccctg
660

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720

aacctgatcg cggtgctggg cgagcacgac ctacgcgagc acgacgggga tgagcagagc
780

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ctgccgaac ggacgttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc
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Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
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Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35 40 45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
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Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
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Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
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Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
245 250 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
260 265 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
275 280 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
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 Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
 305 310 315 320
 Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
 325 330 335
 Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
 340 345 350
 Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 355 360 365
 Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
 370 375 380
 Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
 385 390 395 400
 Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
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 <213> Homo sapiens

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 ggatatctac tcagtgtgta atgtacagtt tttcttgatc atgaaaacgc caacaaaatt
 120
 ctgaatcggc caagaggta taattcaggt aaattggaag agtttgttca agggaacctt
 180
 gagagagaat gtatggaaga aaagtgtagt tttgaagaac cagcagaagt ttttgaaaac
 240
 actgaaaaga caactgaatt ttggaagcag tatgttgatg gagatcagtg tgagtccaat
 300
 ccatgtttta atggcggcag ttgcaaggat gacattaatt cctatgaatg ttgggtgtccc
 360
 tttggatttg aaggaaagaa ctgtgaatta gatgtaacat gtaacattaa gaatggcaga
 420
 tgcgagcagt tttgtaaaaa tagtgctgat aacaaggtgg tttgctcctg tactgagggg
 480

tatcgaattg cagaacaaacca gaagtcctgt gaaccagcag tgccatttcc atgtggaaga
540

gtttctgttt cacaaacttc taagctcacc cgtgctgagg ctgtttttcc tgatgtggac
600

tatgtaaatc ctactgaagc tgaaccatt ttggataaca tcaactcaagg cacccaatca
660

tttaatgact tcaactcgggt tgttggtgga gaagatgcca aaccagggtca attoccttgg
720

caggttgttt tgaatggtaa agttgatgca ttctgtggag gctctatcgt taatgaaaaa
780

tggattgtaa ctgctgcca ctgtgttgaa actggtgtta aaattacagt tgcgcagggt
840

gaacataata ttgaggagac agaacataca gagcaaaagc gaaatgtgat tcgagcaatt
900

attcctcacc acaactacaa tgcagctatt aataagtaca accatgacat tgcccttctg
960

gaactggacg aacccttagt gctaaacagc tacgttacac ctatttgcat tgctgacaag
1020

gaatacacga acatcttcct caaatttgga tctggctatg taagtggctg ggcaagagtc
1080

ttccacaaag ggagatcagc tttagttctt cagtacctta gagttccact tgttgaccga
1140

gccacatgtc ttgatctac aaagttcacc atctataaca acatgttctg tgctggcttc
1200

catgaaggag gtagagattc atgtcaagga gatagtgggg gaccccatgt tactgaagtg
1260

gaagggacca gtttcttaac tggaattatt agctgggggtg aagagtgtgc aatgaaaggc
1320

aaatatggaa tatataccaa ggtatcccg tatgtcaact ggattaagga aaaaacaaag
1380

ctcaattaat gaaagatgga tttccaaggt taattcattg gaattgaaaa ttaacag
1437

<210> 10
<211> 462
<212> PRT
<213> Homo sapiens

<400> 10
Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr
1 5 10 15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
20 25 30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn

35	40	45
Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys 50 55 60		
Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn 65 70 75 80		
Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln 85 90 95		
Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile 100 105 110		
Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys 115 120 125		
Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe 130 135 140		
Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly 145 150 155 160		
Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe 165 170 175		
Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala 180 185 190		
Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu 195 200 205		
Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe 210 215 220		
Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp 225 230 235 240		
Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile 245 250 255		
Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly 260 265 270		
Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu 275 280 285		
His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His 290 295 300		
Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu 305 310 315 320		
Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys 325 330 335		
Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly 340 345 350		
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu 355 360 365		

Val Leu Gln Tyr Leu Arg^u Val Pro Leu Val Asp Arg Ala Thr Cys Leu
 370 375 380

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe
 385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His
 405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp
 420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val
 435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
 450 455 460

<210> 11
 <211> 603
 <212> DNA
 <213> Homo sapiens

<400> 11
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gtttctccatt ccgctcctga tgtgcaggat tgcccagaat gcacgctaca ggaaaaccca
 120

ttcttctccc agccgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca
 180

tatcccactc cactaagggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag
 240

tccacttgct gtgtagctaa atcatataac agggtcacag taatgggggg tttcaaagtg
 300

gagaaccaca cggcgtgccca ctgcagtact tgttattatc acaaatttta aatgttttac
 360

caagtgtgtt cttgatgact gctgattttc tggaatggaa aattaagttg tttagtgttt
 420

atggctttgt gagataaaac tctccttttc cttaccatac cactttgaca cgcttcaagg
 480

atatactgca gctttactgc cttcctcgtt atoctacagt acaatcagca gtctagttct
 540

tttcatttgg aatgaataca gcattaagct tgttccactg caaataaagc cttttaaatc
 600

atc
 603

<210> 12
 <211> 116
 <212> PRT

<213> Homo sapiens

<400> 12

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
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Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
20 25 30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
35 40 45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
100 105 110

Tyr His Lys Ser
115

<210> 13

<211> 390

<212> DNA

<213> Homo sapiens

<400> 13

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60

tgtgagctga ccaacatcac cattgcaata gagaaagaag aatgtcggtt ctgcataagc
120

atcaacacca ctggtgtgc tggctactgc tacaccaggg atctggtgta taaggaccca
180

gccaggccca aaatccagaa aacatgtacc ttcaaggaac tggatatatga aacagtgaga
240

gtgcccggct gtgctcacca tgcagattcc ttgtatacat acccagtggc caccagtgt
300

cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggccagc
360

tactgtcct ttggtgaaat gaaagaataa
390

<210> 14

<211> 129

<212> PRT

<213> Homo sapiens

<400> 14

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile

1

5

10

15

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
20 25 30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
35 40 45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
50 55 60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
65 70 75 80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
85 90 95

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
100 105 110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys
115 120 125

Glu

<210> 15

<211> 1342

<212> DNA

<213> Homo sapiens

<400> 15

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60

ccgccctctc ctccaggccc gtggggctgg cctgcaccg ccgagcttc cgggatgagg
120

gccccgggtg tggtcacccg gcgcgcccc ggtcgctgag ggaccccggc caggcgcgga
180

gatgggggtg caogaatgtc ctgcctggct gtggcttctc ctgtccctgc tgtcgctccc
240

tctgggcctc ccagtcctgg gcgccccacc acgcctcctc tgtgacagcc gagtccctga
300

gaggtacctc ttggaggcca aggaggccga gaatatcacg acgggctgtg ctgaacactg
360

cagcttgaat gagaatatca ctgtcccaga caccaaagtt aatttctatg cctggaagag
420

gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaagc
480

tgtcctgcgg ggccaggccc tgttggtcaa ctcttcccag ccgtgggagc cctgcagct
540

gcattgtgat aaagccgtca gtggccttcg cagcctcacc actctgcttc gggctctgcg
600

agcccagaag gaagccatct cccctccaga tggggcctca gctgctccac tccgaacaat
660

cactgctgac actttccgca aactcttccg agtctactcc aatttcctcc ggggaaagct
720

gaagctgtac acaggggagg cctgcaggac aggggacaga tgaccagggtg tgtccacctg
780

ggcatatcca ccacctccct caccaacatt gcttggtgcca caccctcccc cgccactcct
840

gaaccccgtc gaggggctct cagctcagcg ccagcctgtc ccatggacac tccagtgcc
900

gcaatgacat ctcaggggcc agaggaactg tccagagagc aactctgaga tctaaggatg
960

tcacagggcc aacttgaggg cccagagcag gaagcattca gagagcagct ttaaactcag
1020

ggacagagcc atgctgggaa gacgcctgag ctactcggc accctgcaaa atttgatgcc
1080

aggacacgct ttggaggcga tttacctgtt ttgcaccta ccatcagggg caggatgacc
1140

tggagaactt aggtggcaag ctgtgacttc tccaggtctc acgggcatgg gcactccctt
1200

ggtggcaaga gcccccttga caccggggtg gtgggaacca tgaagacagg atgggggctg
1260

gcctctggct ctcatggggt ccaagttttg tgtattcttc aacctcattg acaagaactg
1320

aaaccaccaa aaaaaaaaaa aa
1342

<210> 16
<211> 193
<212> PRT
<213> Homo sapiens

<400> 16
Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Arg

<210> 17
<211> 435
<212> DNA
<213> Homo sapiens

<400> 17
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60

cgctcgccca gcccagcac gcagccctgg gagcatgtga atgccatcca ggaggcccg
120

cgctctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcac
180

tcagaaatgt ttgacctcca ggagccgacc tgcttacaga cccgcttga gctgtacaag
240

cagggcctgc ggggcagcct caccaagctc aagggcccct tgaccatgat ggccagccac
300

tacaagcagc actgccctcc aaccccgga acttctgtg caaccagat tatcaccttt
360

gaaagtttca aagagaacct gaaggacttt ctgcttgtca tcccctttga ctgctgggag
420

ccagtccagg agtga
435

<210> 18
<211> 144
<212> PRT
<213> Homo sapiens

<400> 18
Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile

1				5						10							15
Ser	Ala	Pro	Ala	Arg	Ser	Pro	Ser	Pro	Ser	Thr	Gln	Pro	Trp	Glu	His		
			20					25					30				
Val	Asn	Ala	Ile	Gln	Glu	Ala	Arg	Arg	Leu	Leu	Asn	Leu	Ser	Arg	Asp		
		35					40					45					
Thr	Ala	Ala	Glu	Met	Asn	Glu	Thr	Val	Glu	Val	Ile	Ser	Glu	Met	Phe		
	50					55					60						
Asp	Leu	Gln	Glu	Pro	Thr	Cys	Leu	Gln	Thr	Arg	Leu	Glu	Leu	Tyr	Lys		
65					70					75					80		
Gln	Gly	Leu	Arg	Gly	Ser	Leu	Thr	Lys	Leu	Lys	Gly	Pro	Leu	Thr	Met		
				85					90					95			
Met	Ala	Ser	His	Tyr	Lys	Gln	His	Cys	Pro	Pro	Thr	Pro	Glu	Thr	Ser		
			100					105					110				
Cys	Ala	Thr	Gln	Ile	Ile	Thr	Phe	Glu	Ser	Phe	Lys	Glu	Asn	Leu	Lys		
		115					120					125					
Asp	Phe	Leu	Leu	Val	Ile	Pro	Phe	Asp	Cys	Trp	Glu	Pro	Val	Gln	Glu		
	130					135					140						

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<210> 19
<211> 501
<212> DNA
<213> Homo sapiens
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<400> 19
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tgttactgcc aggaccata tgtaaaagaa gcagaaaacc ttaagaaata ttttaatgca
120

gggtcattcag atgtagcgga taatggaact cttttcttag gcattttgaa gaattggaaa
180

gaggagagtg acagaaaaat aatgcagagc caaattgtct ctttttactt caaacttttt
240

aaaaacttta aagatgacca gagcatccaa aagagtgtgg agaccatcaa ggaagacatg
300

aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat
360

tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgatg
420

gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga
480

ggtcgaagag catcccagta a
501

$\langle 210 \rangle$	20
$\langle 211 \rangle$	166

<212> PRT

<213> Homo sapiens

<400> 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
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Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
 20 25 30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
 35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
 50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
 65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
 85 90 95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
 100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
 115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
 130 135 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
 145 150 155 160

Gly Arg Arg Ala Ser Gln
 165

<210> 21

<211> 1352

<212> DNA

<213> Homo sapiens

<400> 21

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cctgtgctgc ctggctccctg tctccctggc tgaggatccc caggagatg ctgcccagaa
 120

gacagataca tcccaccatg atcaggatca cccaaccttc aacaagatca cccccaacct
 180

ggctgagttc gccttcagcc tataccgcc gctggcacac cagccaaca gcaccaatat
 240

cttctttctcc ccagttagca togtacagc ctttgcaatg ctctccctgg ggaccaaggc
 300

tgacaactcac gatgaaatcc tggagggcct gaatttcaac ctcacggaga ttccggaggc
 360

tcagatccat gaaggcttcc aggaactcct ccgtaccctc aaccagccag acagccagct
420

ccagctgacc accggcaatg gcctgttcct cagcgagggc ctgaagctag tggataagtt
480

tttgaggat gttaaaaagt tgtaccactc agaagccttc actgtcaact tcggggacac
540

cgaagaggcc aagaaacaga tcaacgatta cgtggagaag ggtactcaag ggaaaattgt
600

ggatttggtc aaggagcttg acagagacac agtttttgcct ctggtgaatt acatcttctt
660

taaaggcaaa tgggagagac cctttgaagt caaggacacc gaggaagagg acttccacgt
720

ggaccaggtg accaccgtga aggtgcctat gatgaagcgt ttaggcatgt ttaacatcca
780

gcactgtaag aagctgtcca gctgggtgct gctgatgaaa tacctgggca atgccaccgc
840

catcttcttc ctgcctgatg aggggaaaact acagcactctg gaaaatgaac tcaccacga
900

tatcatcacc aagttcctgg aaaatgaaga cagaaggtct gccagcttac atttaccxaa
960

actgtocatt actggaacct atgatctgaa gagcgtcctg ggtcaactgg gcactactaa
1020

ggtcttcagc aatggggctg acctctccgg ggtcacagag gaggcacccc tgaagctctc
1080

caaggccgtg cataaggctg tgctgaccat cgacgagaaa gggactgaag ctgctggggc
1140

catgttttta gaggccatac ccatgtctat ccccccgag gtcaagttca acaaaccctt
1200

tgtcttctta atgattgaac aaaataccaa gtotccctc ttcattggaa aagtggtgaa
1260

tcacaccaa aaataactgc ctctcgctcc tcaacccctc cctccatcc ctggccccct
1320

ccctggatga cattaaagaa gggttgagct gg
1352

<210> 22
<211> 418
<212> PRT
<213> Homo sapiens

<400> 22
Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
1 5 10 15
Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala

20
 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
 35 40 45
 Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 50 55 60
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
 65 70 75 80
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
 85 90 95
 His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
 100 105 110
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
 115 120 125
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
 130 135 140
 Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
 145 150 155 160
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
 165 170 175
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
 180 185 190
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
 195 200 205
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
 210 215 220
 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
 225 230 235 240
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
 245 250 255
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
 260 265 270
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
 275 280 285
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 290 295 300
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 305 310 315 320
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 325 330 335
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 340 345 350

Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 355 360 365
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 370 375 380
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 385 390 395 400
 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 405 410 415

Gln Lys

<210> 23
 <211> 2004
 <212> DNA
 <213> Homo sapiens

<400> 23
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 ctctatcctt cagagactct ggaacccctg tggctcttctc ttcattctaata gacctgagg
 120
 ggatggagtt ttcaagtcct tccagagagg aatgtcccaa gcctttgagt agggtaagca
 180
 tcatggctgg cagcctcaca ggtttgcttc tacttcaggc agtgtoctgg gcatcagggtg
 240
 cccgcccctg catccctaaa agcttcgggt acagctcggg ggtgtgtgtc tgcaatgcca
 300
 catactgtga ctcttttgac cccccgaact ttcttgccct tggtagcttc agccgctatg
 360
 agagtacacg cagtgggcga cggatggagc tgagtatggg gcccatccag gctaatacaca
 420
 cgggcacagg cctgctactg acctgcagc cagaacagaa gttccagaaa gtgaagggat
 480
 ttggaggggc catgacagat gctgctgctc tcaacatcct tgccctgtca cccctgccc
 540
 aaaatttgct acttaaactg tactttctctg aagaaggaat cggatataac atcatccggg
 600
 tacccatggc cagctgtgac ttctccatcc gcacctacac ctatgcagac accctgatg
 660
 atttccagtt gcacaacttc agcctcccag aggaagatac caagctcaag ataccctga
 720
 ttcaaccgagc cctgcagttg gccagcgtc ccgtttcact ccttgccagc cctggacat
 780

" caccacttg gctcaagacc aatggagcgg tgaatgggaa ggggtcacc aagggacagc
840

cggagacat ctaccaccag acctgggcca gatactttgt gaagttcctg gatgcctatg
900

ctgagcaciaa gttacagttc tgggcagtga cagctgaaaa tgagccttct gctgggctgt
960

tgagtggata ccccttcag tgcctgggct tcaccctga acatcagcga gacttcattg
1020

cccgtgacct aggtcctacc ctgcacaaca gtactcacca caatgtccgc ctactcatgc
1080

tggatgacca acgcttgctg ctgcccact gggcaaagggt ggtactgaca gaccagaaag
1140

cagctaaata tgttcatggc attgctgtac attggtacct ggactttctg gctccagcca
1200

aagccaccct aggggagaca caccgcctgt tccccaacac catgctcttt gcctcagagg
1260

cctgtgtggg ctccaagttc tgggagcaga gtgtgcggct aggtccttg gatcgaggga
1320

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<212> PRT
<213> Homo sapiens

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Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
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Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
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Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
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Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
115 120 125
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Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
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Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
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Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
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Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
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Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
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Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
225 230 235 240
Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
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Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
260 265 270
Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu

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Gln	Tyr	Ser	His	Ser	Ile	Ile	Thr	Asn	Leu	Leu	Tyr	His	Val	Val	Gly
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Asp	Pro	Ala	Val	Gly	Phe	Leu	Glu	Thr	Ile	Ser	Pro	Gly	Tyr	Ser	Ile
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240

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Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
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Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
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Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
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Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
100 105 110

Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
115 120 125

Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
130 135 140

Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
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Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
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Gln	Lys	Phe	Glu	Val	Glu	Lys	Tyr	Ile	Val	His	Lys	Glu	Phe	Asp	Asp		
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Pro	Ala	Asp	Leu	Gln	Leu	Pro	Asp	Trp	Thr	Glu	Cys	Glu	Leu	Ser	Gly		
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Glu	Ala	His	Val	Arg	Leu	Tyr	Pro	Ser	Ser	Arg	Cys	Thr	Ser	Gln	His		
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Arg	Ser	Gly	Gly														

Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val
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 <212> DNA
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Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
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Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys Gln Leu Gln
 65 70 75 80

Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
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Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
 100 105 110

Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
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Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
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Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
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His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
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Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
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Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
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Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr

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Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp 225 230 235 240		
Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr 245 250 255		
Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val 260 265 270		
Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile 275 280 285		
Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser 290 295 300		
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Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp 355 360 365		
Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser 370 375 380		
Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr 385 390 395 400		
Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro 405 410 415		
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Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met 435 440 445		
Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu 450 455 460		
Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu 465 470 475 480		
Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro 485 490 495		
His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys 500 505 510		
Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe 515 520 525		

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Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
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Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
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Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
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Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
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Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
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Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
 645 650 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
 660 665 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
 675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
 690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
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Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
 725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
 740 745 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg
 755 760 765

Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp
 770 775 780

Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys
 785 790 795 800

Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser
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Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr
 820 825 830

Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
 835 840 845

Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
 850 855 860

Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
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Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
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Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
 900 905 910

Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
 915 920 925

Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
 930 935 940

Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
 945 950 955 960

Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
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Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
 980 985 990

Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
 995 1000 1005

Leu Phe Lys Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser
 1010 1015 1020

Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser
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Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu
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Ser Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg
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Met Leu Met Asp Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met
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Ser Asn Lys Thr Thr Ser Ser Lys Asn Met Glu Met Val Gln Gln
 1085 1090 1095

Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala Gln Asn Pro Asp Met
 1100 1105 1110

Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg Trp Ile
 1115 1120 1125

Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro
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Ser Pro Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu
 1145 1150 1155

Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys Val Val Val Gly Lys

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Lys Lys Glu Thr Leu Ile Gln	Glu Asn Val Val Leu Pro Gln Ile	
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His Thr Val Thr Gly Thr Lys	Asn Phe Met Lys Asn Leu Phe Leu	
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Leu Ser Thr Arg Gln Asn Val	Glu Gly Ser Tyr Asp Gly Ala Tyr	
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Arg Thr Lys Lys His Thr Ala	His Phe Ser Lys Lys Gly Glu Glu	
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Glu Asn Leu Glu Gly Leu Gly	Asn Gln Thr Lys Gln Ile Val Glu	
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Lys Tyr Ala Cys Thr Thr Arg	Ile Ser Pro Asn Thr Ser Gln Gln	
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Pro	Gly	His	Leu	Asp	Leu	Val	Glu	Gly	Ser	Leu	Leu	Gln	Gly	Thr
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Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu 1835 1840 1845
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Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His 1865 1870 1875
Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln 1880 1885 1890
Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp 1895 1900 1905
Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn 1910 1915 1920
Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His 1925 1930 1935
Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met 1940 1945 1950
Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser 1955 1960 1965
Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr 1970 1975 1980
Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr 1985 1990 1995
Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly 2000 2005 2010
Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly 2015 2020 2025
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Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His 2060 2065 2070
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Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile 2150 2155 2160		
Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg 2165 2170 2175		
Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys 2180 2185 2190		
Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln 2195 2200 2205		
Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser 2210 2215 2220		
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Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
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Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
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Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
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Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
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Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
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Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser

210	215	220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser :		
225	230	235 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly		
	245	250 255
Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly		
	260	265 270
Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys		
	275	280 285
Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro		
	290	295 300
Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu		
305	310	315 320
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser		
	325	330 335
Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly		
	340	345 350
Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser		
	355	360 365
Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile		
	370	375 380
Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln		
385	390	395 400
Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro		
	405	410 415
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser		
	420	425 430
Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro		
	435	440 445
Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser		
	450	455 460

<210> 33

<211> 1475

<212> DNA

<213> Homo sapiens

<400> 33

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agcgccccga cctcgcacc atgagagccc tgotggcgcg cctgcttctc tgcgtcctgg
120

tctgtagcga ctccaaaggc agcaatgaac ttcatcaagt tccatcgaac tgtgactgtc
180

taaatggagg aacatgtgtg tccaacaagt acttctccaa cattcactgg tgcaactgcc
240

caaagaaatt cggagggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga
300

atggtcactt ttaccgagga aaggccagca ctgacaccat gggcggccc tgccctgcct
360

ggaactctgc cactgtcctt cagcaaact accatgccca cagatctgat gctcttcagc
420

tgggcctggg gaaacataat tactgcagga acccagacaa ccggagggcga cccctgggtgt
480

atgtgcagggt gggcctaaag ccgcttgtcc aagagtgcac ggtgcatgac tgcgcagatg
540

gaaaaaagcc ctctctctct ccagaagaat taaaatttca gtgtggccaa aagactctga
600

ggccccgctt taagattatt gggggagaat tcaccaccat cgagaaccag cccctggtttg
660

cggccatcta caggaggcac cgggggggct ctgtcaccta cgtgtgtgga ggcagcctca
720

tcagcccttg ctgggtgatc agcgccacac actgcttcat tgattacca aagaaggagg
780

actacatcgt ctacctgggt cgotcaaggc ttaactccaa cacgcaaggg gagatgaagt
840

ttgaggtgga aaacctcatc ctacacaagg actacagcgc tgacacgctt gctcaccaca
900

acgacattgc cttgctgaag atccgttcca aggagggcag gtgtgcgag ccatcccga
960

ctatacagac catctgcctg cctcogatgt ataacgatcc ccagtttggc acaagctgtg
1020

agatcactgg ctttggaata gagaattcta ccgactatct ctatccggag cagctgaaga
1080

tgactgttgt gaagctgatt tcccaccggg agtgtcagca gcccactac tacggctctg
1140

aagtcaccac caaatgctg tgtgtctgtg acccacagtg gaaaacagat tcctgccagg
1200

gagactcagg gggacccctc gtctgttccc tccaaggccg catgactttg actggaattg
1260

tgagctgggg ccgtggatgt gccctgaagg acaagccagg cgtctacacg agagtctcac
1320

acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgaggggt
1380

ccccagggag gaaacgggca ccaccgctt tcttgctggt tgtcattttt gcagtagagt
1440

catctccatc agctgtaaga agagactggg aagat
1475

<210> 34
<211> 431
<212> PRT
<213> Homo sapiens

<400> 34
Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1 5 10 15
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
20 25 30
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
35 40 45
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
50 55 60
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65 70 75 80
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
85 90 95
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
100 105 110
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
115 120 125
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
130 135 140
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
145 150 155 160
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
165 170 175
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
180 185 190
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
195 200 205
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
210 215 220
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
225 230 235 240
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
245 250 255
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His

260

265

270

His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
 275 280 285
 Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
 290 295 300
 Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
 305 310 315 320
 Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val
 325 330 335
 Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly
 340 345 350
 Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
 355 360 365
 Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
 370 375 380
 Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
 385 390 395 400
 Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
 405 410 415
 Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
 420 425 430

 <210> 35
 <211> 107
 <212> PRT
 <213> Mus musculus

 <400> 35
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
 20 25 30
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 36
 <211> 120

<212> PRT

<213> Mus musculus

<400> 36

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 37

<211> 120

<212> PRT

<213> Mus musculus

<400> 37

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 38

<211> 106

<212> PRT

<213> Mus musculus

<400> 38

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 39

<211> 1039

<212> DNA

<213> Homo sapiens

<400> 39

tcctgcacag gcagtgcctt gaagtgcctc ttcagagacc tttcttcata gactactttt
 60

ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag
 120

cattctcgtc atctctgagg^{*}acatcacat catotcagga tgaggggcat gaagctgctg
 180

ggggcgctgc tggcactggc ggccctactg cagggggcog tgtccctgaa gatcgcagcc
 240

ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt
 300

gtgcagatcc tgagccgcta tgacatcgcc ctgggtccagg aggtcagaga cagccacctg
 360

actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac
 420

gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg
 480

cctgaccagg tgtctgoggt ggacagctac tactacgatg atggctgcga gccctgcggg
 540

aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccgtt cacagaggto
 600

agggagtgtg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac
660

gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg
720

atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtgggc atccatccgc
780

ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca
840

cccacgcact gtgcctatga caggatcgtg gttgcagga tgctgctccg aggcgccgtt
900

gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg
960

gcccagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agccccctccc
1020

cacaccagtt gaactgcag
1039

<210> 40
<211> 282
<212> PRT
<213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu
1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
100 105 110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
145 150 155 160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val

165

170

175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
 180 185 190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
 195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
 210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
 225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
 245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
 260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys
 275 280

<210> 41
 <211> 678
 <212> DNA
 <213> Mus musculus

<400> 41
 gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt
 60

ttctcctgca gggccagtca gtctgttggc tcaagcatcc actggtatca gcaaagaaca
 120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatgtctgg gatcccttcc
 180

aggtttagtg gcagtggtac agggacagat ttactotta gcatcaaac tgtggagtct
 240

gaagatattg cagattatta ctgtcaacaa agtcatagct ggccattcac gtccggctcg
 300

gggacaaatt tggaagtaaa agaagtgaag cttgaggagt ctggaggagg cttggtgcaa
 360

cctggaggat ccatgaaact ctctgtgtt gcctctggat tcattttcag taaccactgg
 420

atgaactggg tccgccagtc tccagagaag gggcttgagt gggttgctga aattagatca
 480

aaatctatta attctgcaac acattatgcg gagtctgtga aaggagggtt caccatctca
 540

agagatgatt ccaaaagtgc tgtctacctg caaatgaccg acttaagaac tgaagacact
 600

ggcgtttatt actgttccag gaattactac ggtagtacct acgactactg gggccaaggg
 660

accactctca cagtctcc
678

<210> 42
<211> 226
<212> PRT
<213> Mus musculus

<400> 42
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
65 70 75 80
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
85 90 95
Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu
100 105 110
Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser
115 120 125
Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val
130 135 140
Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser
145 150 155 160
Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg
165 170 175
Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met
180 185 190
Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn
195 200 205
Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
210 215 220

Val Ser
225

<210> 43
<211> 450
<212> DNA
<213> Homo sapiens

<400> 43

gctgcatcag aagaggccat caagcacatc actgtccttc tgccatggcc ctgtggatgc
60

gcctcctgcc cctgtctggcg ctgtctggccc tctggggacc tgaccacagcc gcagcctttg
120

tgaaccaaca cctgtgcggc tcacacctgg tggaagctct ctacctagtg tgcggggaaac
180

gaggtcttctt ctacacaccc aagaccogcc gggaggcaga ggacctgcag gtggggcagg
240

tggagctggg cggggggccct ggtgcaggca gcctgcagcc cttggccctg gaggggtccc
300

tgcagaagcg tggcattgtg gaacaatgct gtaccagcat ctgtccctc taccagctgg
360

agaactactg caactagacg cagcccgagc gcagcccccc acccgccgcc tcttgcaccg
420

agagagatgg aataaagccc ttgaaccagc
450

<210> 44
<211> 110
<212> PRT
<213> Homo sapiens

<400> 44
Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1 5 10 15
Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
20 25 30
Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
35 40 45
Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
50 55 60
Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
65 70 75 80
Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
85 90 95
Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
100 105 110

<210> 45
<211> 1203
<212> DNA
<213> Hepatitis B virus

<400> 45
atgggaggtt ggtottocaa acctcgacaa ggcattggga cgaatctttc tgttcccaat
60

cctctgggat tctttccoga tcaccagttg gacctgcgt tcggagccaa ctcaaacaa
120

ccagattggg acttcaaccc caacaaggat cactggccag aggcaatcaa ggtaggagcg
180

ggagacttcg ggccagggtt caccacacca caggcggtc tttggggtg gagccctcag
240

gctcagggca tattgacaac agtgccagca gcgcctctc ctgtttccac caatcggcag
300

tcaggaagac agcctactcc catctctcca cctctaagag acagtcaccc tcaggccatg
360

cagtggaaact ccacaacatt ccaccaagct ctgctagatc ccagagttag gggcctatat
420

tttctgctg gtggctccag ttccggaaca gtaaaccctg ttccgactac tgtctcacc
480

atatogtcaa tcttctcgag gactggggac cctgcaccga acatggagag cacaacatca
540

ggattcctag gacctctgct cgtgttacag gcggggtttt tcttggtgac aagaatctc
600

acaataccac agagtctaga ctggtggtg acttctctca atttcttagg gggagcacc
660

acgtgtcctg gccaaaattc gcagtcccca acctccaatc actcaccaac ctcttgctc
720

ccaatttgc ctggttatcg ctggatgtgt ctggcggtt ttatcatatt cctcttcac
780

ctgctgctat gctcatctt cttgttggtt cttctggact accaaggat gtgcccgtt
840

tgtcctctac ttccaggaac atcaactacc agcacgggac catgcaagac ctgcacgatt
900

cctgctcaag gaacctctat gtttccctct tgttgctgta caaaccttc ggacggaaac
960

tgcacttgta ttcccatccc atcatctcg gctttcgcaa gattcctatg ggagtgggcc
1020

tcagtccgtt tctctggct cagtttacta gtgccatttg ttcagtgggt cgcagggtt
1080

tccccactg tttggctttc agttatatgg atgatgtggt attgggggcc aagtctgtac
1140

aacatcttga gtccctttt acctctatta ccaattttct tttgtctttg ggtatacatt
1200

tga
1203

<210> 46

<211> 400
 <212> PRT
 <213> Hepatitis B virus

<400> 46

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45

Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly
 50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
 65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser
 85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
 100 105 110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
 115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
 130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
 145 150 155 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
 165 170 175

Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
 180 185 190

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 195 200 205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
 225 230 235 240

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
 245 250 255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
 260 265 270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
 275 280 285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
 290 295 300

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
305 310 315 320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
325 330 335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
340 345 350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val
355 360 365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
370 375 380

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
385 390 395 400

<210> 47
<211> 799
<212> DNA
<213> Homo sapiens

<400> 47
cgaaccactc agggctcctgt ggacagctca cctagctgca atggctacag gctcccggac
60

gtccctgctc ctggcttttg gctgctctg cctgccctgg cttcaagagg gcagtgcctt
120

cccaaccatt cccttatcca ggccttttga caacgctatg ctccggcgccc atcgtctgca
180

ccagctggcc tttgacacct accaggagtt tgaagaagcc tatatcccaa aggaacagaa
240

gtattcattc ctgcagaacc cccagacctc cctctgtttc tcagagtcta ttccgacacc
300

ctccaacagg gaggaaacac aacagaaatc caacctagag ctgctccgca tctccctgct
360

gctcatccag tcgtggctgg agcccgtgca gttcctcagg agtgtcttcg ccaacagcct
420

ggtgtacggc gcctctgaca gcaacgtcta tgacctccta aaggacctag aggaaggcat
480

ccaaacgctg atggggaggc tggaagatgg cagcccccg actgggcaga tcttcaagca
540

gacctacagc aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg
600

gctgctctac tgcttcagga aggacatgga caaggctgag acattcctgc gcctogtgca
660

gtgccgtctt gtggagggca gctgtggctt ctagctgcc gggtggcatc cctgtgaccc
720

ctccccagtg cctctcctgg ccttggaagt tgccactcca gtgcccacca gccctgtcct
780

aataaaatta agttgcac
799

<210> 48
<211> 217
<212> PRT
<213> Homo sapiens

<400> 48
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15
Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
20 25 30
Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
35 40 45
Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
50 55 60
Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65 70 75 80
Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
85 90 95
Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
100 105 110
Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val
115 120 125
Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
130 135 140
Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
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Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
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His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
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<400> 49

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 Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro
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 Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
 65 70 75 80
 Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
 85 90 95
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
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 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 115 120 125
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 130 135 140
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 145 150 155 160
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
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 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
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 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
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 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 225 230 235 240
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
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 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 260 265 270
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
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 <211> 107
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 <213> Homo sapiens

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Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
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Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
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Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
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Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
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Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
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<210> 52

<211> 107

<212> PRT

<213> Mus musculus

<400> 52

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Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
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Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
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Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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<210> 53

<211> 119

<212> PRT

<213> Homo sapiens

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Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
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Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
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Thr Leu Val Thr Val Ser Ser
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<210> 54
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 <212> PRT
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<400> 54
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Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
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Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly
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Thr Leu Val Thr Val Ser Ala
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<210> 55
 <211> 214
 <212> PRT
 <213> Homo sapiens

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Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
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Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

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45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
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<210> 56
<211> 448
<212> PRT
<213> Homo sapiens

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Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
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 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
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 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190
 Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205
 Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220
 Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 225 230 235 240
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350
 Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
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720

gagctcactg ttctggtgct ggttaacacc atttacttca agggcctgtg gaagtcaaag
780

ttcagccctg agaacacaag gaaggaactg ttctacaagg ctgatggaga gtcgtgttca
840

gcattctatga tgtaccagga aggcaagttc cgttatcggc gcgtggctga aggcaccag
900

gtgcttgagt tgcccttcaa aggtgatgac atcaccatgg tctcatctt gcccaagcct
960

gagaagagcc tggccaaggt ggagaaggaa ctcacccag aggtgctgca ggagtggctg
1020

gatgaattgg aggagatgat gctggtggtc cacatgccc gcttccgcat tgaggacggc
1080

ttcagtttga aggagcagct gcaagacatg ggccttgctg atctgttcag ccctgaaaag
1140

tccaaactcc caggtattgt tgcagaaggc cgagatgacc tctatgtctc agatgcattc
1200

cataaggcat ttcttgaggt aaatgaagaa ggcagtgaag cagctgcaag taccgctgtt
1260

gtgattgctg gccgttcgct aaaccccaac agggtgactt tcaaggccaa caggcctttc
1320

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1380

ccttggtgta agtaa
1395

<210> 64
<211> 464
<212> PRT
<213> Homo sapiens

<400> 64
Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val
1 5 10 15

Tyr Leu Leu Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys
20 25 30

His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
35 40 45

Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
50 55 60

Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
65 70 75 80

Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
85 90 95

His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
100 105 110

Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
115 120 125

Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
130 135 140

Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
145 150 155 160

Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
165 170 175

Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
180 185 190

Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
 195 200 205
 Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
 210 215 220
 Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
 225 230 235 240
 Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
 245 250 255
 Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
 260 265 270
 Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
 275 280 285
 Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
 290 295 300
 Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
 305 310 315 320
 Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
 325 330 335
 Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
 340 345 350
 Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
 355 360 365
 Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
 370 375 380
 Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
 385 390 395 400
 His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
 405 410 415
 Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val
 420 425 430
 Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
 435 440 445
 Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 450 455 460
 <210> 65
 <211> 1962
 <212> DNA
 <213> Homo sapiens
 <400> 65
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120

tggccctgc ggcgttctg gaggagcaca ggcttctgcc ccccgctgcc acacagccag
180

gctgaccagt acgtcctcag ctgggaccag cagctcaacc tcgcctatgt ggggcgcgtc
240

cctcaccgog gcatcaagca ggtccggacc cactggctgc tggagcttgt caccaccagg
300

gggtccactg gacggggcct gagctacaac ttcaccacc tggacgggta cttggacctt
360

ctcagggaga accagctcct ccaggggttt gagctgatgg gcagcgcctc gggccacttc
420

actgactttg aggacaagca gcaggtgttt gagtgggaagg acttgggtctc cagcctggcc
480

aggagataca tcggtaggta cggactggcg catgtttoca agtggaactt cgagacgtgg
540

aatgagccag accaccacga ctttgacaac gtctccatga ccatgcaagg cttcctgaac
600

tactacgatg cctgctcgga gggctctgcg gcgcgcagcc ccgccctgcg gctgggaggg
660

ccggcgact ccttccacac cccaccgga tccccgctga gctggggcct cctgcgcac
720

tgccacgacg gtaccaactt cttoactggg gaggcggcg tgcggctgga ctacatctcc
780

ctccacagga agggtgogcg cagctccatc tccatcctgg agcaggagaa ggtcgtcgcg
840

cagcagatcc ggcagctott cccaagttc gcggacacc ccatttaca cgacgagggc
900

gacccgctgg tgggctggtc cctgccacag ccgtggaggg cggacgtgac ctacgcggcc
960

atggtggtga aggtcatgc gcagcatcag aacctgctac tggccaacac cacctccgcc
1020

ttccctacg cgtcctgag caacgacaat gccttctga gctaccacc gcaccccttc
1080

gogcagcgca cgctcaccgc gcgcttcag gtcaacaaca cccgcccgc gcacgtgcag
1140

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1200

ctctgggccc aagtgtcgca ggccgggacc gtctggaca gcaaccacac ggtgggcgtc
1260

ctggccagcg cccaccgccc ccagggcccg gccgacgcct ggcgcgccgc ggtgctgac
1320

tacgcgagcg acgacacccg cgcccacccc aaccgcagcg tcgcggtgac cctgcggctg
1380

cgcggggtgc cccccggccc gggcctggtc tacgtcacgc gctacctgga caacgggctc
1440

tgcagccccc acggcgagtg gcggcgcccg ggccggcccg tcttccccac.ggcagagcag
1500

ttccggcgca tgcgcgcggc tgaggacccg gtggccgcgg cgccccgccc cttaaccgcc
1560

ggcgcccgcc tgacctgcg ccccgcgctg cggctgccgt cgcttttgcg ggtgcacgtg
1620

tgtgcgcgcc ccgagaagcc gcccgggcag gtcacgcggc tcgcgcacct gccctgacc
1680

caagggcagc tggttctggt ctggctggat gaacacgtgg gctccaagt cctgtggaca
1740

tacgagatcc agttctctca ggacggtaag ggtacacccc cggtcagcag gaagccatcg
1800

accttcaacc tctttgtgtt cagcccagac acaggtgctg totctggctc ctaccgagtt
1860

cgagccctgg actactgggc ccgaccaggc cccttctcgg accctgtgcc gtacctggag
1920

gtccctgtgc caagagggcc cccatccccg ggcaatccat ga
1962

<210> 66
<211> 653
<212> PRT
<213> Homo sapiens

<400> 66
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
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Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
20 25 30

Gln Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
35 40 45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
50 55 60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65 70 75 80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
85 90 95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr

	100	105	110
His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro	115	120	125
Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu	130	135	140
Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala	145	150	155
Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn	165	170	175
Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser	180	185	190
Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly	195	200	205
Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser	210	215	220
Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His	225	230	235
Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu	245	250	255
Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile	260	265	270
Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro	275	280	285
Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val	290	295	300
Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala	305	310	315
Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn	325	330	335
Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe	340	345	350
Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg	355	360	365
Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys	370	375	380
Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln	385	390	395
Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His	405	410	415
Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp	420	425	430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
 435 440 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
 450 455 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
 465 470 475 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
 485 490 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
 500 505 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
 515 520 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
 530 535 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
 545 550 555 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
 565 570 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
 580 585 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
 595 600 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
 610 615 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
 625 630 635 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
 645 650

<210> 67

<211> 1290

<212> DNA

<213> Homo sapiens

<400> 67

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 120

accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca
 180

gattcctgca tcagtgagaa gctcttcattg gagatggcag agctcatggt ctcagaaggg
 240

tggaaggatg cagggttatga gtacctctgc attgatgact gttggatggc tccccaaaga
300

gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat tgcgcagcta
360

gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa
420

acctgogcag gcttccctgg gagtttttga tactacgaca ttgatgccca gacctttgct
480

gactggggag tagatctgct aaaatttgat ggttggtact gtgacagttt ggaaaatttg
540

gcagatgggt. ataagcacat gtccttggcc ctgaatagga ctggcagaag catttgttac
600

tcctgtgagt ggctcttcta tatgtggccc ttcaaaagc ccaattatac agaaatccga
660

cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag
720

agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg
780

ggttggaatg acccagatat gttagtgatt ggcaactttg gcctcagctg gaatcagcaa
840

gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc
900

cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat
960

caggacccct tgggcaagca agggtagcag cttagacagg gagacaactt tgaagtgtgg
1020

gaacgacctc tctcaggctt agcctgggct gtagctatga taaaccggca ggagattggt
1080

ggacctcgct cttataccat cgcagttgct tccctgggta aaggagtggc ctgtaatcct
1140

gcctgcttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaatggact
1200

tcaagggttaa gaagtcacat aaatcccaca ggcactgttt tgcttcagct agaaaataca
1260

atgcagatgt cattaaaaga cttactttta
1290

<210> 68

<211> 429

<212> PRT

<213> Homo sapiens

<400> 68

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu

91

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
 370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
 405 410 415

Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu
 420 425

<210> 69
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 69
 atggattact acagaaaata tgcagctatc tttctgggtca cattgtcggg gtttctgcat
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gtttctccatt ccgctcctga tgtgcaggat tgcccagaat gcacgctaca ggaaaaccca
 120

tttttctccc agccgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca
 180

tatcccactc cactaagggtc caagaagacg atgttgggtcc aaaagaacgt cacctcagag
 240

tccacttgct gtgtagctaa atcatataac agggtcacag taatggggggg tttcaaagtg
 300

gagaaccaca cggcgtgccca ctgcagtact tgttattatc acaaattctta a
 351

<210> 70
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 70
 Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
 1 5 10 15

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
 20 25 30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
 35 40 45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
 50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
100 105 110

Tyr His Lys Ser
115

<210> 71
<211> 498
<212> DNA
<213> Homo sapiens

<400> 71
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60

tccaaggagc cgcttcggcc acggtgccgc cccatcaatg ccacctggc tgtggagaag
120

gagggctgcc ccgtgtgcat caccgtcaac accaccatct gtgcgggcta ctgccccacc
180

atgaccgcg tgctgcagg ggtcctgccg gccctgcctc aggtgggtgtg caactaccgc
240

gatgtgcgt tgcagtcacat ccggctccct ggctgcccgc gcggcgtgaa ccccggtgtc
300

tcctacgccg tggtctcag ctgtcaatgt gcaactctgcc gccgcagcac cactgactgc
360

gggggtccca aggaccaccc cttgacctgt gatgaccccc gcttccagga ctctcttcc
420

tcaaaggccc ctccccccag ccttccaagc ccatcccgc tcccggggcc ctcgacacc
480

ccgatacctcc cacaataa
498

<210> 72
<211> 165
<212> PRT
<213> Homo sapiens

<400> 72
Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly
1 5 10 15

Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile
20 25 30

Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr
35 40 45

Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val

50

55

60

Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg
65 70 75 80

Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val
85 90 95

Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu
100 105 110

Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu
115 120 125

Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro
130 135 140

Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
145 150 155 160

Pro Ile Leu Pro Gln
165

<210> 73

<211> 165

<212> PRT

<213> Homo sapiens

<400> 73

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
1 5 10 15

Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
20 25 30

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
35 40 45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
50 55 60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65 70 75 80

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
85 90 95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
100 105 110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
115 120 125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
130 135 140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145 150 155 160

Cys Arg Thr Gly Asp
165

<210> 74
 <211> 588
 <212> DNA
 <213> Homo sapiens

<400> 74
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 120
 ctgcacaaa tgaggagaat ctcccctttc ttgtgtctca aggacagaag agacttcagg
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 240
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 aacatgaccc tcctagacca actccacact ggacttcacg agcaactgca acacctggag
 360
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 420
 ctgaccttga ggaggtactt ccagggaatc cgtgtctacc tgaaagagaa gaaatacagc
 480
 gactgtgcct gggaagtgtt cagaatggaa atcatgaaat ccttggttctt atcaacaaac
 540
 atgcaagaaa gactgagaag taaagataga gacctgggct catcttga
 588

<210> 75
 <211> 195
 <212> PRT
 <213> Homo sapiens

<400> 75
 Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
 1 5 10 15
 Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
 20 25 30
 Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
 35 40 45
 Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
 50 55 60
 Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
 65 70 75 80
 His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
 85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
 100 105 110
 His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
 115 120 125
 Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
 130 135 140
 Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
 145 150 155 160
 Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
 165 170 175
 Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
 180 185 190
 Gly Ser Ser
 195

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